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LIGAND BINDING AND SIGNAL TRANSDUCTION OF VERTEBRATE SOMATOSTATIN RECEPTORS RECOMBINANTLY EXPRESSED IN CCL39 CELLS

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Abbreviations

A. albifrons	Apteronotus albifrons (gymnotiform fish)
AC	adenylate cyclase
ADP	adenosine-5`-diphosphate
AIDS	aquired immunodeficiency syndrome
ATP	adenosine-5`-triphosphate
B _{max}	receptor density
bp	basepairs
BSA	bovine serum albumin
$[Ca^{2+}]_i$	intracellular calcium concentration
cAMP	cyclic adenosine monophosphate
CCL39 cells	Chinese hamster lung fibroblast cells
cDNA	copy DNA
°C	Celcius degree(s)
cGMP	cyclic guanosine monophosphate
CHO cells	Chinese hamster ovary cells
Ci	$Curie = 3.7 \times 10^{10} Bequerel (Bq)$
CMV	Cytomegalie virus (promotor)
CNS	central nervous system
COS cells	CV1 Origin SV40 cells (derived from monkey kidney)
cpm	counts per minute
CST	cortistatin
DAG	1,2-diacylglycerol
dATP	desoxy ATP
dCTP	desoxy cytosine-5`-triphosphate
DEAE	diethylaminoethyl-dextran
dGTP	desoxy GTP
DMSO	dimethyl sulfoxide
DNA	desoxyribonucleic acid

dpm	decreases per minute
DTT	dithiothreitol
dTTP	desoxy thymidine-5`-triphosphate
EC_{50}	concentration of half-maximal effect
EDTA	ethylene diaminetetraacetic acid
e.g.	for example
E _{max}	maximal effect
FBS	foetal bovine serum
f.c.	final concentration
FLIPR	Fluorometric Imaging Plate Reader
FSAC	forskolin-stimulated adenylate cyclase activity
$fsst_3$	fish somatostatin receptor subtype 3
g	acceleration due to gravity
G418	geneticin sulphate
GDP	guanosine-5'-diphosphate
GEP	gastroenteropancreatic
GppNHp	5`-guanylyl-imidodiphosphate
G-protein, G	guanyl-nucleotide binding protein
GTP	guanosine-5`-triphosphate
GTPγS	guanosine-5'-O-3'-thio-triphosphate
h	hour(s)
HBS	HEPES-buffered saline
HBSS	Hank's balanced salt solution
HEK293 cells	human embryonic kidney cells
HEPES	N-[2-Hydroxyethyl]piperazine-N`[2-ethanesulfonic acid]
hsst ₁₋₅	human somatostatin receptor subtypes 1-5
5-HT	5-hydroxytryptamin, serotonin
Hz	Hertz
icv	intracerebroventral
IP ₁	inositol monophosphate
IP_2	inositol diphosphate
IP ₃	inositol triphosphate

IP _x	inositol x-phosphate
kb	kilo basepairs
K _d	equilbrium dissociation constant
М	mol/l
МАРК	mitogen-activated protein kinase
MBq	Mega-Bequerel
MEM	minimal essential medium
μF	μ-Farad
min	minute(s)
mJ	m-Joule
mM	mmol/l
μΜ	μmol/l
mol wt	molecular weight
MOPS	3-[N-morpholino]-propanesulphonic acid
mRNA	messenger RNA
NK	neurokinin
nM	nmol/l
Р	probability
PACAP	pituitary adenylate cyclase activating polypeptide
PBS	phosphate-buffered saline
PCR	polymerase chain reaction
pEC ₅₀	potency, negative logarithm of the EC_{50}
P _i	inorganic phosphate (PO ₃ ²⁻)
рК _в	potency of an antagonist
pK _d	negative logarithm of the equilibrium dissociation constant
PLC	phospholipase C
pМ	pmol/ l
PTX	pertussis toxin
r	correlation coefficient
RGS	regulators of G-protein signalling
RNA	ribonucleic acid
RSV	Rous Sarcoma virus (promotor)

RT	reverse transcriptase
S	second(s)
SDS	sodium dodecyl sulphate
SEM	standard error of the mean
SPA	scintillation proximity assay
SRIF	somatotropin-release-inhibiting factor = somatostatin
SSC	standard saline citrate
sst ₁₋₅	somatostatin receptor subtypes 1-5
TM	transmembrane domain
Tris	tris(hydroxymethyl)-aminomethane
UV	ultravilolett
V	Volt
WGA	wheatgerm agglutinin

amino acids

Ala	А	alanine	Leu	L	leucine
Arg	R	arginine	Lys	K	lysine
Asn	Ν	asparagine	Met	Μ	methionine
Asp	D	aspartic acid	Phe	F	phenylalanine
Cys	С	cysteine	Pro	Р	proline
Glu	Е	glutamic acid	Ser	S	serine
Gln	Q	glutamine	Thr	Т	threonine
Gly	G	glycine	Trp	W	tryptophan
His	Н	histidine	Tyr	Υ	tyrosine
Ile	I	isoleucine	Val	V	valine

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Summary

Somatostatin (SRIF = somatotropin release inhibiting factor) is a hormone/ neuropeptide with multiple endocrine and exocrine effects, effects on inhibition of hormone release, cognitive functions, behaviour, sleep activity and inhibition of tumour growth. The SRIF analogue octreotide is used to treat acromegaly, hormone-secreting tumours, and AIDS-related diarrhoea. In mammals, the SRIF family includes SRIF₁₄, SRIF₂₈, and the recently identified and putative neuropeptide cortistatin (CST); nonmammalian vertebrates posses SRIF₁₄ and a second SRIF variant.

A class of G-protein-coupled receptors, the somatostatin receptors, mediate the actions of SRIF, and five mammalian subtypes (sst_{1-5}) have been cloned; SRIF receptors are specifically expressed in brain, periphery, and many tumours. The third cytoplasmatic loop of G-protein-coupled receptors is suggested to link the receptors to G-proteins, which couple the receptors to specific intracellular signalling cascades. Many cellular effector proteins such as phospholipase C (PLC), phospholipase A₂, calcium channels, potassium channels, Na⁺/H⁺ exchanger, adenylate cyclase (AC), protein tyrosine phosphatases, mitogen-activated protein kinase (MAPK) or p53 are reported to be specifically modulated by SRIF receptor subtypes.

In this study, the five human SRIF receptor subtypes, and the first cloned nonmammalian SRIF receptor, fish sst₃ receptor (of *Apteronotus albifrons*), were characterised by analysing their binding and transductional features under the same environment, i.e. by stable receptor expression in CCL39 hamster lung fibroblast cells.

 $CST_{14/17}$ and the iodinated analogue $[^{125}I][Tyr^{10}]CST_{14}$, bound with similar high affinity to all five human SRIF receptors, and thus the pharmacological profiles of the iodinated peptide was established with a number of SRIF/ CST analogues; the affinity profiles were comparable to those established using $[^{125}I]LTT$ -SRIF₂₈. This underlines the close relation of CST and SRIF peptides, although specific CST receptors may also exist.

Very marked differences in peptide affinities for SRIF receptors have been described in the literature; therefore additional synthetic radioligands ($[^{125}I]CGP$ 23996, $[^{125}I][Tyr^3]$ octreotide) were used to establish affinity profiles. Surprisingly, $[^{125}I][Tyr^3]$ octreotide labelled beside human sst₂ also sst₅ receptor sites with high affinity, and some other classically sst₂ –selective compounds (octreotide, seglitide etc.) showed high affinity to sst₅ receptors; hence, sst₅ receptors may mediate physiological effects of octreotide, which previously were attributed to the sst₂ subtype solely.

Ligand affinities and receptor densities were radioligand-dependent at human sst₅, but not at sst_{1.4} receptors: e.g. [¹²⁵I]LTT-SRIF₂₈ labelled seven times more sst₅ receptor sites than [¹²⁵I][Tyr³]octreotide, and the affinity of e.g. octreotide defined with [¹²⁵I]LTT-SRIF₂₈ was 100-fold lower compared to that defined with [¹²⁵I][Tyr³]octreotide.

Although the non-iodinated analogues of the four radioligands are full agonists in functional studies, their binding to sst_5 receptors was differently modulated by the GTP-analogue guanylylimidodiphosphate (GppNHp): e.g. $[^{125}I][Tyr^3]$ octreotide binding was highly affected suggesting selective labelling of G-protein-coupled sst_5 receptors, whereas $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I][Tyr^{10}]CST_{14}$ seem to label rather uncoupled receptors and hence a higher density; radioligand binding at sst_2/sst_3 receptors was markedly inhibited, and rather unaffected at sst_1/sst_4 receptors.

The data do not fit the ternary complex model, instead the existence of multiple G-protein-coupled/-uncoupled agonist-specific receptor states may be proposed.

In functional studies, all five SRIF receptors inhibited forskolin-stimulated adenylate cyclase (FSAC) activity, hsst₂₋₅ receptors stimulated [35 S]GTP γ S binding (G-protein activation), and sst₃/ sst₅ activated PLC activity (measured by IP_x accumulation, intracellular Ca²⁺ increase), the latter effect being only partially pertussis toxin (PTX) sensitive (i.e. partly mediated by G_{i/o}).

Pharmacological profiles of human SRIF receptors established in these three functional assays correlated significantly, but to various extents even at the same receptor with the different radioligand binding profiles; functional data of sst_1/sst_2 receptors correlated only modestly with the affinity profiles suggesting other effector pathways to be more important. In addition, the potency rank orders of SRIF/ CST ligands examined at each human SRIF receptor subtype was distinct from one functional assay to the other, and compared to the affinity profiles. These findings support the hypothesis of receptor induced effector trafficking by presumably different agonist-specific receptor states.

In the brain, fish sst₃ receptor transcripts, as detected by RT-PCR, and fish sst₃ protein seem to be present, since the profile of fsst₃ receptors expressed in CCL39 cells correlated highly with that of native brain receptors [¹²⁵I]LTT-SRIF₂₈ binding; however, biphasic curves in brain and low correlation with liver sites suggest additional fish SRIF receptors. At recombinant fsst₃ receptors radioligand-dependency of receptor densities, affinities, and GppNHp-sensitivity was documented using [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide, similar to the human sst₅ receptor. Coupling to signalling pathways seems to be highly conserved between fish and mammalian SRIF receptors: fsst₃ receptors mediate stimulation of [³⁵S]GTPγS binding, inhibition of FSAC via G_i/G_o, and PLC activation partly via G_i/G_o. Pharmacological profiles of radioligand binding and functional tests correlated with each other with variations, supporting again a model of specific agonist-induced receptor conformations; species differences on pharmacology: fsst₃ profiles fitted best with the hsst₅ receptor profiles, in spite of the highest sequence homology with the hsst₃ subtype.

Keywords: somatostatin (SRIF), cortistatin (CST), octreotide, human recombinant somatostatin receptors (hsst₁₋₅), fish somatostatin receptor 3; (fsst₃), CCL39 Chinese hamster lung fibroblast cells, guanylylimidodiphosphate (GppNHp), guanosine-5'O-(3-thio)-triphosphate (GTP γ S), adenylate cyclase (AC), phospholipase C (PLC), inositol phosphate (IP_x), intracellular calcium, pertussis toxin (PTX).

Kurzfassung

Somatostatin (SRIF = Somatotropin-Freisetzung-inhibierender Faktor) ist ein Hormon/ Neuropeptid mit zahlreichen endokrinen und exokrinen Wirkungen, Wirkungen auf Inhibition von Hormon-Freisetzungen, kognitive Funktionen, Verhalten, Schlafaktivität, und auf Hemmung von Tumorwachstum. Das SRIF-Analog Octreotide wird zur Behandlung von Akromegalie, Hormon-sekretierenden Tumoren, und von AIDSabhängiger Diarrhoea verwendet. Bei Säugern umfasst die SRIF-Familie SRIF₁₄, SRIF₂₈, sowie das kürzlich identifizierte und vermutlich existente Neuropeptid Cortistatin (CST); Wirbeltiere, die nicht der Klasse der Säuger angehören, besitzen SRIF₁₄ und eine zweite SRIF-Variante.

Eine Klasse von G-Protein-gekoppelten Rezeptoren, die Somatostatin-Rezeptoren, vermitteln die Wirkungen von SRIF, und fünf Subtypen (sst₁₋₅) sind bei Säugern kloniert worden; SRIF-Rezeptoren sind im Gehirn, in der Peripherie, und in vielen Tumoren spezifisch exprimiert. Die dritte cytoplasmatische Schleife von G-Protein-gekoppelten Rezeptoren verbindet vermutlich die Rezeptoren mit G-Proteinen, welche die Rezeptoren an spezifische intrazelluläre Signalkaskaden koppeln. Es wird berichtet, dass viele zelluläre Effektorproteine, wie z. B. Phospholipase C (PLC), Phospholipase A₂, Calciumkanäle, Kaliumkanäle, Na⁺/H⁺-Austauschpumpen, Adenylat-Cyclase (AC), Proteintyrosin-Phosphatasen, Mitogen-aktivierte Proteinkinase (MAPK) oder p53 von SRIF-Rezeptorsubtypen spezifisch moduliert werden.

In dieser Studie wurden die fünf humanen SRIF-Rezeptorsubtypen, und der erste von einem Nichtsäuger klonierte SRIF-Rezeptor, der Fish sst₃ Rezeptor (von *Apteronotus albifrons*), durch Analyse von Bindungs- und Transduktionseigenschaften im gleichen System charakterisiert, d. h. durch stabile Rezeptorexpression in CCL39 Hamster-Lungenfibroblastenzellen.

 $CST_{14/17}$ und das iodierte Analog [¹²⁵I][Tyr¹⁰]CST₁₄, banden mit ähnlich hoher Affinität an alle fünf menschlichen SRIF-Rezeptoren, und somit wurden die pharmakologischen Profile des iodierten Peptids mit einer Anzahl an SRIF/ CST Analogas erstellt; die Affinitätsprofile waren vergleichbar mit den unter Verwendung von [¹²⁵I]LTT-SRIF₂₈ erstellten Profilen. Dies unterstreicht die enge Verwandtschaft von CST- und SRIF-Peptiden, obgleich auch spezifische CST-Rezeptoren existieren könnten.

Für SRIF-Rezeptoren wurden grosse Unterschiede von Peptidaffinitäten in der Literatur beschrieben; deshalb wurden zusätzliche, synthetische Radioliganden ($[^{125}I]CGP$ 23996, $[^{125}I][Tyr^3]Octreotide)$ verwendet, um Affinitätsprofile zu erstellen. Überaschenderweise markierte $[^{125}I][Tyr^3]Octreotide neben humanen sst_2 auch humane$ $sst_5 Rezeptorstellen mit hoher Affinität, und einige andere klassisch sst_2-selektiven$ $Verbindungen (Octreotide, Seglitide etc.) zeigten hohe Affinität für sst_5 Rezeptoren;$ $folglich vermitteln sst_5 Rezeptoren möglicherweise physiologische Wirkungen von$ $Octreotide, welche zuvor einzig dem sst_2-Subtyp zugeordnet wurden.$

Ligandenaffinitäten und Rezeptordichte waren bei menschlichen sst₅ Rezeptoren Radioliganden-abhängig, nicht aber bei sst₁₋₄ Rezeptoren: z. B. markierte [¹²⁵I]LTT-SRIF₂₈ siebenmal mehr sst₅ Rezeptorstellen als [¹²⁵I][Tyr³]Octreotide, und die von z. B. Octreotide ermittelte Affinität war mit [¹²⁵I]LTT-SRIF₂₈ 100-mal niedriger als mit [¹²⁵I][Tyr³]Octreotide.

Obwohl die nicht-iodierten Analoga der vier Radioliganden in funktionellen Studien volle Agonisten sind, war deren Bindung an sst₅ Rezeptoren durch das GTP-Analog Guanylylimidodiphosphat (GppNHp) unterschiedlich moduliert: die Bindung von z. B. [¹²⁵I][Tyr³]Octreotide war stark inhibiert, was auf ein selektives Markieren von G-Protein-gekoppelten sst₅ Rezeptoren hinweist, während [¹²⁵I]LTT-SRIF₂₈ und [¹²⁵I][Tyr¹⁰]CST₁₄ eher ungekoppelte Rezeptoren und daher eine höhere Dichte zu markieren scheinen; die Radioligandenbindung von sst₂/ sst₃ Rezeptoren war deutlich inhibiert, und eher unbeinträchtigt bei sst₁/ sst₄ Rezeptoren. Diese Daten passen nicht in das ternäre Komplex-Modell, stattdessen kann die Existenz von multiplen G-Protein-gekoppelten/-ungekoppelten Agonist-spezifischen Rezeptorzuständen vermutet werden.

In funktionellen Studien inhibierten alle fünf SRIF-Rezeptoren Forskolin-stimulierte Adenylat-Cyclase (FSAC)-Aktivität, hsst₂₋₅ Rezeptoren stimulierten [³⁵S]GTP γ S-Bindung (G-Protein-Aktivierung), und sst₃/ sst₅ Rezeptoren aktivierten PLC-Aktivität (gemessen durch IP_x-Akkumulation, intrazellulären Ca²⁺-Anstieg), wobei der letztere Effekt nur teilweise Pertussis-Toxin (PTX)-sensitiv (d. h. nur teils durch G_{i/o} vermittelt) war.

Die in diesen drei funktionellen Versuchsmethoden an menschlichen SRIF-Rezeptoren erstellten pharmakologischen Profile korrelierten signifikant, aber selbst am gleichen Rezeptor zu einem unterschiedlichem Grad mit den verschiedenen Radioliganden-Bindungsprofilen; funktionelle Daten von sst₁/ sst₂ Rezeptoren korrelierten nur mässig mit den Affinitätsprofilen, was darauf hinweist, dass andere Effektor-Signalwege bedeutsamer sind. Ausserdem war bei jedem SRIF-Rezeptorsubtypen die untersuchten Reihenfolgen der Potenzen von SRIF/ CST- Liganden von einem funktionellen Assay zum anderen verschieden, sowie verglichen zu den Affinitätsprofilen. Diese Ergebnisse unterstützen die Hypothese von Rezeptor-induziertem Effektor-"Trafficking" durch vermutlich verschiedene Agonist-spezifische Rezeptorzustände.

Im Gehirn scheinen Fisch sst3 Rezeptor-Transkripte, welche durch RT-PCR nachgewiesen wurden, und Fisch sst₃ Protein vorhanden zu sein, da das [¹²⁵I]LTT-SRIF₂₈-Bindungsprofil von in CCL39-Zellen exprimierten fsst₃ Rezeptoren stark mit dem von natürlich vorkommenden Gehirnrezeptoren korreliert; jedoch lassen biphasische Kurven im Gehirn und die schwache Korrelation mit Leber-Bindungsstellen zusätzliche Fisch-SRIF-Rezeptoren vermuten. Beim rekombinanten fsst₃ Rezeptor wurde unter Verwendung von [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, und [¹²⁵I][Tyr³]Octreotide Radioliganden-Abhängigkeit der Rezeptordichte, der Affinitäten, und der GppNHp-Sensitivität gemessen - ähnlich wie beim menschlichen sst5 Rezeptor. Das Koppeln an Signalwege scheint bei Fisch- und Säuger-SRIF-Rezeptoren hoch konserviert zu sein: Fisch sst₃ Rezeptoren vermitteln Stimulation von $[^{35}S]$ GTP γ S-Bindung, Inhibition von FSAC über G_i/G_0 , und PLCüber G_i/G_o . Die pharmakologischen Aktivierung teilweise Profile von Radioligandenbindung und funktionellen Tests korrelierten unterschiedlich stark was erneut das Modell der spezifischen Agonist-induzierten miteinander, Rezeptorkonformationen unterstützt; pharmakologische Arten-Unterschiede: die fsst3 Profile stimmten am besten mit den hsst, Profilen überein, trotz der grössten Sequenzhomologie mit dem hsst₃ Subtyp.

Stichworte: Somatostatin (SRIF), Cortistatin (CST), Octreotide, menschliche rekombinante Somatostatin-Rezeptoren (hsst₁₋₅), Fisch-Somatostatin-Rezeptor 3; (fsst₃), CCL39 Hamster-Lungenfibroblastenzellen, Guanylylimidodiphosphat (GppNHp), Guanosine-5'O-(3-thio)-Triphosphat (GTP γ S), Adenylat-Cyclase (AC), Phospholipase C (PLC), Inositolphosphat (IP_x), intrazelluläres Calcium, Pertussis-Toxin (PTX).

Chapter 1

Introduction

1.1. The Somatostatin peptide family

1.1.1. Mammalian somatostatin peptides

In mammals, the two physiologically active forms of somatostatin are the tetradecapeptide SRIF₁₄ (SRIF = somatotropin release inhibiting factor) (Brazeau et al., 1973), which was originally discovered from bovine hypothalamic extracts and found to inhibit somatotropin secretion (Krulich et al., 1968), and the N-terminally extended SRIF₂₈, which was originally isolated from porcine duodenum (figure 1) (Pradayrol et al., 1980). The "cyclic" peptides SRIF₁₄ and SRIF₂₈ are the products of a common gene, and they are released from their prepropeptide by enzymatic processing; other cleavage products of the precursor molecule reveal no biological activity (figure 2) (Patel et al., 1985; Robbins and Reichlin, 1983; Shen et al., 1982; Zingg and Patel, 1982).

The more recently cloned cortistatin (CST) is the (putative) product of a second gene, and the corresponding preprocortistatin shows especially in the carboxy terminus high structural similarity to preprosomatostatin; therefore, it may be proteolysed at analogous endonuclease restriction sites to CST_{14} in rodents, and to CST_{17} in human (figure 2) (De Lecea et al., 1996; 1997b; Fukusumi et al., 1997). The primary sequence of CST is very similar to that of mature SRIF: e.g. CST_{14} shares 11 of 14 amino acid residues with SRIF₁₄ (figure 1) (De Lecea et al., 1996).

The neuropeptide SRIF is widely expressed in the mammalian organism both in the central nervous system (CNS), and also in peripheral tissues: SRIF transcripts were found in the submandibular glands, in the thyroid, in gut, pancreas, kidney, adrenals, prostate, and in placenta (Aguila et al., 1991; Finley et al., 1981; Johansson et al., 1984; Reichlin, 1983; Vincent et al., 1985). SRIF₁₄ is the predominant form found in neurones, whereas SRIF₂₈ is the predominant peptide found in some peripheral organs like e.g. stomach and intestine (Patel et al., 1981; 1985). In contrast to SRIF, the prepro-CST mRNA has been located solely to the CNS: in cortex, hippocampus and spinal cord (De Lecea et al., 1996; 1997b; Fukusumi et al., 1997). There is currently no final proof for the existence of mature CST, since CST-selective antibodies have not yet become available, although it is clear that synthetic CST is biologically active.



Figure 1: Primary structure of somatostatin, cortistatin and some widely used analogues.

The four amino acids which appear to be crucial for activity in the β -turn (SRIF₁₄: Phe⁷-Trp⁸-Lys⁹-Thr¹⁰) are marked in bold; in CST₁₄ three further amino acids, which underline the differences to SRIF₁₄, are indicated in bold, in CST₁₇ the four further amino acids in bold emphasise the differences to CST₁₄. Abbreviations: Asu = amino suberic acid; Aha = amino heptanoic acid; Bzl = Benzyl-substituent.

1.1.2. Non-mammalian somatostatin peptides

SRIF₁₄ has been found not only in every mammalian species examined thus far, but also in representatives of other vertebrate classes, like birds (Conlon and Hicks, 1990; Spiess et al., 1979), reptiles (Wang and Conlon, 1993), amphibia (Vaudry et al., 1992), and fish (Andrews and Dixon, 1981; Conlon et al., 1985; 1988a; 1988b; 1995; Noe et al., 1979; Plisetskaya et al., 1986; Taylor et al., 1981); therefore, SRIF₁₄ seems to be highly conserved among vertebrates. Variants of SRIF₁₄, like [Pro²]SRIF₁₄, [Pro², Met¹³]SRIF₁₄, [Ser⁵]SRIF₁₄, [Ser¹²]SRIF₁₄, appear to be rather rare and could be isolated in a few species only (Andrews et al., 1988; Conlon, 1990; Nishii et al., 1995; Vaudry et al., 1992).

Two somatostatin genes are known from various fish species: one encodes the prepropeptide of SRIF₁₄, whereas the second gene encodes a precursor molecule which is processed to a SRIF peptide varying with the systematic group (Eilertson et al., 1993; Goodmann et al., 1980; Hobart et al., 1980); this SRIF variant molecule comprises 22-37 amino acids and its primary structure is much less conserved in the course of evolution, particularly in the N-terminal region: e.g. $SRIF_{22}$ in catfish, $SRIF_{25}$ in salmon and eel (Andrews et al., 1984; Conlon et al., 1988b; Eilertson et al., 1993; Fletcher et al., 1983; Hobart et al., 1980; Magazin et al., 1982; Plisetskaya et al., 1986; Uesaka et al., 1995).

SRIF mRNA has been identified in fish tissue of various organs. In the fish CNS, SRIF is expressed throughout the neuraxis in specific areas (Sas and Maler, 1991; Zupanc et al., 1991; 1994), and possesses multiple physiological functions such as regulation of postnatal development (Stroh and Zupanc, 1993; 1995; 1996; Zupanc, 1996, 1999; Zupanc and Maler, 1997).



Figure 2: Prepropeptide processing of mammalian somatostatin and human cortistatin.

Proteolytic processing of mammalian preprosomatostatin at monobasic (Arg) and dibasic (Arg-Lys) cleavage sites (Robbins and Reichlin, 1983; Shen et al., 1982; Zingg and Patel, 1982), and putative cleavage of human preprocortistatin (Fukusumi et al., 1997). The preprohormones contain a N-terminal signal sequence; the mature products, which are indicated in bold, are released from the carboxy terminus, in which the highest sequence homology of preprohormones is found. Abbreviation: Aa = amino acids.

1.1.3. Synthetic somatostatin analogues

SRIF binding sites were initially studied with [³H] ligands (Whitford et al., 1985, 1986, 1987), however iodinated ligands offer a number of advantages. Their theoretical specific activity (2175 Ci/ mmol = 1 iodine/ molecule) is much higher than that of tritiated ligands (20- 60 Ci/ mmol), which allows the use of very low amounts of receptors to perform studies. In addition, when autoradiographic studies are to be performed, high specific activity shortens dramatically the exposure time for the autoradiography film. Finally, if needed, the Chloramine T method for iodination offers clearly some economic advantages.

Since SRIF and CST cannot be iodinated, synthetic analogues with tyrosine residues for iodination were created to allow radioligand binding studies to their respective binding sites. Structure-activity studies have shown that analogues containing the Phe⁷-Trp⁸-Lys⁹-Thr¹⁰ residues of SRIF₁₄ in an appropriate cyclic conformation are sufficient to function as highly potent agonists. The presence of Trp⁸-Lys⁹ in the peptide is essential, whereas Phe⁷ and Thr¹⁰ can undergo minor substitutions (Brazeau et al., 1972; Epelbaum, 1986; Freidinger et al., 1984; Veber et al., 1981).

To increase the half-life, the peptides were metabolically stabilised by the introduction of D-amino acids. An example of such a metabolically stable peptide which is important for clinical use is the short synthetic SRIF analogue octreotide (figure 1) (SMS 201-995, Sandostatin[®], Bauer et al., 1982). Octreotide inhibits, like SRIF, the release of GH (growth hormone, somatotropin), and hence is used to treat acromegaly, which is caused by hypersecretion of somatotropin from the anterior pituitary; acromegaly is primarily associated with a pituitary adenoma, and leads to abnormal skeletal and tissue enlargement (Lancranjan et al., 1996). In addition, octreotide has antiproliferative properties *in vitro* in a number tumour cell lines and *in vivo* in a variety of neuroendocrine and gastroenteropancreatic (GEP) tumours; therefore, octreotide inhibits tumour growth, or even induces tumour shrinkage (Cheung et al., 1995; Kubota et al., 1994; Lamberts et al., 1987; 1991; 1995; Srikant, 1995; Weckbecker et al., 1993) and is currently indicated for the treatment of a number of GEP tumours.

Similar to SRIF, octreotide stimulates water and electrolyte absorption and inhibits epithelial transport and intestinal motility, and the release of gut hormones (Edwards et al., 1986; Efendic and Mattson, 1978; Kraenzlin et al., 1985). Thus, it is used in the control of refractory diarrhoea associated with acquired immunodeficiency syndrome (AIDS) (Cello et al., 1991; Monte et al., 1989). The radionuclide-coupled peptide [¹²⁵In]octreoscan (Penteotride®) is used to visualise tumours positive for SRIF binding sites by scintigraphy, whereas [⁹⁰Y]SMZ 487 is currently undergoing clinical trials for tumour radiotherapy (Krenning et al., 1994; 1995).

1.1.4. Physiological relevance

SRIF (and CST) possesses multiple physiological functions including regulation of endocrine and exocrine secretion, neurotransmission, neuromodulation, cognitive functions, behaviour, regulation of embryonic and postnatal development of neurones, inhibition of tumour growth and modulation of sleep activity (Brazeau et al., 1972; Brown et al., 1977; Buscail et al., 1993; 1994; De Lecea et al., 1996; 1997a; 1997b; Epelbaum, 1986; 1994; Feniuk et al., 1993; Fujii et al., 1994; Fukusumi et al. 1997; Krulich et al., 1968; Mandarino et al., 1981; for review, Patel, 1997; Raynor and Reisine, 1992; Reichlin, 1983; Schally et al., 1988).

SRIF expression is known to be altered in numerous diseases: decreased SRIF production was observed in the brain and/or CSF (cerebro spinal fluid) of patients suffering from Alzheimer's disease, schizophrenia, and epilepsy (Beal et al., 1985; Davies et al., 1980; Nemeroff et al., 1983; Riekkinen et al., 1990), whereas an increased SRIF expression could be determined in the brain of patients with Huntington's chorea, Parkinson's disease, and AIDS (Aronin et al., 1983; Chesselet and Reisine, 1983; Da Cunha et al., 1995; Nemeroff et al., 1983).

1.2. Somatostatin receptors

1.2.1. Receptor subtypes

SRIF and CST exert their biological effects via membrane-bound receptors - the socalled somatostatin receptors-, which have seven transmembrane-spanning helices and belong to the superfamily of G-protein coupled receptors (Bell and Reisine, 1993); they contain the consensus sequence Asp-Arg-Tyr (= DRY) at the boundary of their third transmembrane domain and their second cytoplasmatic loop, which is characteristic for a subfamily of G-protein-coupled receptors (figure 3) (Reisine and Bell, 1995).

Five mammalian receptor subtypes – designated as $sst_{1.5}$ (Hoyer et al., 1995a) - have been cloned from human, rat and mouse (Bell and Reisine, 1993; Bruno et al., 1992; Demchyshyn et al., 1993; Kluxen et al., 1992; Li et al., 1992; Lublin et al., 1997; Meyerhof et al., 1992; O'Carroll et al., 1992; 1994; Panetta et al., 1994; Rohrer et al., 1993; Vanetti et al., 1992; Xu et al., 1993; Yamada et al., 1992a; 1992b; 1993; Yasuda et al., 1992); additionally, the porcine and bovine homologues of the sst₂ receptor were cloned (Matsumoto et al., 1994; Xin et al., 1992). Based on structural and operational features, two classes of SRIF receptors can be distinguished: the SRIF₁-family comprising sst₂, sst₃ and sst₅, and the SRIF₂-family including sst₁ and sst₄ receptors (Hoyer et al., 1995a).

All cloned receptor subtypes are intron-less in their protein-coding region with the exception of the rodent sst_2 receptor: in addition to the unspliced sst_{2A} receptor, the sst_{2B} receptor splice variant, which differs only by a shorter carboxy tail from the unspliced form, was identified in mouse and rat (Schindler et al., 1998b; Vanetti et al., 1992; 1993). Two differentially sized transcripts were detected for the human sst_2 receptor, suggesting alternative splicing to take place also in man (Yamada et al., 1992a), although the existence of the spliced form has not been confirmed so far by cloning.



Figure 3: Transmembrane model of the human somatostatin sst₅ receptor.

CHO = putative N-linked glycosylation site, PO_4 = putative phosphorylation site, Σ = putative palmitoyl membrane anchor site (Leu-rich), C-C = disulfide bond between cysteine residues. Black amino acids indicate the proposed ligand binding pocket of SRIF₁₄ within the transmembrane domains 3-7. The model was taken from Patel et al. (1995).

The genes of the different SRIF receptor subtypes are localised on separate chromosomes; the human sst_{1-5} receptors were localised on chromosome 14, 17, 22, 20 and 16, and their protein consists of 391, 369, 356, 418, 388 and 364 amino acids, respectively (Corness et al., 1993; Demchyshyn et al., 1993; Yamada et al., 1993; Yasuda et al., 1993; Panetta et al., 1994; Patel, 1997).

The primary structure of SRIF receptors suggests the presence of seven transmembrane spanning α -helices, in which highest sequence similarities are found when comparing the different receptor subtypes; in addition, there is suggested to be a disulfide bound between two cysteine residues of the second and the third extracellular loop, as well as several subtype- and species-specific glycosylation and phosphorylation sites (figure 3) (Bell et al., 1995; Dournaud et al., 1996; Nehring et al., 1995; Meyerhof et al., 1992). The ligand binding pocket of SRIF receptors is species-, subtype- and ligand-specific, but the responsible amino acids are predominantly located within the transmembrane domains 3- 7, and partially in the second and/ or third extracellular loop, as suggested from studies performed with numerous deletion mutants and by site-directed mutagenesis (Fitzpatrick and Vandlen, 1994; Liapakis et al., 1996; Kaupmann et al., 1995; Ozenberger and Hadcock, 1995). The agonist binding of SRIF₁ receptors, but not of SRIF₂ receptors, is negatively modulated by sodium ions (Reubi and Maurer, 1986; Raynor et al., 1993a, 1993b), for which a conserved aspartate residue in the second the transmembrane domain is responsible (Kong et al., 1993).

All SRIF receptor subtypes bind the endogenous peptides SRIF₁₄, SRIF₂₈ and CST with similar high affinity and only little or no selectivity (Fukusumi et al. 1997; Hoyer et al., 1994). In contrast, the short cyclic analogues octreotide and seglitide (MK678) (figure 1) bind selectively to members of the SRIF₁-receptor family with preferential affinity for sst₂ and sst₅ receptors compared to sst₃ receptors, whereas their affinity to SRIF₂ receptors is very low (Hoyer et al., 1994b; Martin et al., 1991; Patel and Srikant, 1994; Raynor et al., 1993a; Reisine and Bell, 1995; Reubi, 1984; Tran et al., 1985). The iodinated forms of octreotide and seglitide, [¹²⁵I][Tyr³]octreotide and [¹²⁵I]MK 678, were suggested to label exclusively sst₂ receptors *in situ*, e.g. in native brain membranes or slices (Hoyer et al., 1994b; Piwko et al., 1997; Schoeffter et al., 1995). The SRIF₂-family - sst₁ and sst₄ receptors - can be selectively labelled *in situ* with radioligands in the presence of high sodium concentrations, e.g. with [¹²⁵I][Tyr¹¹]SRIF₁₄ or [¹²⁵I]CGP 23996 (Hoyer et al., 1994b; 1995b; Reubi and Maurer, 1986; Thoss et al, 1997).

1.2.2. Tissue distribution of receptor subtypes

In mammals, SRIF receptor subtypes were found to be specifically expressed in brain and many peripheral tissues (Bell and Reisine, 1993; Breder et al., 1992; Kaupmann et al., 1993; Raulf et al., 1994; Thoss et al. 1996; 1997), as well as in a number of tumours (Reubi et al., 1984; 1987; 1990a; 1990b); their expression undergoes changes in a spatial and temporal manner during ontogenesis (Wulfsen et al., 1993; Hartmann et al., 1995; Thoss et al., 1995; 1996).

In brain, the transcripts of sst_{1-4} receptors are widely distributed and high levels were found in cortex, hippocampus and hypothalamus; however, sst_5 receptor mRNA was detected primarily in the preoptic area and hypothalamus (Bito et al., 1994; Bruno et al., 1993; Meyerhof et al., 1992; Perez and Hoyer, 1995; Raulf et al., 1994; Thoss et al., 1996; 1997). Among the two sst_2 receptor splice variants, the sst_{2A} receptor form is preferentially expressed over the sst_{2B} variant in brain and pituitary of rat, but not of mouse (Sarret et al., 1998; Vanetti et al., 1992). Also cellular coexpression of different receptor subtypes has been reported, e.g. of sst_3 and sst_4 (Perez and Hoyer, 1995).

In the periphery, expression of human sst_{1-5} receptors $(hsst_{1-5})$ was observed in pituitary, stomach and various tumours. In addition, the expression of the $hsst_1$ receptor was detected in liver and ovary, of the $hsst_2$ receptor in kidney, adrenals and pancreas, of the $hsst_3$ receptor in spleen, liver, pancreas, lymph nodes and smooth muscle, of the $hsst_4$ receptor in lung, and of the $hsst_5$ receptor in liver, adrenals, pancreas and heart (Kubota et al., 1994a; Le Romancier et al., 1996; O'Carroll et al., 1994; Panetta et al., 1994; Raulf et al., 1994; Reubi et al., 1998; Vikic-Topic et al., 1995; Yamada et al., 1992a).

Receptor-specific antibodies are being used to localise the corresponding receptor proteins. Human sst_{1-3} receptors were immunolocalised in tumour tissues (Reubi et al., 1998; Schulz et al., 1998b), and $hsst_2$ receptors in the cerebral cortex, hippocampus and cerebellum of brain (Schindler et al., 1998a), as well as in the peripheral nervous system, in lymphatic tissue and in the gastrointestinal smooth muscle (Reubi et al., 1999).

In rat, the sst₂ receptor protein was similarly found in brain and spinal cord, and also in pancreas (Dournaud et al., 1996; Hunyady et al., 1997; Schindler et al., 1997; Schulz et al., 1998a); the sst₁ receptor protein was widely distributed in brain (Helboe et al., 1998; Hervieu et al., 1998), and the sst₃ receptor was immunolocalised in neuronal cilia (Händel et al., 1999); preliminary reports suggest sst₅ receptors to be present in the rat brain, but with very low abundance, and they seem to be limited to the more rostral regions of the brain (Stroh et al., 1998).

1.2.3. Receptor subtype-specific functions

The sst, receptor subtype is suggested to regulate intrahypothalamic pulsatility of somatotropin (Lanneau et al., 1999). Mainly responsible for the inhibition of somatotropin release from anterior pituitary is the sst, receptor subtype (Raynor et al., 1993b); the sst₂ receptor additionally plays a major role in the inhibition of glucagon release from the pancreas, of histamine release from the antrum, of gastrin release from the mucosa, of acid and ion secretion in the colon, of cell firing in the locus coeruleus, and mediates inhibition of neurotransmission in the ileum (Coy and Taylor, 1996; Feniuk et al., 1995; Prinz et al., 1994; Rossowski and Coy, 1994; Warhurst et al., 1996; Zaki et al., 1996). Sst, receptor knockout mice were devoid of severe defects, but were refractory to the somatotropin-mediated negative feedback, and revealed an increased gastric acid secretion (Zheng et al., 1997; Martinez et al., 1998). The sst, receptor is suggested to mediate inhibition of gastric smooth muscle contraction, and partially functions in inhibition of insulin release (Coy et al., 1998; Gu et al., 1995). No functional effects have been attributed to sst₄ receptors so far. The sst₅ receptor subtype is suggested to be involved in inhibition of amylase release, of insulin release from the pancreas, as well as of mitogen-induced regeneration of aortic vascular smooth muscle cells (Coy and Taylor, 1996; Coy et al., 1998; Lauder et al., 1997; Rossowski et al., 1994).

1.3. Signal transduction

1.3.1. Coupling to G-proteins

Mammalian SRIF receptors are specifically coupled to intracellular signal transduction cascades via various pertussis toxin (PTX)-sensitive (G_i and G_o) and PTX-insensitive G-proteins (e.g. G_q , G_{14} , G_{16}) (Bell and Reisine, 1993; Kagimoto et al., 1994; Kleuss et al., 1991; Komatsuzaki et al., 1997; Kubota et al., 1994b; Law et al., 1991; 1994; Murthy et al., 1996; Patel et al., 1994; Reisine et al., 1995; Yatani et al., 1987). The third cytoplasmatic loop of agonist-activated G-protein-coupled receptors binds to the C-terminus of G α -subunits, which forms heterotrimeric complexes with G $\beta\gamma$ subunits (for review, Hamm et al., 1998; Kobilka et al., 1988; Reisine et al., 1994).

The activated receptor bound to the inactive G-protein catalyses the exchange of GDP to GTP on the G α subunit, which activates the G-protein; it is assumed that the G α -subunit dissociates from the G $\beta\gamma$ -subunit upon G-protein activation, although dissociation may not be the rule under physiological conditions (Rebois et al., 1997). The GTP-bound G-protein modulates the activity of downstream effector molecules, and is deactivated by G α -catalysed hydrolysis of GTP to GDP and P_i (Birnbaumer and Birnbaumer, 1995; Gilman, 1987; Hamm et al., 1998). In addition, GTPase-activating proteins, the so-called regulators of G-protein-signalling (RGS), modulate G-protein-signalling, especially of G_i-proteins (Roush et al., 1996).

The binding rate of GTP and thereby the ability of a receptor to activate G-proteins can be measured using the non-hydrolysable GTP-analogue guanosine-5`O-(3-[³⁵S]GTP_YS) triphosphate ([³⁵S]GTP_YS). The agonist-induced receptor/ G-protein/ [³⁵S]GTP_YS complexes can be determined quantitatively by measuring the bound radioactivity, which is a reflection of the capacity of agonists to trigger intracellular signalling events (Lorenzen et al., 1993). In addition, binding of GTP or analogues to the G-protein induces dissociation of the agonist from the receptor/ G-protein complex, and therefore inhibits ligand binding (Brown and Schonbrunn, 1993; Hjorth et al., 1996; Koch and Schonbrunn, 1984; Rens-Domiano et al., 1992). Multiple subunits isoforms of heterotrimeric G-proteins couple SRIF receptor subtypes specifically to the different intracellular targets (for review, Birnbaumer and Birnbaumer, 1995; Gutkind, 1998). Thus, SRIF receptors mediate inhibition of adenylate cyclase activity via $G\alpha_{i1}$, $G\alpha_{i2}$, $G\alpha_{i3}$ and $G\alpha_{o}$ depending on the receptor subtype and the cell system, but they also activate phospholipase C via $G\alpha_{i1}$, $G\alpha_{o}$, $G\alpha_{14}$ and $G\alpha_{16}$ (Patel, 1997); for instance, sst₂ receptors are coupled via $G\alpha_{i1}$ to inhibition of adenylate cyclase (Kagimoto et al., 1994), via $G\alpha_{i3}$ to stimulation of K⁺-channels (Yatani et al., 1987), and via $G\alpha_{o}(\beta_{1}/\gamma_{2})$ to stimulation of Ca²⁺-channels (Kleuss et al., 1991).

1.3.2. Modulation of adenylate cyclase

Each of the five mammalian SRIF receptors has been shown to couple to inhibition of adenylate cyclase (AC) activity as suggested from earlier work performed in tissue and cell preparations (Chneiweiss et al. 1987; Jakobs et al., 1983; Kaupmann et al., 1993; Koch and Schonbrunn, 1984; Patel et al., 1994; Raynor and Reisine 1992; Reisine et al., 1995); the inhibition of AC by somatostatin is blocked by pertussis toxin, which ADPribosylates and thereby inactivates the α subunits of G_i and G_o (Reisine et al., 1985). Nine distinct mammalian AC variants, which are membrane-spanning, are known. G_i and G_0 -proteins effectively inhibit the activity of the Ca²⁺-calmodulin-stimulated AC type I; G_i additionally inhibits AC's type V and VI (for review, Sunahara et al., 1996; Taussig et al., 1993; 1994). AC type I is primarily expressed in neurones, while type V and VI are ubiquitously expressed (for review, Birnbaumer and Birnbaumer, 1995). The $G\alpha$ subunit of G_i and G_o is myristoylated, which is required for membrane anchoring and interaction with the AC enzyme (Jones et al., 1990; Mumby et al., 1990; Taussig et al., 1993). SRIF receptors have been reported to couple to inhibition of AC via G_{i1} , G_{i2} , and G_{i3}, depending on the receptor subtype and the cell line (Kagimoto et al., 1994; Kubota et al., 1994b; Law et al., 1993a; 1993b; Liu et al., 1994; Senogles, 1994; Tallent and Reisine, 1992; Yajima et al., 1993).

SRIF-induced inhibition of AC activity, and thereby decreased cAMP levels, cause inhibition of protein kinase A activation, and subsequently inhibition of phosphorylation and therefore activation of the cAMP response element-binding protein - CREB - (Tentler et al., 1997).

In mammals, AC inhibition by somatostatin was measured in various tissues/ organs such as brain (Chneiweiss et al., 1984), pituitary (Epelbaum et al., 1987), pancreas (Rodriguez et al., 1997; Viguerie et al., 1988), retina (Colas et al., 1992), enteric cells (Barber et al., 1987), intestinal smooth muscle cells (Murthy et al., 1996), kidney-derived cells (Roy, 1984), and astrocytes, in which somatostatin inhibits interleukin 6 release (Grimaldi et al., 1997).

In fish, SRIF has been reported to inhibit AC activity in the pituitary (Helms et al., 1991); the nature of the AC isozymes has not yet been characterised in fish, but adenylate cyclases are present in many tissues like in pituitary, heart, liver, ovary, and gill (Fabbri et al., 1992; Guibbolini et al., 1992; Helms et al., 1991; Srivastava et al., 1994; Vornanen, 1998).

1.3.3. Modulation of phospholipase C

All five human SRIF receptor subtypes have been described to couple to activation of phospholipase C (PLC), when expressed in COS-7 cells (Akbar et al., 1994). In F_4C_1 rat pituitary cells, mouse sst₂ receptors mediated activation of PLC, but not rat sst₁ receptors (Chen et al., 1997). In intestinal smooth muscle cells, endogenously expressed sst₃ receptors induced activation of PLC_{β3} and Ca²⁺-release via Gβγ-subunits of G_{i1}/G_o (Murthy et al., 1996). The activation of PLC by human sst₁₋₅, mouse sst₂, and guinea pig sst₃ receptors was only partially pertussis toxin (PTX)-sensitive (Akbar et al., 1994; Chen et al., 1997; Murthy et al., 1996). PTX ADP-ribosylates $G_{i/o}\alpha$ at a specific cysteine residue at –4 position, and $G_o\alpha$ additionally at –3 position from the carboxy terminus, which inactivates these G-proteins by preventing their interaction with receptors (Avigan et al., 1992; West et al.; 1985).

The PLC enzyme family comprises at least 9 different isoforms, which all require Ca²⁺ for activity; G-protein-coupled receptors primarily stimulate the activity of the 4 β isoforms, $PLC_{\beta 1}$ -4, via direct interaction of activated G-proteins. The α subunits of $G_{i/o}$ do not directly activate PLC_B, but as a result of activation of $G_{i/o}\alpha\beta\gamma$, the $\beta\gamma$ -complex will activate PLC_{B2}/ PLC_{B3}. $G_{q}\alpha$ and $G_{11}\alpha$ are primarily responsible for coupling of receptors to $PLC_{\beta 1}$ and $PLC_{\beta 3}$; in addition, $G_q \alpha$ activates $PLC_{\beta 4}$ (Berridge, 1993; for review: Exton, 1996; Simon et al., 1991; Sternweiss et al., 1992). Receptor-mediated stimulation of membrane-associated PLC activity acts on phosphatidylinositol 4,5biphosphate hydrolysis, which leads to generation of the second messengers inositol 1,4,5-triphosphate (IP₃) and 1,2-diacylglycerol (DAG). IP₃ molecules bind to their respective receptors at the membranes of the intracellular Ca2+-stores, the Endoplasmatic Reticulum and the Golgi apparatus, which results in an increase of cytoplasmatic Ca²⁺ levels. Ca²⁺ and DAG activate the protein kinase C enzyme, that regulates cell growth and cell differentiation. Ca2+ activates also other Ca2+ binding proteins such as calmodulins. IP_3 is specifically degraded by phosphatases to IP_2 , IP_1 , and finally inositol; degradation to inositol can be blocked by lithium ions, and phospholipase C activity determined by measurement of total IP_x levels (Berridge, 1993; Clapham, 1995; Mikoshiba, 1997).

1.3.4. Modulation of further signalling proteins

In addition to adenylate cyclase and phospholipase C, multiple effector molecules are reported to be modulated by SRIF receptor subtypes. SRIF receptors induce activation of cGMP-dependent protein kinases (Meriney et al., 1994), and the sst₄ receptor was found to activate arachidonic acid release and phospholipase A_2 (Shimizu et al., 1996; Schweitzer et al., 1990). Potassium channels are stimulated by the sst₂ receptor (Wang et al., 1987; 1989; Yatani et al., 1987), calcium channels are inhibited by sst₂ and sst₅ receptors (Fujii et al., 1994; Ikeda and Schonfield, 1989; Rosenthal et al., 1988; Tallent et al., 1996; Wang et al., 1990), and Na⁺/H⁺ exchanger proteins are positively or negatively modulated by sst₁ and sst₅ receptors (Barber et al., 1989; Hou et al., 1994).

Activation and inhibition of the p42/p44 mitogen-activated protein kinase (= MAPK, Erk1/2) by sst_{1-5} receptors has been observed in diverse cellular systems, and consequently modulation of the transcription factor elk-1 (Bito et al., 1994; Buscail et al., 1994; 1995; Florio et al., 1994; 1999; Lopez et al., 1997; Todisco et al., 1995; 1997); sst₁ receptor-induced MAPK activation was shown to involve the tyrosine phosphatase SHP-2, the tyrosine kinase c-src, and Ras and Raf-1 (Florio et al., 1999). Stimulation of protein tyrosine phosphatases, particularly SHP-1 and SHP-2, was observed for sst_{1-4} receptors (Buscail et al., 1994; 1995; Florio et al., 1994; 1999; Reardon et al., 1996; 1997; Lopez et al., 1997; Srikant and Shen, 1996). Further, the recombinantly expressed sst₃ receptor is reported to induce p53 and apoptosis (Sharma et al., 1996).

1.4. Outline of the thesis

The aim of the present study was to characterise ligand binding and ligand-modulated signal transduction pathways of the five different human somatostatin sst₁₋₅ receptor subtypes and of the first non-mammalian somatostatin receptor, the fish sst₃ receptor, all studied in the same environment, i.e. the same cell line. For this purpose, the receptors were stably expressed in CCL39 Chinese hamster lung fibroblast cells, which contain high levels of G-protein isoforms known to couple somatostatin receptors to their effector molecules.

The recently identified CST, which is structurally related to SRIF, was investigated for its ability to bind to the human SRIF receptor subtypes, and pharmacological profiles were established using iodinated CST ([125I][Tyr10]CST14), and SRIF/ CST and analogues at cell membrane preparations. Since there is historically great variation in data reported by various groups on the pharmacological profiles of the different mammalian receptor subtypes even when expressed in the same cell line, the affinity $([^{125}I]LTT-SRIF_{28}, [^{125}I]CGP$ 23996, radioligands further profiles using [¹²⁵I][Tyr³]octreotide) were determined, and compared to each other. The stable and nonhydrolysable GTP-analogue guanylylimidodiphosphate was used to study inhibition of radioligand binding at membrane preparations, and therefore to indirectly examine Gprotein coupling of the receptor populations labelled by the various radioligands.

Agonist-induced G-protein activation was investigated at the human SRIF receptors by measuring agonist-stimulated guanosine-5`O-($3-[^{35}S]$ thio)-triphosphate ($[^{35}S]$ GTP γ S) binding using microsome preparations; assay conditions were established, and the agonist rank orders of potency and efficacy determined. Inhibition of forskolinstimulated adenylate cyclase activity by SRIF ligands was examined at human sst₁₋₅ receptors by measuring cellular cyclic adenosine monophosphate (cAMP) levels. Activation of phospholipase C activity mediated by the human SRIF receptor subtypes was indirectly measured by determining total cellular [³H]-inositolphosphate accumulation; in addition, stimulated intracellular calcium levels were measured using a calcium-dye and by monitoring fluorescence. The agonist profiles of human sst_{1-5} receptors obtained in [³⁵S]GTP γ S binding, adenylate cyclase inhibition, and phospholipase C stimulation were compared to each other, and to the affinity profiles determined in competition binding assays using the four distinct radioligands.

To characterise the fish sst₃ receptor cloned from the teleost fish *Apteronotus albifrons*, pharmacological profiles were established in radioligand binding using distinct iodinated ligands, in [³⁵S]GTP γ S binding, in forskolin-stimulated adenylate cyclase inhibition, and in phospholipase C stimulation, and compared to each other, and compared to data obtained at the human somatostatin receptor subtypes. The interest was to elucidate the binding properties as well as the signal transduction machineries in non-mammalian vertebrates. Further, the presence and nature of native somatostatin receptors was studied in various tissues prepared from *Apteronotus albifrons*.

COS-1 cells (SV40 CV-1 cells, which originate from kidney cells of the African Green Monkey; American Type Culture Collection) and CCL39 cells (established line of Chinese hamster lung fibroblasts; American Type Culture Collection) were cultured in a 1:1 mixture of Dulbecco's Modified Eagle's Medium (DMEM; Seromed, Biochrom, Berlin, Germany; 3.7 g/ 1 NaHCO₃; 1.0 g/ 1 D-glucose; with stable glutamine) and Ham's F-12 Nutrient Mixture (Seromed; 1.176 g/ 1 NaHCO₃; with stable glutamine) supplemented with 10 % (v/ v) foetal bovine serum (FBS; Gibco BRL) and penicillin (100 u/ml final concentration)/ streptomycin (100 μ g/ ml final concentration) (both from Sigma-Aldrich Chemie, Deisenhofen, Germany) at 37°C, 5 % CO₂ and 95 % relative humidity. For passaging, the cells were detached from the cell culture flask by washing with phosphate-buffered saline (PBS, pH 7.4, Gibco BRL) and by brief incubation with trypsin (0.5 mg/ ml)/ EDTA (0.2 mg/ ml) (Gibco BRL). The cells were passaged every 2 days. For storage, the cells were resuspended in medium containing dimethyl sulfoxide (10 % final concentration), and frozen in liquid nitrogen.

2.2. Transient transfection

Transient expression of the fish sst₃ receptor gene in COS-1 cells was carried out by using the diethylaminoethyl (DEAE)-dextran transfection method. Cells were splitted 12- 16 h prior to transfection on culture plates (diameter 10 cm) to obtain a density of approximately 10^4 cells/ plate. For transfection, cells of each plate were covered with 4 ml medium. The transfection mix containing 10- 40 µg pcDNA3-fsst₃ plasmid DNA (G.K.H. Zupanc, Manchester, England), 40 ml HBS buffer pH 7.4 (130 mM NaCl, 0.9 mM NaH₂PO₄, 0.8 mM MgSO₄, 5.4 mM KCl, 1.8 mM CaCl₂, 25 mM D(+)-glucose, 20 mM HEPES, 5 ng/ ml phenol red) and 80 µl DEAE-dextran (10 mg/ ml) was distributed in each plate. Two hours later, 40 µl chloroquine (10 mM in H₂O) were added. 6 h after transfection, cells were washed twice with PBS, restored in culture medium, and harvested after additional 32- 36 h.

As a control, cells were transfected in parallel with RSV-lacZII plasmid (constructed by W. Ankenbauer, Heidelberg, Germany) containing the *Escherichia coli* β -galactosidase gene, and harvested 24 h later. Cells were washed twice with PBS, incubated for 10 min at room temperature with 1 % glutaraldehyde in PBS for fixation, washed 3 times with PBS, and incubated overnight in a sealed plate with staining solution (5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 2 mM MgCl₂, 1 mg/ ml 5-bromo-4-chloro-3-indolyl- β -D-galactoside), pH 7.0, at 37°C and 0 % CO₂. A blue staining can normally be observed by microscopy in roughly 20 % of the cells.

2.3. Stable transfection

CCL39 cells were used for stable expression of the human SRIF receptor genes. Cells were splitted 1 day prior to transfection for logarithmic growth. 1.6 x 10^8 cells resuspended in 800 µl electroporation buffer (272 mM sucrose, 1 mM MgCl₂, 7 mM Na₂HPO₄/NaH₂PO₄), pH 7.4, were mixed with 10- 80 µg DNA pcDNAI-hsst₁+pNeo, pcDNAI-hsst₂+pNeo, pcDNAI-hsst₃+pNeo (G.I. Bell, Chicago, USA), pcDNAI-hsst₄+pNeo (F. Raulf, Basel, Switzerland), pRc/CMV-hsst₅ (S. Seino, Chiba, Japan), or pcDNA3-fsst₃ (G.K.H. Zupanc, Manchester, England), and incubated on ice for 10 min. Cells were electroporated at 500 V/ 25 µF, cooled down at 4°C for 10 min, and supplemented with cell culture medium in 260 ml culture flasks. After 2 days, the antibiotic G418 (geneticin sulphate; Gibco BRL) was added to the cell culture medium (0.4 mg/ml 100 % active G418 final concentration) for selection of SRIF receptor-expressing cells. Receptor expression of single cell-derived colonies was tested by radioligand binding. Stable transfected cells were permanently cultured in G418-containing medium.

2.4. Radioligand binding assay

For crude cell membrane preparations, cells were harvested by washing with 10 mM HEPES, pH 7.5, scrapping off the culture plates with 4 ml of the same buffer, and centrifugation at 4° C for 5 min at 2500 x g.
The cell pellet was either stored at -80°C or directly used. The cell preparations were resuspended in binding assay buffer (10 mM HEPES, pH 7.5, 0.5 % (w/v) bovine serum albumin (BSA)) by homogenisation with the Polytron at 50 Hz for 20 s.

For preparation of crude tissue membranes, the different fish tissues were briefly rinsed in 10 mM HEPES, pH 7.5, weighed, resuspended in 10 mM HEPES, pH 7.5, by homogenisation with the Polytron at 50 Hz for 40 s (100 mg/ ml each), and stored at -80°C. Tissue homogenates were diluted in assay buffer to a concentration of 4- 7 mg/ml.

In competition experiments, 150 µl of the cell or tissue homogenate (CCL39 cells: hsst₁ and hsst₂: ca. 1.5 x 10⁵ cells/ 4 μ g protein, hsst₃, hsst₅ and fsst₃: 0.75 x 10⁵ cells/ 2 μ g protein, and hsst₄: 4.5 x 10^5 cells/ 6 µg protein, depending on the expression level of each receptor; 750 µg brain or 600 µg liver, respectively), were incubated with 50 µl of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, or [¹²⁵I][Tyr³]octreotide (2175 Ci/mmol: 25- 35 pM; final concentration), in binding assay buffer containing MgCl₂ (5 mM) and the protease inhibitor bacitracin (5 μ g/ ml), and either 50 μ l binding assay buffer (total binding) or with 50 µl of various peptide/ GppNHp concentrations. Nonspecific binding was determined in the presence of SRIF₁₄ (1 µM). After 1 h at room temperature, the incubation was terminated by vacuum filtration through glass fibre filters pre-soaked in 0.3 % (w/v) polyethyleneimine. The filters were rinsed twice with ice-old 10 mM Tris/HCl buffer, pH 7.4, and dried. Bound radioactivity was measured in a γ -counter using scintillation liquid (80 % counting efficiency). Data were analysed by non-linear regression curve fitting with the computer program SCTFIT (De Lean, 1979). In saturation experiments, 150 µl of cell homogenates were incubated with 50 µl of 8 different concentrations (approximately 25- 300 pM) of [¹²⁵I]LTT-SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996, or $[^{125}I][Tyr^{3}]$ octreotide, and 50 µl of binding assay buffer (total binding) or 1 µM SRIF₁₄ (non-specific binding). If GppNHp (10⁻⁵ M; final concentration) was used, it was included in each well. Data were analysed using the computer program SCTFIT (De Lean, 1979). Protein concentration was determined according to Bradford (1976) by means of the BioRad Protein Assay Kit with BSA as a standard.

For statistical analysis, data from radioligand binding studies were compared by paired t-Test analysis for individual values using the statistical package in GraphPad Prism. Affinity profiles were compared by correlation and significance indicated by P values; they were also compared one way ANOVA and Dunnett's multiple comparison test.

2.5. [³⁵S]GTPγS binding assay

Cells were harvested for microsome preparations, by washing with 10 mM HEPES, pH 7.5, scrapping off the culture plates with 4 ml of the same buffer and centrifugation at 4°C for 5 min at 2500 x g. The cell preparations were resuspended in 10 mM HEPES, pH 7.5 by homogenisation with the Polytron at 50 Hz for 20 s, and centrifuged at 4°C for 30 min at 15000 x g. The microsome pellets were resuspended in assay buffer (10 mM HEPES pH 7.4, 100 mM NaCl, 5 mM MgCl₂, 0.1 mM EDTA pH 8.0, 10 μ g/ ml bacitracin), and either stored at -80°C or directly used.

100 µl of the microsome preparation from CCL39 cells (hsst₁: ca. 3 x 10⁵; hsst₂, hsst₃ and hsst₄: 1.5 x 10⁵; hsst₅, fsst₃: 0.75 x 10⁵ cells, depending on the expression level of each receptor) were incubated with 20 µl GDP (1 µM; final concentration), and either 10 µl assay buffer (total binding) or with 10 µl of various peptide concentrations, and with 10 µl of [³⁵S]GTPγS (200 ρ M; final concentration) in 96-well Viewplates (Dynatech Laboratories). Non-specific binding was determined by addition of 10 µl GTPγS (10 µM; final concentration), in all other wells 10 µl assay buffer were added. After 5 min preincubation, 50 µl wheatgerm agglutinin (WGA) SPA (scintillation proximity assay)-beads were supplemented (1.5 mg beads per well; beads in 50 mM Tris pH 7.4, 0.1 % sodium azide, and diluted 1:3 in assay buffer), the plates sealed, incubated for 1 h at room temperature, and centrifuged for 10 min at 1000 x g. [³⁵S]GTPγS bound to a G-protein/ receptor-complex, and thereby to the WGA SPAbeads stimulated those to emit light, which was measured in a β-scintillation counter (Packard TopCount). Data were calculated and standardised to the level of basal activity (= 100 %). Stimulatory concentration-response curves were analysed by non-linear regression curve fitting using the computer program "GraphPad Prism". pK_B -values were determined using the Schild-Gaddum-equation.

2.6. Adenylate cyclase activity (cAMP accumulation) measurement

In cAMP-Scintillation Proximity Experiments (indirect cAMP measurements), cells were splitted 1 day prior to the experiment in 96-well Viewplates (Dynatech Laboratories) (5 x 10^4 cells per well). The assay was performed as described for the cAMP-Scintillation Proximity Assay (SPA)-kit (Amersham). Cell culture medium was flicked out, and cells were incubated for 15 min at 37°C (5 % CO₂, 95 % relative humidity) with 50 µl Minimum Essential Medium (MEM; Gibco BRL; with Earle's red, phenol with stable glutamine) containing 1 mM salts. without isobutylmethylxanthine (IBMX; Sigma) as a phosphodiesterase-inhibitor, either without forskolin (basal enzyme activity) or with 10 µM forskolin (Sigma) and various concentrations of the tested peptides. Experiments were conducted in triplicates. Medium was flicked out, and for cell lysis 50 µl Lysis Reagent I (1 % Dodecyltrimethylammoniumbromide, 0.01 % sodium azide, 0.05 M acetate buffer, pH 5.8) were added to each well, and the plate was shaken for 5 min followed by another incubation period of 5 min. Equal volumes of [¹²⁵I]cAMP (3`,5`-cyclic phosphoric acid-2'-O-succinyl-3-[¹²⁵I]-iodotyrosine methyl ester in Lysis Reagent II), of rabbit-anticAMP-serum (diluted in Lysis Reagent II), and of SPA anti-rabbit reagent (SPA fluomicrospheres (polyvinyl toluene based beads), diluted in Lysis Reagent II) were mixed, and 150 µl of the mixture was added per well. Plates were sealed and incubated for 15-20 hrs at room temperature. [¹²⁵I]cAMP bound to the rabbit-anti-cAMP-serum/ SPA anti-rabbit reagent-complex stimulated the SPA beads to emit light, which was measured in a β -scintillation counter (Packard TopCount).

cAMP of the cell lysate, which competes with [¹²⁵I]cAMP in binding to the rabbit-anticAMP-serum/ SPA anti-rabbit reagent-complex (radioimmunoassay), was calculated and normalised to the level reached in the presence of forskolin. Forskolin induces a ca. 20-30 fold stimulation of AC in CCL39 cells. Inhibitory concentration-response curves were analysed by non-linear regression curve fitting with the computer program "GraphPad Prism" using the equation $y = E_{max}/(1+x /EC_{50})+(100-E_{max})$, where y represents the percentage of cAMP produced and x the agonist concentration. pK_Bvalues were determined using the Schild-Gaddum-equation.

In direct cAMP measurements, cells were grown to confluence in 24-well plates. Following washing with assay buffer (130 mM NaCl, 5.4 mM KCl, 1.8 mM CaCl₂, 0.8 mM MgSO₄, 0.9 mM NaH₂PO₄, 25 mM glucose, 20 mM HEPES, pH 7.4), the cells were incubated with 6 μ Ci [³H]adenine (1 mCi/ ml) in 500 μ l assay buffer for 2 h at 37°C, 5 % CO₂ and 95 % relative humidity. When pertussis toxin (PTX; Sigma; 100 ng/ml medium) was used, cells were treated for 24 h before the incubation with 6 μ Ci [³H]adenine. Cells were then washed twice with assay buffer containing 1 mM IBMX (Sigma). The cells were incubated at 37°C in 1 ml assay buffer containing IBMX either without (basal enzyme activity) or with 10 μ M forskolin (Sigma) and various ligand concentrations. Experiments were conducted in duplicate. After 15 min, cells were extracted with 5 % trichloroacetic acid containing 100 μ M adenosine triphosphate (ATP) and 100 μ M cyclic adenosine monophosphate (cAMP).

[³H]ATP and [³H]cAMP were separated by sequential chromatography on Dowex AG 50W-X4 and alumina columns. Dowex columns were washed with 10 ml H₂O, then cell-extract and 3 ml H₂O were loaded, and the eluate ([³H]ATP) measured in a β-counter. 8 ml H₂O were loaded onto the Dowex columns, the eluate was loaded on alumina columns, which had been washed with 10 ml 100 μ M imidazole, and the flow-through discarded. The [³H]cAMP was eluted from the alumina columns with 6 ml 100 μ M imidazole and measured in a β-counter. The recovery of [³H]cAMP, as measured in separate experiments using a [³H]cAMP standard, was 76 ± 1 % (n = 5).

Dowex- columns were regenerated with 10 ml 2 N HCl, the alumina columns with 3 ml 1 M imidazole. Data were calculated as cAMP/(cAMP+ATP) ratios and normalised to the level reached in the presence of forskolin. Inhibition concentration-response curves were analysed using the computer program ORIGIN.

2.7. Measurement of phosphoinositide turnover (total [³H]-IP_x accumulation)

 2×10^5 cells per well were splitted 24 h prior to the experiment on 24-well plates and incubated in 1 ml cell culture medium containing 2 µCi myo-[2-³H(N)]-inositol (74 MBq/ ml; American Radiolabelled Chemicals). When pertussis toxin (PTX) was used, cells were pre-treated with the toxin (Sigma; 100 ng/ ml) for at least 3 h during labelling with myo-[2-³H(N)]-inositol. Following washing with HBS buffer (130 mM NaCl, 5.4 mM KCl, 1.8 mM CaCl₂, 0.8 mM MgSO₄, 0.9 mM NaH₂PO₄, 25 mM glucose, 20 mM HEPES, pH 7.4) containing 20 mM LiCl to block inositol monophosphatase activity, the cells were incubated for 5 min at 37° C. Various compound concentrations were added, and the cells were incubated at 37° C for another 50 min. Preliminary experiments were conducted in triplicates, ligand testing was performed in duplicates.

Cells were extracted with 750 µl 10 mM ice-cold formic acid. After 30 min, the extracts containing inositol phosphates and free inositol are diluted into 3 ml of 5 mM NH₄OH (final pH = 8-9), and applied to AG 1-X8 anion exchange columns (Biorad; 0.7 ml sediment volume/ column). Columns were equilibrated with 4 ml 2.5 mM NH₄OH, loaded, and washed with 4 ml 40 mM ammonium formate buffer (pH 5) to eliminate free inositol and glycerophosphoinositol. Total inositol phosphates were eluted with 4 ml 2 M ammonium formate buffer (pH 5), and radioactivity was determined by liquid scintillation counting in a β -counter.

The columns were regenerated by washing with 4 ml 2M ammonium formate buffer, 8 ml H_2O , and 4 ml 2.5 mM NH_4OH . Stimulatory concentration-response curves were analysed by non-linear regression curve fitting using the computer program "GraphPad Prism". pK_B-values were determined using the Schild-Gaddum-equation.

2.8. Measurement of intracellular Ca²⁺

5 x 10⁴ cells per well were splitted 24 h prior to the experiment on black 96-well plates (Costar). For dye loading, cells were incubated for 1 h at 37° C (in darkness) with 100 μ l dye solution/ well containing 5 μ M Fluo-4/ acetoxymethyl ester (Molecular Probes), 0.02 % Pluronic acid (Molecular Probes), 5 mM Probecenid (Sigma; freshly prepared), 20 mM Hepes pH 7.4, in cell culture medium (DMEM/ F-12 1:1, 10 % FBS). Cells were washed 2x with 125 μ l wash solution containing 2.5 mM Probecenid, 20 mM Hepes pH 7.4, in Hanks Balanced Salt Solution (HBSS; Gibco BRL; with 1.25 mM Ca²⁺) to remove extracellular dye, and 100 μ l wash solution per well were finally added. Cells were incubated about 30 min at room temperature (darkness) for intracellular enzymatic de-esterification of Fluo-4.

Intracellular calcium was measured using the FLIPRTM II system (Fluorometric Imaging Plate Reader; Molecular Devices, USA). Fluorescence excitation was yielded by 480 nm of an argon ion laser; emission was kinetically monitored at 515 nm for 5 min. Various $SRIF_{14}$ concentrations were automatically pipetted; 1 unit/ ml f.c. bovine thrombin (Sigma) was used as a positive control. Data were quantified subtracting the minimal from the maximal relative fluorescence units of each curve (well) using FLIPRTM II statistical software. Stimulatory concentration-response curves were analysed by non-linear regression curve fitting using the "GraphPad Prism" software.

2.9. Ligands

(1) BIM 23014 (lanreotide; somatuline; D-Nal-c[Cys-Tyr-D-Trp-Lys-Val-Cys]-Thr-NH₂),

(2) BIM 23030 (c[Mpr-Tyr-D-Trp-Lys-Val-Cys]-D-Phe-NH₂),

(3) BIM 23052 (D-Phe-Phe-Phe-D-Trp-Lys-Thr-Phe-Thr-NH₂),

(4) BIM 23056 (D-Phe-Phe-Tyr-D-Trp-Lys-Val-Phe-D-Nal-NH₂),

(5) CGP 23996 (c[Asu-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Tyr-Thr-Ser]),

(6) mouse/ rat CST₁₄ (cortistatin 14; Pro-c[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Ser-Ser-Cys]-Lys),

(7) [Tyr¹⁰]CST₁₄ (Pro-c[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Tyr-Ser-Ser-Cys]-Lys),

(8) human CST₁₇ (cortistatin 17; Asp-Arg-Met-Pro-c[Cys-Arg-Asp-Phe-Phe-Trp-Lys-

Thr-Phe-Ser-Cys]-Lys),

(9) cycloantagonist (SA; c[Aha-Phe-D-Trp-Lys-Thr(Bzl)]),

(10) L363,301 (c[Pro-Phe-D-Trp-Lys-Thr-Phe]),

(11) L362,855 (c[Aha-Phe-Trp-D-Trp-Lys-Thr-Phe]),

(12) octreotide (SMS 201-995; D-Phe-c[Cys-Phe-D-Trp-Lys-Thr-Cys]-Thr-OH),

(13) [Tyr³]octreotide (SMS 204-090; D-Phe-c[Cys-Tyr-D-Trp-Lys-Thr-Cys]-Thr-OH),

(14) RC160 (vapreotide; octastasin; D-Phe-c[Cys-Tyr-D-Trp-Lys-Val-Cys]-Trp-NH₂),

(15) seglitide (MK678; c[N-Met-Ala-Tyr-D-Trp-Lys-Val-Phe]),

(16) SRIF₁₄ (Ala-Gly-c[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys]-OH),

(17) SRIF₂₂ (Asp-Asn-Thr-Val-Thr-Ser-Lys-Pro-Leu-Asn-c[Cys-Met-Asn-Tyr-Phe-Trp-Lys-Ser-Arg-Thr-Ala-Cys]-OH),

(18) SRIF₂₅ (Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-c[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys]-OH);

(19) SRIF₂₈ (Ser-Ala-Asn-Ser-Asn-Pro-Ala-Met-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Glyc[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-Phe-Thr-Ser-Cys]-OH),

(20) LTT-SRIF₂₈([Leu⁸,D-Trp²²,Tyr²⁵]-SRIF₂₈; Ser-Ala-Asn-Ser-Asn-Pro-Ala-Leu-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-c[Cys-Lys-Asn-Phe-Phe-D-Trp-Lys-Thr-Tyr-Thr-Ser-Cys]-OH),

(21) [¹²⁵I]CGP 23996 (c[Lys-Asu-Phe-Phe-Trp-Lys-Thr-(¹²⁵I-Tyr)-Thr-Ser]),

(22) [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]Tyr¹⁰-CST (Pro-c[Cys-Lys-Asn-Phe-Phe-Trp-Lys-Thr-(¹²⁵I-Tyr)-Ser-Ser-Cys]-Lys),

(23) [¹²⁵I][Tyr³]octreotide (D-Phe-c[Cys-(¹²⁵I-Tyr)-D-Trp-Lys-Thr-Cys]-Thr-OH),

(24) [¹²⁵I]LTT-SRIF₂₈ ([Leu⁸,D-Trp²²,¹²⁵I-Tyr²⁵]SRIF₂₈, Ser-Ala-Asn-Ser-Asn-Pro-Ala-

Leu-Ala-Pro-Arg-Glu-Arg-Lys-Ala-Gly-c[Cys-Lys-Asn-Phe-Phe-D-Trp-Lys-Thr-(¹²⁵I-Tyr)-Thr-Ser-Cys]-OH).

Abbreviations: Asu = amino suberic acid; Aha = amino heptanoic acid; Mpr = 3mercaptopropionic acid; D-Nal = Naphthyl-D-Ala; Bzl = Benzylsubstituent. 5'-Guanylylimidodiphosphate (GppNHp) was from Sigma (St-Louis, Mo). BIM 23014, cycloantagonist SA, LTT-SRIF₂₈, SRIF₁₄, SRIF₂₅, and SRIF₂₈ were purchased from Bachem AG (Bubendorf, Switzerland), RC160 was purchased from Peninsula Laboratories (Heidelberg, Germany), CST₁₇ was kindly provided by Drs. JG. Sutcliffe and L. de Lecea (The Scripps Research Institute, La Jolla, CA) or synthesised at ANAWA AG (Wangen, Switzerland); CST₁₄ and [Tyr¹⁰]CST₁₄ were from ANAWA. Other ligands were synthesised at Novartis Pharma AG (Basel, Switzerland). [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, and [¹²⁵I][Tyr³]octreotide were custom synthesised from ANAWA AG (Wangen, Switzerland).

2.10. Northern blot analysis

Poly(A)⁺-RNA (brain, gut, liver, spleen, stomach) was prepared according to the manuals of Quiagen RNA extraction kits: 4 μ g Poly(A)⁺-RNA, and from brain an additional sample of 8 μ g Poly(A)⁺-RNA, were diluted 1:1 with loading buffer (20 % formaldehyde, 70 % deionisized formamide, 6 % glycerol, 0.5 % bromphenol blue, in 2x MOPS (= 3-[N-morpholino]propanesulfonic acid) buffer) (1x MOPS buffer: 200 mM MOPS, 50 mM NaAc pH 7.0, 10 mM EDTA pH 8.0, pH 7.0 with NaOH). Following 10 min denaturation at 55°C, the samples and the RNA marker (0.2- 9.5 kb) were loaded on a 1 % MOPS-agarose gel (1 % agarose in 1x MOPS buffer, 0.06 % ethidium bromide), and in 1x MOPS buffer separated at 70 V. The quality of the Poly(A)⁺-RNA was checked under UV-light: sharpeness of the 28S and 18S ribosomal RNA signals (in fish: 3.5 kb and 1.8 kb, respectively). The RNA was overnight blotted onto a nylon membrane (HybondTM-N, Amersham) in 20x SSC (3 M NaCl, 0.3 M Na₃-citrate) according to standard protocols (Sambrook et al., 1989), and the membrane was UV-crosslinked (120 mJ/ cm²; UV-Stratalinker, Stratagene).

The ³²P-DNA hybridization probe was obtained by specific PCR-amplification: a PCR reaction of 50 µl was carried out in a MicroAmp reaction tube in a GeneAmp PCR System 9600 (Perkin Elmer Cetus).

Final concentrations of the reaction components were 4 ng pcDNA3-fsst₃ plasmid DNA, 200 μ M each of dGTP, dCTP, dTTP, 1 μ M each of the fsst₃-specific oligonucleotides 5'-AGGTCCTAAACCGGCCAAG-3' and 5'-ATGAGCACCCCGGCGGCG-3' (206 bp product), 1x PCR-buffer (Stratagene; 1.5 mM MgCl₂), 10 μ Ci [α -³²P]-dATP and 5 units Taq 2000TM DNA polymerase (Stratagene). The PCR conditions were as follows: an initial denaturation step at 95°C for 7 min, during which the enzyme was mixed with other components (Hot Start), then 30 cycles consisting of 95°C for 30 s, 55°C for 30 s, and 72°C for 30 s. For final elongation, the reactions were held at 72°C for 3 min; an in parallel amplified product containing additional 200 μ M of dATP and no [α -³²P]-dATP was checked on a 1 % agarose gel stained with ethidium bromide. The hybridization probe was filter purified (Millipore; 0.025 μ m pore size).

Pre-hybridisation (> 2 h) and hybridisation (overnight) of the nylon membrane were carried out at 43°C in 50 % formamide, 50 mM Tris pH 7.5, 0.8 M NaCl, 1 % SDS, 0.2 % BSA, 0.2 % Ficoll 400, 0.2 % polyvinylpyrrolidone, and 100 µg/ml salmon sperm DNA. For hybridisation, 1.25 x 10⁶ dpm/ ml denaturated ³²P-DNA probe were added. The membrane was washed at 65°C three times for 20 min in 1 x SSC, 0.1 % SDS, and exposed to a X-OMATTM autoradiography film (Kodak). As a positive control for the hybridization probe different amounts of pcDNA3-fsst₃ plasmid DNA (10 ρ g- 1 ng) were pipetted onto a second membrane, denaturated and renatured (see RT-PCR protocol), cross-linked, and hybridized and washed in parallel. The oligonucleotides were purchased from Microsynth (Balgach, Switzerland).

2.11. Reverse transcriptase-polymerase chain reaction (RT-PCR)

 $Poly(A)^+$ -RNA (brain) and total RNA (fsst₃-expressing CCL39 cells) was prepared according to the manuals of Quiagen RNA extraction kits.

To eliminate potential contamination of the RNA with genomic DNA (since the fsst₃ receptor gene contains, like mammalian SRIF receptor genes, no introns) 0.5 μ g Poly(A)⁺-RNA from brain and 2 μ g total RNA from fsst₃ receptor-expressing CCL39 cells (positive control) were incubated for 30 min at 37°C with 0.5 units RQ1 RNase-free-DNase, 20 units rRNasin (Promega) in 25 μ l of 10 mM Tris-HCl pH 7.0, 10 mM MgCl₂, 1 mM DTT, 1 mM EDTA pH 8.0. After addition of 6 μ l DNase-Stopmix (50 mM EDTA pH 8.0, 1.5 M NaAc pH 7.0), phenol/ chloroform extraction and ethanol precipitation was performed.

The RNA was denaturated by heating for 5 min at 65°C and then reverse transcribed into first strand cDNA by using 500 ng Oligo(dT) primers (Gibco BRL) for Poly(A)⁺-RNA and 3 µg random hexamer primers (Gibco BRL) for total RNA, 20 units rRNasin and 200 units SuperscriptTM II reverse transcriptase (Gibco BRL) in 20 µl of 1x first strand buffer (Gibco BRL), 250 µM each of dATP, dGTP, dCTP, dTTP, and 10 mM DTT. The reactions were incubated 60 min at 37°C, followed by denaturation for 5 min at 95°C. 3 µl of the first strand cDNA reaction mixture were subjected to PCR amplification. As a control for digestion of genomic DNA, DNase-digested, but not reverse transcribed Poly(A)⁺-RNA (brain), was subjected to PCR in parallel. PCR reactions of 50 µl were carried out in MicroAmp reaction tubes in a GeneAmp PCR System 9600 (Perkin Elmer Cetus). Final concentrations of the reaction components were 200 µM each of dATP, dGTP, dCTP, dTTP, 1 µM each of the fsst₃-specific oligonucleotides 5'-AGGTCCTAAACCGGCCAAG-3' 5`and ACGTGACGTTCACGCTTTG-3' (569 bp product), 1x PCR-buffer (Stratagene; 1.5 mM MgCl₂) and 5 units Taq 2000TM DNA polymerase (Stratagene). The PCR conditions were as follows: an initial denaturation step at 95°C for 2 min, during which the enzyme was mixed with other components (Hot Start), then 40 cycles consisting of 95°C for 20 s, 62°C for 30 s, and 72°C for 90 sec. For final elongation, the reactions were held at 72°C for 7 min. The amplified products were analysed on a 1 % agarose gel stained with ethidium bromide using φ X174 RF DNA/Hae III fragments (Gibco BRL) as a molecular weight marker.

Quality and amount of the cDNA was analysed by specific amplification of β -actin with the primers 5'-TCTCGCACCACCACCTTCTACAA-3' and 5'-GTCTCATGGATACCGCAGGACT-3', which were derived from the β -actin sequence of the teleostean fish *Oryzias latipes*.

To confirm fsst₃-specific amplification, the agarose gel was analysed by Southern Blot. After denaturation (0.5 N NaOH, 1.5 M NaCl) and neutralisation (1.5 N NaOH, 0.5 M Tris pH 7.4) of the gel, the DNA was blotted in 20 x SSC onto a HybondTM-N membrane (Amersham) according to standard protocols (Sambrook et al., 1989), and the membrane was UV-crosslinked with 120 mJ/ cm². The ³²P-DNA probe (206 bp) was obtained by specific PCR-amplification of pcDNA3-fsst₃ plasmid DNA with the 5'-5'-AGGTCCTAAACCGGCCAAG-3' oligonucleotides and ATGAGCACCCCGGCGGCG-3' and filter purification (Millipore; 0.025 µm pore size). Pre-hybridisation and hybridisation were carried out at 43°C in 50 % formamide, 50 mM Tris pH 7.5, 0.8 M NaCl, 1 % SDS, 0.2 % BSA, 0.2 % Ficoll 400, 0.2 % polyvinylpyrrolidone, and 100 μ g/ ml salmon sperm DNA. For hybridisation, 1.25 x 10⁶ dpm/ ml denaturated ³²P-DNA probe were added. The membrane was washed at 65°C three times for 20 min in 1 x SSC, 0.1 % SDS, and exposed to a X-OMAT $^{\rm TM}$ autoradiography film (Kodak). All oligonucleotides were purchased from Microsynth (Balgach, Switzerland).

Chapter 3

[¹²⁵I]Tyr¹⁰-cortistatin₁₄ labels all five somatostatin receptors

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3.1. Abstract

The recently cloned rat preprocortistatin, which shows homology to the preprosomatostatin peptide, is thought to be enzymatically cleaved to cortistatin₁₄ (CST_{14}) similarly to somatostatin₁₄ $(SRIF_{14})$. High structural similarity of cortistatin₁₄ compared to SRIF₁₄ suggested binding properties to somatostatin receptors similar to SRIF₁₄. In the present study, we expressed stably the five human somatostatin receptor subtypes (hsst,-hssts) in CCL39 cells (Chinese hamster lung fibroblast cells). The receptors were labelled with an iodinated analogue of CST_{14} ([¹²⁵I]Tyr¹⁰-cortistatin₁₄, ¹²⁵I]Tyr¹⁰-CST) to establish the pharmacological profile of hsst₁-hsst₅ sites labelled with [¹²⁵I]Tyr¹⁰-CST. In parallel, [Leu⁸,D-Trp²²,¹²⁵I-Tyr²⁵]-SRIF₂₈ ([¹²⁵I]LTT-SRIF₂₈) was used as a control at the five recombinant SRIF receptors stably expressed in CCL39 cells. High affinity [¹²⁵I]Tyr¹⁰-CST binding could be demonstrated to all five recombinant somatostatin receptor subtypes. The $pK_{\rm d}$ (-log mol/l) and $B_{\rm max}\mbox{-values (fmol/mg)}$ for $hsst_{1-5}$ receptors were: 10.02 ± 0.04 , 220 ± 30 ; 9.45 ± 0.09 , 340 ± 70 ; 10.06 ± 0.11 , 340 \pm 50; 9.67 \pm 0.14, 340 \pm 110 and 10.33 \pm 0.03, 5630 \pm 330, respectively. The pharmacological profiles determined with [125I]Tyr10-CST and [125I]LTT-SRIF28 were very similar at every receptor studied. These data suggest that cortistatin and somatostatin have similar high affinity for SRIF receptors. None of the receptors showed marked selectivity for either CST_{14} / CST_{17} or the somatostatins. In conclusion, the data show that cortistatin and somatostatin have very similar high affinity to all five recombinant somatostatin receptors. It remains to be seen whether there are specific receptors which bind only somatostatins or cortistatins.

3.2. Results

 $[^{125}I]Tyr^{10}$ -cortistatin₁₄ ($[^{125}I]Tyr^{10}$ -CST) specifically bound to the human somatostatin receptors sst₁₋₅ and was used as a radioligand to determine the pharmacological profile in CCL39 cells. Saturation experiments (table 1) revealed high affinity and saturable binding of $[^{125}I]Tyr^{10}$ -CST to hsst₁₋₅ receptors similarly to $[^{125}I]LTT$ -SRIF₂₈. No specific binding and therefore no presence of endogenous SRIF receptors was detectable in nontransfected CCL39 cells (data not shown). RT-PCR revealed expression of hsst₁₋₅ in the stably transfected cells, but not in non transfected CCL39 cells (data not shown). The saturation isotherms were apparently monophasic suggesting a homogenous population of receptor sites (figure 1). The B_{max}-values obtained at each receptor were roughly comparable between the two radioligands. The non specific binding of $[^{125}I]Tyr^{10}$ -CST was usually higher than that of $[^{125}I]LTT$ -SRIF₂₈, except for sst₅ receptors which however showed higher expression levels than the other SRIF receptors.

Table 1: Comparison of saturation data obtained with $[^{125}I]Tyr^{10}$ -CST and $[^{125}I]LTT$ -SRIF₂₈ at human sst_{1.5} receptors

	[¹²⁵ I] LTT	-SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ -CST		
	pK _d	B _{max} [fmol/mg]	pK _d	B _{max} [fmol/mg]	
CCL39/hsst ₁	9.96 ± 0.00	470 ± 30	10.02 ± 0.04	220 ± 30	
CCL39/hsst ₂	9.89 ± 0.04	370 ± 60	9.45 ± 0.09	340 ± 70	
CCL39/hsst ₃	10.28 ± 0.06	560 ± 60	10.06 ± 0.11	340 ± 50	
CCL39/hsst ₄	9.64 ± 0.03	440 ± 50	9.67 ± 0.14	340 ± 110	
CCL39/hsst ₅	10.48 ± 0.04	6950 ± 220	10.33 ± 0.03	5630 ± 330	

The data represent the mean of pK_d -values (-log M) \pm standard error (SEM) of three determinations.

Figure 1: Saturation curves using $[^{125}I]Tyr^{10}$ -CST (left column) and $[^{125}I]LTT$ -SRIF₂₈ (right column) to membranes prepared from CCL39 cells stably expressing human sst₁₋₅ receptors.



Crude membrane preparations from sst_{1-5} receptor expressing cells were incubated with increasing concentrations of $[1251]Tyr^{10}$ -CST or [1251]LTT-SRIF₂₈, and assayed for receptor binding. The plots depict specific (\bullet) and non-specific binding (\blacksquare) expressed as amount of radioligand bound (fmol/mg) versus free radioligand concentration (pM). The figures represent one representative example of 3 different experiments.

SRIF₁₄, SRIF₂₈, CST₁₄, CST₁₇ and the unlabelled Tyr¹⁰-CST bound with K_d 's in the nMrange to sst_{1-5} receptors. CST_{17} which is derived from the human prepropeptide, showed slightly higher affinity at the five human receptors compared to CST₁₄ which is derived from the rat prepropeptide. The pharmacological profile of human sst₁₋₅ receptors labelled with [¹²⁵I]Tyr¹⁰-CST and [¹²⁵I]LTT-SRIF₂₈ were compared (table 2 & 3, figure 2). The short cyclic SRIF-analogues seglitide, octreotide, RC160 and BIM 23014 bound all with high affinity (< 1 nM) to the sst, receptor, but displayed very low affinity to sst_1 and sst₄ receptors. Seglitide showed high affinity for the sst₅ receptor whereas other peptides of this group displayed intermediate affinity. The rank order of potency of compounds for sst₁ sites labelled with [¹²⁵I]Tyr¹⁰-CST: CST₁₇ > SRIF₂₈ \approx SRIF₁₄ \approx > BIM $23052 > CGP 23996 > CST_{14} >> octreotide >> seglitide, was similar to that at sst_4$ sites: $CST_{17} > CST_{14} = CGP \ 23996 \approx SRIF_{28} \approx SRIF_{14} \approx BIM \ 23052 >> octreotide >$ seglitide. On the other hand, the affinity rank orders for the other three receptors were typical for the SRIF₁ receptor family, i.e. sst₂: SRIF₂₈ \approx SRIF₁₄ > seglitide = RC160 > $CST_{17} \approx BIM \ 23014 \approx octreotide > L362,855 > CST_{14} = BIM \ 23052 = L363,301; \ sst_3:$ $\mathrm{SRIF}_{28} \approx \, \mathrm{SRIF}_{14} \approx \, \mathrm{BIM} \,\, 23052 \approx \mathrm{CST}_{17} > \mathrm{CGP} \,\, 23996 > \mathrm{CST}_{14} > \mathrm{octreotide} > \mathrm{L362}, 855$ > BIM 23014, and sst₅: CST₁₇ > SRIF₂₈ \approx SRIF₁₄ \approx seglitide > CST₁₄ > octreotide = BIM 23014 > BIM 23030.

The profiles defined using [¹²⁵I]Tyr¹⁰-CST and [¹²⁵I]LTT-SRIF₂₈ were comparable independently of the receptor type examined. The sst₃ receptor though, may represent an exception, since some of the compounds (seglitide, octreotide BIM 23052, cycloantagonist) showed an approximately 10 fold higher affinity for [¹²⁵I]Tyr¹⁰-CST- as compared to [¹²⁵I]LTT-SRIF₂₈-labelled sites. The receptor profiles determined with the two radioligands showed high correlation coefficients (see figure 3) at each of the five SRIF receptor subtypes (sst₁: r = 0.981; sst₂: r =0.985; sst₃: 0.956; sst₄: 0.985; sst₅: 0.968).

Table 2: Comparison of the pharmacological profiles of human sst₁ and sst₄ receptors labelled with [¹²⁵I]Tyr¹⁰-CST or [¹²⁵I]LTT-SRIF₂₈. The affinity values are expressed as $pK_d \pm SEM$ of 3-4 independent experiments

	CCL3	9/hsst ₁	$CCL39/hsst_4$		
	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ - CST	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ - CST	
SRIF ₁₄	9.12 ± 0.05	9.08 ± 0.07	8.91 ± 0.15	8.39 ± 0.28	
SRIF ₂₈	9.22 ± 0.02	9.26 ± 0.07	9.08 ± 0.12	8.44 ± 0.30	
seglitide	4.50 ± 0.04	4.32 ± 0.06	5.37 ± 0.08	5.11 ± 0.07	
CGP 23996	8.33 ± 0.06	8.31 ± 0.04	8.77 ± 0.03	8.67 ± 0.14	
octreotide	6.65 ± 0.05	6.41 ± 0.04	6.40 ± 0.09	5.76 ± 0.08	
L362,855	6.25 ± 0.07	6.30 ± 0.07	7.31 ± 0.07	6.76 ± 0.32	
L363,301	5.32 ± 0.08	5.38 ± 0.15	5.61 ± 0.03	5.06 ± 0.06	
RC160	7.08 ± 0.08	6.96 ± 0.24	7.25 ± 0.05	6.56 ± 0.44	
BIM 23030	5.06 ± 0.04	4.85 ± 0.02	5.98 ± 0.04	5.56 ± 0.14	
BIM 23014	6.75 ± 0.04	6.66 ± 0.18	6.64 ± 0.07	6.25 ± 0.28	
BIM 23056	6.61 ± 0.10	6.46 ± 0.07	7.17 ± 0.10	6.47 ± 0.35	
BIM 23052	8.37 ± 0.04	8.62 ± 0.05	8.63 ± 0.04	8.20 ± 0.11	
cycloantagonist	7.02 ± 0.00	6.80 ± 0.17	6.48 ± 0.13	6.07 ± 0.26	
Tyr ¹⁰ -CST	8.56 ± 0.08	9.04 ± 0.13	8.44 ± 0.06	8.17 ± 0.09	
CST ₁₄	8.76 ± 0.06	7.74 ± 0.09	8.76 ± 0.02	8.75 ± 0.14	
CST ₁₇	9.61 ± 0.04	9.61 ± 0.17	9.24 ± 0.02	9.55 ± 0.03	

3.3. Discussion

The putative neuropeptides CST_{14} and CST_{17} bound to all five known human somatostatin receptor subtypes with high affinity. There was no preferential affinity of either of the cortistatins to any of the receptors, although the putative human peptide CST_{17} showed somewhat higher affinity than its rat equivalent CST_{14} .

Table 3: Comparison of the pharmacological profiles of human sst₂, sst₅ and sst₃ receptors labelled with [¹²⁵I]Tyr¹⁰-CST or [¹²⁵I]LTT-SRIF₂₈. The affinity values are expressed as $pK_d \pm SEM$ of 3-4 independent experiments

	CCL39/hsst ₂		CCL3	CCL39/hsst ₅		CCL39/hsst ₃	
	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ - CST	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ - CST	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ - CST	
SRIF ₁₄	10.00 ± 0.01	10.06 ± 0.07	9.53 ± 0.13	9.01 ± 0.24	9.54 ± 0.05	9.67 ± 0.07	
SRIF ₂₈	9.92 ± 0.03	10.16 ± 0.11	9.39 ± 0.22	9.18 ± 0.19	9.65 ± 0.04	9.80 ± 0.08	
seglitide	9.96 ± 0.02	9.62 ± 0.17	8.70 ± 0.26	9.14 ± 0.30	6.88 ± 0.08	7.89 ± 0.25	
CGP 23996	8.58 ± 0.07	8.94 ± 0.02	6.59 ± 0.41	6.67 ± 0.24	8.82 ± 0.05	9.28 ± 0.19	
octreotide	9.19 ± 0.03	9.11 ± 0.14	7.17 ± 0.30	7.31 ± 0.18	7.88 ± 0.04	8.60 ± 0.16	
L362,855	8.36 ± 0.05	8.79 ± 0.19	7.17 ± 0.30	7.17 ± 0.12	7.62 ± 0.23	8.25 ± 0.06	
L363,301	8.39 ± 0.11	8.47 ± 0.18	7.69 ± 0.13	7.17 ± 0.15	6.34 ± 0.06	6.83 ± 0.08	
RC160	9.35 ± 0.09	9.60 ± 0.02	7.51 ± 0.06	7.27 ± 0.11	7.37 ± 0.15	7.91 ± 0.03	
BIM 23030	7.77 ± 0.07	7.66 ± 0.07	6.02 ± 0.09	5.56 ± 0.17	7.17 ± 0.08	7.85 ± 0.11	
BIM 23014	9.27 ± 0.06	9.26 ± 0.07	7.76 ± 0.13	7.38 ± 0.19	7.86 ± 0.41	8.02 ± 0.14	
BIM 23056	6.33 ± 0.10	6.23 ± 0.12	7.17 ± 0.05	6.68 ± 0.05	6.90 ± 0.04	7.08 ± 0.11	
BIM 23052	8.30 ± 0.14	8.50 ± 0.32	7.92 ± 0.19	7.45 ± 0.24	8.42 ± 0.12	9.55 ± 0.12	
cycloantagonist	5.40 ± 0.06	5.74 ± 0.05	6.38 ± 0.23	6.02 ± 0.11	6.23 ± 0.03	7.08 ± 0.04	
Tyr ¹⁰ -CST	8.77 ± 0.09	8.91 ± 0.21	8.67 ± 0.24	8.06 ± 0.40	8.70 ± 0.18	8.90 ± 0.08	
CST ₁₄	8.75±0.20	8.54±0.44	8.71±0.02	8.40±0.04	9.06±0.12	9.13±0.09	
CST ₁₇	9.07±0.01	9.29±0.13	9.54±0.10	9.37±0.09	9.43±0.06	9.52±0.10	

When $[^{125}I]Tyr^{10}$ -CST was used as a radioligand, the data compared well with $[^{125}I]LTT$ -SRIF₂₈ binding, as indicated by the high correlation observed at each of the five SRIF receptors. Some differences could be observed at the sst₃ receptor for a number of compounds, but these may well lie within the experimental variation, although the somatostatins and cortistatins displayed no such differences. The pharmacological profile established at human recombinant receptors in CCL39 cells reveals some discrepancy to literature data. The cyclic heptapeptide L362,855 reported to be sst₅-selective (O'Carroll et al., 1994; Raynor et al., 1993a, 1993b; Williams et al., 1997) shows higher affinity to sst, receptors in CCL39 cells. Similarly, the linear octapeptide BIM 23052 claimed to be sst₅-selective (Raynor et al., 1993a, 1993b), shows no selectivity in the present study. Further, we have not been able to reproduce the very high affinity and selectivity for sst, receptors which has been reported for BIM 23056. To the contrary, it would appear, that this compound is non-selective and has only intermediate affinity for all five SRIF receptors. CST₁₄ and CST₁₇ bound with similar high affinity to all five receptor subtypes in CCL39 cells, as it was found in GH₄ pituitary cells or at recombinant receptors (De Lecea et al., 1996; 1997a; Fukusumi et al., 1997). According to Fukusumi and colleagues, CST₁₇ and CST₁₄, were roughly equipotent and displayed about ten-fold lower affinity for the human sst, receptor compared to the other receptors. Discrepancies may relate to different radioligands used: [¹²⁵I]-Tyr¹¹-SRIF₁₄ (Fukusumi et al., 1997; De Lecea et al., 1996) and [¹²⁵I]CGP 23996 (Raynor et al., 1993a). Some variation was also found when comparing with data obtained with [125I]LTT-SRIF₂₈ (Patel and Srikant, 1994). On the other hand, the use of different cell systems may also provide some grounds for thought. The expression of the recombinant SRIF receptors is often performed in CHO or COS cells.

Post-transcriptional and post-translational mechanisms, like receptor phosphorylation or glycosylation may vary in different cell systems and hence, could affect the conformation of a receptor-ligand complex. Finally, distinct cell lines may express different sets of G-proteins, which are also suggested to influence the agonist binding properties of receptors (Lefkowitz et al., 1993), since SRIF receptor binding is usually performed with agonist radioligands. For instance, Fukusumi et al. (1997) used CHO cells, where apparently the sst₁ receptor does not couple to adenylate cyclase, whereas it does in CCL39 cells (data not shown). However, the present data were compared with those reported for native sst₁, sst₂ and sst₄ receptors described in the human cerebral cortex and in rat lung for the latter (Piwko et al., 1997) and we obtained high correlation coefficients (r = 0.93, 0.96 and 0.98, respectively), suggesting that there is indeed little difference between the receptors expressed recombinantly in CCL39 cells and the native ones.



Figure 2: Competitive radioligand binding assays performed in membranes prepared from CCL39 cells expressing human $sst_{1.5}$ receptors.

Crude membrane preparations from sst_{1-5} receptor transfected cells were incubated with $[125I]Tyr^{10}$ -CST or [125I]LTT-SRIF₂₈ and the indicated concentrations of SRIF₁₄ (\blacksquare), CST₁₄ (\bullet), octreotide (\blacktriangle), seglitide (\bigtriangledown) and BIM 23030 (\blacklozenge). Data are expressed as percentage of specific binding. The data points represent one representative example of at least 3 different experiments.

Figure 3: Correlation between $[^{125}I]Tyr^{10}$ -CST and $[^{125}I]LTT$ -SRIF₂₈ binding at human recombinant sst₁₋₅ receptors expressed in CCL39 cells



The existence of the mature rat peptide CST_{14} has not been documented so far in vivo, although a cortistatin prepropeptide was cloned not only from rat, but also from mouse and human. By in situ hybridisation, the prepropeptide mRNA has been localised in the cerebral cortex and hippocampus of rat (De Lecea et al., 1996) and mouse (De Lecea et al., 1997b) and in the caudate nucleus and spinal cord of human (De Lecea et al. 1997a; Fukusumi et al., 1997). The homology of preprocortistatin to preprosomatostatin suggests analogous cleavage to mature peptides. CST_{14} affects neuronal electrical activity and sleep suggesting that the mature peptide is functional and probably different from somatostatin in its actions (De Lecea et al., 1996). Analogous to the rat peptide, the human preprocortistatin may be cleaved to CST_{17} , which can modulate sleep activity as well (Fukusumi et al., 1997).

The present study shows a close pharmacological similarity between CST_{14} / CST_{17} and the somatostatins. Indeed, CST_{14} has been shown to increase potassium conductance similarly to $SRIF_{14}$ in rat locus coeruleus (Connor et al., 1997). CST_{14} and CST_{17} have been reported to have affinities and activities comparable to those of somatostatin at recombinant human SRIF receptor binding and/ or adenylate cyclase activity (Fukusumi et al., 1997). CST_{14} has also been reported to impair post-training memory in a foot shock avoidance test in mice (Flood et al., 1997). However, CST_{14} has effects on neuronal depression, sleep modulation and slow wave sleep which do not parallel those of somatostatin (De Lecea et al., 1996).

Administration of CST_{17} (icv) to rats induced flattening of cortical and hippocampal electroencephalograms (Fukusumi et al., 1997). As some functional responses of CST_{14} and somatostatin can be differentiated (De Lecea et al., 1996), the existence of yet to be discovered cortistatin receptors may provide a basis for such differences, since the currently known "SRIF" receptors do hardly distinguish between SRIF and cortistatin.

4.1. Abstract

Human somatostatin (somatotropin release inhibiting factor = SRIF) receptor subtypes sst, and sst, were stably expressed in Chinese hamster lung fibroblast (CCL39) cells. $[^{125}\Pi[Tyr^3]$ octreotide labelled with high affinity and in a saturable manner both sst₂ (pK_d $= 9.89 \pm 0.02$, $B_{max} = 210 \pm 10$ fmol/mg, n = 3) and sst₅ sites (pK_d = 9.64 \pm 0.04, B_{max} = 0.02 920 ± 170 fmol/ mg, n = 3). The pharmacological profile of sst₂ sites established in CCL39 cells using SRIF and various peptide analogues was very similar to that described previously in CHO cells and in human cortex: $SRIF_{14} = SRIF_{28} \ge seglitide >$ BIM $23014 = RC160 > octreotide > CGP 23996 \ge L362,855 > BIM 23052 > L361,301$ = cortistatin₁₄ > BIM 23030 > BIM 23056 > cycloantagonist SA. However, peptides classically perceived as sst, receptor selective (e.g. seglitide, octreotide, vapreotide) showed also high affinity for human sst, receptors labelled with [1251][Tyr3]octreotide: $SRIF_{28} > seglitide > SRIF_{14} > L361,301 = octreotide > cortistatin_{14} = BIM 23014 = BIM$ 23052 > L362,855 = RC160 > CGP 23996 > BIM 23056 > cycloantagonist SA > BIM 23030. Further radioligand binding studies were performed with [Leu⁸,D-Trp²²,¹²⁵I-Tyr²⁵]SRIF₂₈ ([¹²⁵I]LTT- SRIF₂₈) and [¹²⁵I]CGP 23996. At sst₂ receptors, B_{max}-values determined with [¹²⁵I][Tyr³]octreotide, [¹²⁵I]LTT- SRIF₂₈ and [¹²⁵I]CGP 23996 were in the same range (180- 370 fmol/ mg). 5'-guanylylimidodiphosphate (GppNHp) displaced all three radioligands to the same extent (85 %) and the pharmacological profiles were superimposable. By contrast, at sst, receptors B_{max}-values ranged were very different: [¹²⁵I][Tyr³]octreotide (920 fmol/mg), [¹²⁵I]CGP 23996 (3530 fmol/ mg) and [¹²⁵I]LTT-SRIF₂₈ (6950 fmol/ mg). GppNHp affected [¹²⁵I][Tyr³]octreotide more than [¹²⁵I]CGP 23996 binding, whereas [125I]LTT-SRIF₂₈ was much less affected. In addition, the affinity values determined in competition experiments at sst₅ receptors, varied markedly; whereas SRIF₁₄, cortistatin₁₄ and SRIF₂₈ showed 2, 4 and 8 fold differences in affinity at sst₅ receptors labelled with [¹²⁵I][Tyr³]octreotide and [¹²⁵I]LTT-SRIF₂₈ compounds such as RC 160, L363,301, L362,855, octreotide or CGP 23996 showed between 42 and 123 fold lower affinity when sst₅ sites were labelled with [¹²⁵I]LTT-SRIF₂₈. The present data suggest caution to be used when comparing affinity profiles determined in binding studies using different radioligands.

In addition, the present results suggest that effects produced by octreotide and related short chain SRIF analogues on hormone release, modulation of tumour growth and central effects may be mediated by either sst_2 and/or sst_5 receptors.

4.2. Results

[¹²⁵I][Tyr³]octreotide showed high specific binding to the human somatostatin receptor subtypes sst₂ and sst₅, non-specific binding was comparatively low. Saturation experiments performed with [¹²⁵I][Tyr³]octreotide suggested labelling of a single population of binding sites (figure 1) in CCL39 cells expressing human sst₂ (pK_d = 9.89 \pm 0.02, B_{max} = 210 \pm 10 fmol/ mg, n = 3) and sst₅ receptors (pK_d = 9.64 \pm 0.04, B_{max} = 920 \pm 170 fmol/ mg, n = 3). No specific binding, i.e. no endogenous SRIF receptors could be detected in non-transfected CCL39 cells (data not shown). RT-PCR revealed only expression of either hsst₂ or hsst₅ in the stably transfected cells, but not in non transfected CCL39 cells (data not shown).

[¹²⁵I][Tyr³]octreotide was used to determine the affinity of SRIF and a range of SRIFanalogues in competition studies in CCL39 cells expressing hsst₂ or hsst₅ receptors (table 1; figures 2 + 3); in addition, hsst₂ receptor binding data reported previously (Piwko et al., 1997) obtained in CHO cells and human cerebral cortex are also listed (see table 3). The rank order of potency of [¹²⁵I][Tyr³]octreotide labelled hsst₂ sites was very similar in human cortex and both CHO and CCL39 cells: SRIF₁₄ = SRIF₂₈ > seglitide > BIM 23014 = RC160 > octreotide > [Tyr¹⁰]cortistatin > CGP 23996 > L362,855 > BIM 23052 > L361,301 = cortistatin₁₄ > BIM 23030 > BIM 23056 > cycloantagonist. At hsst₅ sites, [¹²⁵I][Tyr³]octreotide defined following rank order of affinity: SRIF₂₈ > seglitide > SRIF₁₄ > [Tyr¹⁰]cortistatin = [Leu⁸,D-Trp²²,Tyr²⁵]SRIF₂₈ > L361,301 > octreotide > cortistatin₁₄ = BIM 23052 = BIM 23014 > L362,855 = RC160 > CGP 23996 > [Tyr³]octreotide > BIM 23056 = cycloantagonist > BIM 23030. As expected, the sst₅ receptor showed higher affinity for SRIF₂₈ than SRIF₁₄. The short cyclic SRIF-analogues seglitide, octreotide, RC160 and BIM 23014 bound all with high affinity (between 0.1 and 1 nM) to both receptor subtypes.

Figure 1: Saturation curves of $[^{125}I][Tyr^3]$ octreotide binding to membranes prepared from CCL39 cells stably expressing human sst₂ or sst₅ receptors.



Crude membrane preparations from sst₂ and sst₅ expressing cells (6 μ g or 2 μ g per assay, respectively) were incubated with increasing concentrations of [¹²⁵I][Tyr³]octreotide and assayed for receptor binding activity. The plots depict specific (\bullet) and non-specific binding (\blacksquare) expressed as amount of radioligand bound (cpm/ assay) versus free radioligand concentration (pM). The figure shows one representative example of 3 different experiments.

There was no evidence from competition experiments that two classes of sites fitted the data better than a single class (figure 3). Altogether, the correlation coefficient between both receptor subtypes as labelled with [125 I][Tyr 3]octreotide (see table 1) is r² = 0.536 (data not shown).

Since $[^{125}I][Tyr^3]$ octreotide binding was "atypical", i.e. a number of ligands displayed very similar affinities for both sst₂ and sst₅ receptors, further radioligand binding studies were performed with $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I]CGP$ 23996 at both sst₂ and sst₅ receptors expressing CCL39 cells (see table 2). $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I]CGP$ 23996 showed high affinity and saturable binding for both sst₂ and sst₅ receptors. Saturation experiments were compatible with the presence of a homogeneous population of recognition sites. At sst₂ receptors, B_{max}-values determined with $[^{125}I][Tyr^3]$ octreotide, $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I]CGP$ 23996 were in the same range (180- 370 fmol/ mg).

	CCL39/hsst ₂	CCL39/hsst ₅
SRIF ₂₈	9.99 ± 0.08	10.30 ± 0.25
seglitide	9.81 ± 0.13	10.18 ± 0.22
SRIF ₁₄	10.01 ± 0.04	9.87 ± 0.24
[Tyr ¹⁰]cortistatin	9.00 ± 0.09	9.65 ± 0.22
L361,301	8.39 ± 0.08	9.51 ± 0.14
octreotide	9.10 ± 0.07	9.48 ± 0.11
cortistatin ₁₄	8.35 ± 0.11	9.34 ± 0.23
BIM 23014	9.55 ± 0.03	9.31 ± 0.10
BIM 23052	8.55 ± 0.01	9.28 ± 0.35
L362,855	8.79 ± 0.06	9.17 ± 0.10
RC160	9.50 ± 0.16	9.13 ± 0.35
CGP 23996	8.95 ± 0.07	8.68 ± 0.20
BIM 23056	6.38 ± 0.11	8.32 ± 0.17
cycloantagonist SA	5.77 ± 0.05	8.25 ± 0.17
BIM 23030	7.94 ± 0.22	7.45 ± 0.18

Table 1: Comparison of affinities of SRIF and various SRIF-analogues for human sst_2 and sst_5 receptors labelled with [^{125}I][Tyr 3]octreotide

The data represent the mean of pK_d -values (-log M) \pm standard error of at least three determinations.



Crude membrane preparations from sst₂ and sst₅ transfected cells (6 µg or 2µg per assay, respectively) were incubated with $[^{125}I]$ [Tyr³]octreotide and the indicated concentrations of SRIF₁₄ (**I**), SRIF₂₈ (**•**), seglitide (**A**), octreotide (**V**) and BIM 23056 (**•**) and cortistatin₁₄ (+). Data are expressed as percentage of specific binding. The figure shows one representative example of at least 3 different experiments.

There were however marked differences in B_{max} -values at sst₅ receptors (see table 2): [¹²⁵I][Tyr³]octreotide (920 fmol/mg), [¹²⁵I]CGP 23996 (3530 fmol/ mg) and [¹²⁵I]LTT-SRIF₂₈ (6950 fmol/ mg). In addition, whereas the affinities of the various ligands for sst₂ sites revealed little differences if any (see table 3 and top of figure 4), there were some notable discrepancies in affinity values at the sst₅ receptors, which appeared to be radioligand dependent (see table 4 and bottom of figure 4). These differences are illustrated in figure 4: it can be seen in the top that the competition curves of SRIF₁₄ or the "cycloantagonist" at sst₂ receptors are superimposable whichever radioligand is used. At sst₅ receptors, the competition curves obtained with SRIF₁₄ show little variations, whereas those of the cycloantagonist are shifted by a factor 10 from one radioligand to the other. Finally, the effects of GppNHp, a non-hydrolysable GTP analogue, were investigated on the binding of the three radioligands at both sst₂ and sst₅ receptors. GppNHp displaced all three radioligands to the same extent (85 %) and similar apparent potency at sst₂ receptors (figure 5), whereas again the effects on sst₅ receptors were radioligand dependent. Thus, the binding of $[^{125}I][Tyr^3]$ octreotide was similarly displaced at sst₂ and sst₅ receptors, whereas $[^{125}I]CGP$ 23996 and particularly $[^{125}I]LTT$ -SRIF₂₈ binding were less sensitive to the guanine nucleotide analogue.

Figure 3: Competitive displacement by $SRIF_{28}$ and BIM 23056 of radioligand binding at human sst₅ receptors.



Crude membrane preparations from human sst5 transfected cells (2 µg per assay) were incubated with $[125I][Tyr^3]$ octreotide and 12 concentrations of SRIF₂₈ (\blacksquare) or BIM 23056 (\bullet). Data are expressed as percentage of specific binding. The figure shows one representative example of at least 3 different experiments.

4.3. Discussion

Octreotide (SMS 201-995, Sandostatin®) is currently used for treatment of acromegaly, various gastro-intestinal disorders and cancer in the gastroenteropancreatic system. In addition, since a number of tumours respond to octreotide treatment, a radiolabelled analogue (octreoscan, Penteotride®) is used to visualise SRIF receptor bearing tumours. Octreotide was instrumental in the definition of SRIF receptor subtypes, when Reubi and colleagues (Reubi, 1984; 1985; Reubi and Maurer, 1986) were able to differentiate octreotide-sensitive SRIF binding sites from those which are not sensitive to octreotide, the former were called SS-1 and the latter SS-2. Other ligands were used, such as [¹²⁵I]MK 678 and [¹²⁵I]CGP 23996 which according to Reisine and colleagues were labelling what was called SRIF-1 and SRIF-2 sites (Raynor et al., 1992) and a number of SRIF₁₄ and SRIF₂₈ radiolabelled analogues.

	sst ₂ re	ceptors	sst ₅ receptors		
radioligand	B _{max}	pK _d	B_{max}	pK _d	
[¹²⁵ I][Tyr ³]octreotide	210 ± 10	9.89 ± 0.02	920 ± 170	9.64 ± 0.04	
[¹²⁵ I]CGP 23996	180 ± 20	9.76 ± 0.06	3530 ± 50	9.52 ± 0.08	
[¹²⁵ I]LTT-SRIF ₂₈	370 ± 60	9.89 ± 0.04	6950 ± 220	10.48 ± 0.04	

Table 2: Results of saturation experiments performed with different radioligands at human sst, and sst₅ receptors expressed in CCL39 cells

The data are expressed as B_{max} (fmol/ mg) and pK_d-values (-log mol/ l) ± SEM of at least three experiments. The data represent the mean of pK_d-values (-log M) ± standard error of at least three determinations.

The situation became more complex in 1992 when five SRIF receptor were cloned, but at least it was then convincingly demonstrated that SRIF receptor subtypes exist (see Bell and Reisine, 1993; Hoyer et al., 1995a). It was then established that SRIF analogues e.g. [125 I][Tyr¹¹]SRIF₁₄ or [125 I]LTT-SRIF₂₈ labelled all subtypes. More surprisingly, it was found that [125 I]CGP 23996 also labelled all receptor subtypes (Raynor et al., 1993a, 1993b). By contrast it seemed that [125 I]MK 678 or [125 I][Tyr³]octreotide would only label the currently designated sst₂ receptor (Kluxen et al., 1992; Raynor et al., 1993a). We have investigated that matter further (Schoeffter et al., 1995) and shown that in rat brain and recombinant cells the populations of sites labelled with these two ligands were 1) superimposable with respect to distribution, 2) had close to identical pharmacological profiles in native tissue (e.g. rat brain or human brain, Piwko et al., 1997), 3) that this profile was identical with that of the recombinant sst₂ receptor and 4) that the distribution of sites labelled in the rat or human brain was comparable to that of sst₂ receptor mRNA. Therefore, it was felt adequate to conclude that [125 I][Tyr³]octreotide and [125 I]MK 678 labelled sites represent sst₂ receptors.

radioligand or tissue	[¹²⁵ I][Tyr ³]- octreotide	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]CGP 23996	human cortex	CHO cells hsst ₂
SRIF ₁₄	10.01 ± 0.04	10.00 ± 0.01	10.10 ± 0.12	10.12	10.50
SRIF ₂₈	9.99 ± 0.08	9.92 ± 0.03	9.99 ± 0.14	9.66	10.29
seglitide	9.81 ± 0.13	9.96 ± 0.02	9.82 ± 0.07	10.08	10.64
BIM 23014	9.55 ± 0.03	9.27 ± 0.06	9.43 ± 0.09	8.86	9.67
RC160	9.50 ± 0.16	9.35 ± 0.09	9.56 ± 0.06	8.85	10.23
octreotide	9.10 ± 0.07	9.19 ± 0.03	9.16 ± 0.23	8.57	9.90
CGP 23996	8.95 ± 0.07	8.58 ± 0.07	9.06 ± 0.05	8.78	9.62
L362,855	8.79 ± 0.06	8.36 ± 0.05	8.69 ± 0.24		
BIM 23052	8.55 ± 0.01	8.30 ± 0.14	8.76 ± 0.46	7.78	8.73
L361,301	8.39 ± 0.08	8.39 ± 0.11	8.28 ± 0.61	8.32	9.27
cortistatin ₁₄	8.35 ± 0.11	8.75 ± 0.20	9.04 ± 0.08	-	
BIM 23030	7.94 ± 0.22	7.77 ± 0.07	7.88 ± 0.03	8.14	9.14
BIM 23056	6.38 ± 0.11	6.33 ± 0.10	6.33 ± 0.14	6.14	6.65
cycloantagonist SA	5.77 ± 0.05	5.40 ± 0.06	5.80 ± 0.17	5.43	5.90

Table 3: Comparison of affinities of SRIF and various SRIF-analogues for human sst_2 receptors labelled with [125 I][Tyr 3]octreotide and other radioligands

Human cortex and CHO cell data are from Piwko et al. (1997). The data represent the mean of pK_d -values (-log M) ± standard error of at least three determinations.

On the other hand, we have established that under specific salt conditions (120 mM NaCl) the binding sites labelled with [¹²⁵I][Tyr¹¹]SRIF₁₄ in rat cortex (Hoyer et al., 1995b) had a pharmacological profile that could not be distinguished from that of recombinantly expressed sst₁ receptors (although the sst₄ profile is very close). Thus, one could assume that the so called SS-2 sites of Reubi (1984;1985) corresponded to sst, receptors, although in the lung, sst, receptor show a similar profile (Schloos et al., 1997). However, a number of findings are disturbing: there is indeed great variation in the data reported by different groups (Raynor et al., 1993a, 1993b; Bruns et al., 1994; Patel and Srikant, 1994) on the pharmacological profile of the different receptors, as illustrated at the Ciba Foundation meeting (see Patel et al., 1995; Bruns et al., 1995 and the discussions therein). For instance, it has been reported that [125]CGP 23996 (Czernik & Petrack, 1983) was labelling so called SRIF-2 sites with profiles and distribution different from SRIF-1 sites (Raynor and Reisine, 1989; Raynor et al., 1992b; 1993a; Martin et al., 1991), whereas Epelbaum et al. (1985) had noticed that the pharmacology and distribution of the sites labelled with [¹²⁵I]CGP 23996 was very similar to that of sites labelled with [125I][D-Trp8]SRIF14 and this is fully justified since [125I]CGP 23996 was found later to label all five cloned SRIF receptors.

The present paper shows clearly that [^{125}I][Tyr³]octreotide labels recombinant human sst₅ receptors with high affinity, although the radioligand was thought to label exclusively sst₂ receptors (Hoyer et al., 1994b; Piwko et al., 1997; Schoeffter et al., 1995). The pharmacological profile of [^{125}I][Tyr³]octreotide labelled human sst₂ receptors is very similar in transfected CCL39 and CHO cells and native tissue, i.e. human cerebral cortex. On the other hand, [^{125}I][Tyr³]octreotide-labelled human sst₅ sites bound SRIF₂₈ preferentially compared to SRIF₁₄, and somewhat surprisingly, showed very high affinity for the SRIF-analogues octreotide, seglitide, RC160, BIM 23014, BIM 23052 and BIM 23056. Due to these "atypical" features, the pharmacological profiles of sst₂ and sst₅ receptors expressed in CCL39 cells were further investigated by using [^{125}I]LTT-SRIF₂₈ and [^{125}I]CGP 23996.





Crude membrane preparations from sst₂ and sst₅ transfected cells (6 µg or 2 µg per assay, respectively) were incubated with $[125I][Tyr^3]$ octreotide or [125I]CGP 23996 or [125I]LTT-SRIF₂₈ and the indicated concentrations of SRIF₁₄ (\blacksquare , \bullet , and \blacktriangle for each radioligand, respectively), and cycloantagonist SA (\triangledown , \blacklozenge , and +, respectively). Data are expressed as percentage of specific binding. The figure is representative of at least 3 different experiments.

differences in B_{max} -values (see table 2): receptors, at sst₂ There were [125][Tyr3]octreotide, [125]CGP 23996 and [125]]LTT-SRIF28 labelled about the same number of sites (180- 370 fmol/ mg); by contrast, the differences were particularly marked at sst₅ receptors, where [¹²⁵I][Tyr³]octreotide labelled 920 fmol/ mg, [¹²⁵I]CGP 23996 recognised 3530 fmol/ mg and [125I]LTT-SRIF₂₈ 6950 fmol/ mg, i.e. seven fold a higher value than [¹²⁵I][Tyr³]octreotide. Obviously, such discrepancies have already been reported for peptide receptors e.g. Neurokinin NK1 or opiate receptors (see Hjorth et al., 1996; Schwartz et al., 1996), but were mainly related to the actual nature of the radioligands used, i.e. agonists versus antagonists. Such a point can however, not be made here, since the three radioligands and the non-labelled peptides used behave essentially as agonists (with the limitation that none of the actual radioligands exists as cold iodinated form) when assayed in second messenger tests (inhibition of cAMP production). It is commonly assumed that agonists label a high affinity state of the receptor whereas antagonists label all receptors (high and low affinity states), although it can be debated whether two affinity states exists or whether the receptor-ligand-G protein complex exist under multiple forms.

In the present case, we have evaluated the effects of GppNHp on the binding of all three radioligands. GppNHp reduced the binding to sst₂ receptors to the same extent as would be expected, since all three ligands define binding sites with similar profile and similar receptor density. Similarly, the binding of [¹²⁵I][Tyr³]-octreotide to sst₅ receptors was highly sensitive to GppNHp, whereas that of [¹²⁵I]CGP 23996 was less affected, and [¹²⁵I][Tyr³]-octreotide labelling only weakly inhibited by GppNHp. The data are consistent with [¹²⁵I][Tyr³]-octreotide labelling only a minor part of the sst₅ receptor population which shows high affinity for many of the agonists tested and is almost entirely inhibited by GppNHp. [¹²⁵I]CGP 23996 labels significantly more sites, which show intermediate affinity for the synthetic ligands and is only partly affected by GppNHp. By contrast, [¹²⁵I]LTT-SRIF₂₈ labels a very large number of receptors (6950 fmol/ mg compared to 920 fmol/ mg for [¹²⁵I][Tyr³]-octreotide); but this binding is only little affected by GppNHp and shows low affinity for most of the synthetic analogues of SRIF. Yet, the sites labelled by all three ligands have high affinity for the endogenous peptides (SRIF and cortistatin, see tables and figure 4).

This kind of behaviour is very common for "antagonist" ligands (see Teitler et al., 1990), much less so for agonists binding. However, whereas the binding of [¹²⁵I] pancreatic peptide (PP) to NPY₄ receptors (Walker et al., 1997) is very sensitive to GppNHp, the binding of [¹²⁵I]peptide YY (PYY) is not affected by the guanine nucleotide; PP and PYY are considered as the endogenous agonists. Similarly to the present case, [¹²⁵I]PYY represented only a very minor fraction of the sites labelled by [¹²⁵I]PP at NPY4 receptors (Walker et al., 1997). Obviously, one could invoke other reasons to explain apparent differences in B_{max}-values in cells expressing homogeneous populations of recombinant G-protein receptors such as receptor dimerisation which could be differently affected by agonists as is suggested for dopamine D₂, β_2 adrenoceptors or metabotropic glutamate type 5 receptors (see Hebert et al., 1996; Romano et al., 1996), but there is as yet no positive evidence for such behaviour with SRIF receptors.

radioligand	[¹²⁵ I][Tyr ³] octreotide	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I]CGP 23996
SRIF ₂₈	10.30 ± 0.25	9.39 ± 0.22	10.15 ± 0.23
seglitide	10.18 ± 0.22	8.70 ± 0.26	10.22 ± 0.35
SRIF ₁₄	9.87 ± 0.24	9.53 ± 0.13	9.82 ± 0.19
[Tyr ¹⁰]cortistatin	9.65 ± 0.22	8.67 ± 0.24	9.77 ± 0.24
[Leu ⁸ ,D-Trp ²² ,Tyr ²⁵]SRIF ₂₈	9.60 ± 0.02	8.47 ± 0.02	9.70 ± 0.21
L361,301	9.51 ± 0.14	7.69 ± 0.13	8.77 ± 0.09
octreotide	9.48 ± 0.11	7.17 ± 0.30	8.96 ± 0.10
cortistatin ₁₄	9.34 ± 0.23	8.71 ± 0.02	9.24 ± 0.07
BIM 23014	9.31 ± 0.10	7.76 ± 0.13	9.07 ± 0.04
BIM 23052	9.28 ± 0.35	7.92 ± 0.19	9.59 ± 0.14
L362,855	9.17 ± 0.10	7.17 ± 0.30	8.72 ± 0.04
RC160	9.13 ± 0.35	7.51 ± 0.06	8.72 ± 0.25
CGP 23996	8.68 ± 0.20	6.59 ± 0.41	8.26 ± 0.08
[Tyr ³]octreotide	8.41 ± 0.06	6.49 ± 0.01	8.03 ± 0.05
BIM 23056	8.32 ± 0.17	7.17 ± 0.05	7.77 ± 0.09
cycloantagonist SA	8.25 ± 0.17	6.38 ± 0.23	7.77 ± 0.06
BIM 23030	7.45 ± 0.18	6.02 ± 0.09	7.09 ± 0.05

Table 4: Comparison of affinities of SRIF and various SRIF-analogues for human sst₅ receptors labelled with [¹²⁵I][Tyr³]octreotide and other radioligands

The data represent the mean of $pK_d\mbox{-}values\ (-log\ M)$ \pm standard error of at least three determinations.

As can be taken from table 3, the use of different radioligands has apparently little influence on the affinity of the tested compounds at hsst, receptors. Indeed, the correlation coefficients of the profiles defined with the three radioligands are very high: $r^2 = 0.972-0.975$, and the individual values almost identical. In addition, the data are very comparable to those reported previously with the hsst, receptors expressed in CHO cells and native receptors of human cerebral cortex ($r^2 = 0.939$ - 0.947, see Piwko et al., 1997). By contrast, the profile determined for human sst₅ receptors appeared to be rather radioligand-dependent (table 4). Thus, whereas the affinity values determined using ¹²⁵I]CGP 23996 or ¹²⁵I][Tyr³]octreotide were similar, affinity values determined using [¹²⁵I]LTT-SRIF₂₈ were clearly lower for some compounds: octreotide, seglitide, L363,301, BIM 23014, BIM 23030, BIM 23052, BIM 23056, CGP 23996, L362,855, RC160, [Tyr³]octreotide and cycloantagonist (SA) showed up to 100 fold lower affinities. These affinity values were so markedly low that one would not expect [Tyr³]octreotide or CGP 23996 to label the human sst₅ receptors at the low concentrations used here (between 25 and 30 pM, whereas the affinity for the non labelled compounds are about 1000 fold lower). The correlation coefficient obtained when comparing the three sst, binding profiles were respectively 0.773, 0.833 and 0.922, lower than observed at sst, receptors. On the other hand, the putative endogenous peptides SRIF_{14/28} and cortistatin were little affected by the use of different radioligands since the differences in affinity values were about 2, 4 and 8 fold to the most between the extreme values.

Based on the present results, it would appear that the pharmacological profiles of some G-protein coupled receptors may be radioligand-dependent. The surprising findings are that in two similar situations (i.e. sst_2 and sst_5 receptors expressed in the same CCL39 cells), the results can be so different. Probably, the various agonists are able to induce different kinds of receptor conformations, although this does not apply to every receptor within one family.





Crude membrane preparations from sst₂ and sst₅ transfected cells (6 µg or 2 µg per assay, respectively) were incubated with $[125I][Tyr^3]$ octreotide (\blacktriangle), [125I]CGP 23996 (\bullet) or [125I]LTT-SRIF₂₈ (\blacksquare) and the indicated concentrations of GppNHp at sst₂ receptors (top) and sst₅ receptors (bottom). Data are expressed as percentage of specific binding. One representative example of at least 3 independent experiments.

modifications, such protein and post-translational as Post-transcriptional phosphorylation or glycosylation, may be cell type-specific and as such may affect receptor conformation and influence the binding properties. Coupling to different Gprotein isoforms, which may show different expression pattern depending on the cells, could also be implicated in receptor binding properties (Lefkowitz et al., 1993). In any case, the labelling by $[^{125}I][Tyr^3]$ octreotide with similar affinity of human sst, and sst, receptors and the very high affinity of small cyclic peptides for the sst₅ receptor suggests that in addition to sst₂ receptors, sst₅ receptors could be responsible for mediating a number of effects of short SRIF analogues which may have been assigned primarily to sst₂ receptors. Similarly, in vivo labelling by octreotide analogues may represent both sst, and sst, receptor sites. Finally, from the present data, it is not all too surprising to see differences in affinity reported by different groups at the same recombinant receptor and data obtained by different investigators may not be immediately comparable.

Figure 5: Binding of [¹²⁵I][Tyr³]octreotide, [¹²⁵I]CGP 23996 and [¹²⁵I]LTT-SRIF₂₈ at sst₂
5.1. Abstract

Human somatostatin receptor subtypes 1-5 (sst₁₋₅) were characterised using the agonist radioligands [125 I]LTT-SRIF₂₈, [125 I][Tyr¹⁰]CST₁₄, [125 I]CGP 23996 and [125 I][Tyr³]octreotide in stably transfected CCL39 Chinese hamster lung fibroblast cells. The radioligands used labelled saturable and high affinity populations of sites in each instance; at sst₁₋₄ receptors B_{max}-values were roughly equivalent. By contrast, at sst₅ receptors B_{max}-values determined with [125 I]CGP 23996 and [125 I][Tyr³]octreotide were significantly lower (two and eight fold) compared to [125 I]LTT-SRIF₂₈ and [125 I][Tyr¹⁰]CST₁₄.

Experiments were performed with the stable GTP-analogue guanylylimidodiphosphate (GppNHp) to establish guanine nucleotide sensitivity of agonist binding to sst_{1-5} receptors. The sensitivity towards GppNHp was quite variable depending on receptor and/ or ligand. At sst_1 and sst_4 receptors, GppNHp produced little effect overall, whereas binding to sst_3 and sst_2 receptors was reduced by 70 and > 80 %, respectively. At sst_5 receptors, the binding of [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ was only slightly affected by GppNHp, while [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide binding was almost entirely inhibited. Thus, [¹²⁵I][Tyr³]octreotide labelled about 26-fold less sst_5 receptors than [¹²⁵I]LTT-SRIF₂₈, in the presence of 10 μ M GppNHp. These discrepancies in guanine nucleotide sensitivity, were confirmed in GppNHp competition experiments.

Competition studies were performed at the five receptors labelled with the different radioligands to establish their respective pharmacological profiles: the rank order of affinity was largely radioligand-independent at sst_{1-4} receptors, in contrast to sst_5 receptors, where it was radioligand-dependent. Thus, the pharmacological profile of $[^{125}I][Tyr^{10}]CST_{14}$ - and $[^{125}I]CGP23996$ -labelled sst_5 sites correlated highly significantly, but did not correlate with the affinity profiles defined with $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide binding to sst_5 receptors.

Depending on the agonist radioligand used and the receptor studied, it would appear that binding can be essentially to a guanine nucleotide sensitive state (e.g. sst_2 or sst_3), a guanine nucleotide insensitive state (sst_1 or sst_4) or a mixture of both (sst_5); in the latter case, each radioligand defining a more or less different rank order of affinity at the same receptor.

In summary, the differences in agonist receptor binding and guanine nucleotide sensitivity cannot be explained by the ternary complex model or its variations, but rather suggest the existence of multiple agonist-specific receptor states, which vary from one receptor to another.

5.2. Results

Saturation experiments

 $[^{125}I]LTT-SRIF_{28}$, $[^{125}I][Tyr^{10}]CST_{14}$ and $[^{125}I]CGP$ 23996 labelled human sst₁₋₅ receptors in CCL39 cells with high affinity and in a saturable manner (see figure 1 and table 1); non-specific binding was low for each radioligand. No specific binding was found for any of the radioligands used here in non-transfected cells; RT-PCR confirmed the expression of the respective SRIF receptor subtypes in the stably transfected CCL39 cells, and the absence of expression in the non-transfected cells (data not shown). $[^{125}I][Tyr^3]$ octreotide labelled sst₂ and sst₅ receptors with high affinity, whereas the low affinity of the radioligand for sst₃ receptors precluded any further binding studies; sst₁ and sst₄ receptors could not be labelled with $[^{125}I][Tyr^3]$ octreotide (data not shown). Saturation curves suggested the labelling of a single population of receptor binding sites. Receptor densities (B_{max} -values) obtained with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 (and [¹²⁵I][Tyr³]octreotide) were similar at sst₁₋₄ receptors (see table 1), but rather divergent at human sst₅ receptors (pK_d = 10.48 ± 0.04, 10.33 ± 0.03, 9.52 ± 0.08 and 9.64 ± 0.04, respectively; $B_{max} = 6950 \pm 220$, 5630 ± 330, 3530 ± 50 and 920 ± 170 fmol/mg protein, respectively). Thus, [¹²⁵I][Tyr³]octreotide labelled almost 8-fold less sst₅ receptor sites than [¹²⁵I]LTT-SRIF₂₈, whereas at sst₂ receptors [¹²⁵I][Tyr³]octreotide and the other radioligands labelled similar densities (see table 1). Similarly, there were no profound differences in B_{max} -values at either sst₁ or sst₃ receptors, although there is tendency for [¹²⁵I]LTT-SRIF₂₈ to label more sites than for example [¹²⁵I]CGP 23996.

Effects of GppNHp

To examine, whether differences in receptor densities - especially at sst₅ receptors - may be explained by the radioligands labelling different affinity states of the receptor, the effects of the non-hydrolysable GTP-analogue GppNHp on radioligand binding were investigated. First, saturation experiments were performed with the different radioligands in the presence of 10 µM GppNHp (table 1). The affinities of the four radioligands at sst₁₋₅ receptors were very similar whether saturation experiments were performed with or without GppNHp. At sst₄ receptors, GppNHp produced no significant changes in B_{max} -values for any of the radioligands. At sst₁₋₃ receptors, the effects of GppNHp on B_{max}-values were limited to a 2-fold decrease if at all. At sst₅ receptors B_{max} -values determined with [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ were not affected by GppNHp; in marked contrast, B_{max}-values defined by [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide were 3-4 fold lower in the presence compared to the absence of GppNHp (figure 1 and table 1). In other words, in the presence of GppNHp, [¹²⁵I][Tyr³]octreotide labelled about 24- 26 fold less sst₅ receptor sites ($B_{max} = 270 \pm 90$ fmol/mg) compared to $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I][Tyr^{10}]CST_{14}$ (B_{max} = 6560 ± 560 and 6960 ± 760 , respectively) (table 1). Similarly, [¹²⁵I]CGP 23996 labelled about 7 times less sst₅ receptor sites than the latter two radioligands.

Table 1: Comparison of saturation experiments in the absence or the presence of GppNHp (10⁻⁵ M) using [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide at human sst₁₋₅ receptors

	[¹²⁵ I]L	ΓT-SRIF ₂₈	[¹²⁵ I][T	yr ¹⁰]CST ₁₄	[¹²⁵ I]C	GP 23996	[¹²⁵]][Tyr ³]
							oct	reotide
	pK _d	B _{max}	pK _d	B _{max}	pK _d	B _{max}	pK _d	B _{max}
		[fmol/mg]		[fmol/mg]		[fmol/mg]		[fmol/mg]
hsst ₁	9.96	470	10.02	220	9.63	260	-	-
	± 0.00	± 30	± 0.04	± 30	± 0.09	± 30		
hsst ₁	10.15	200	9.75	320	9.33	310	_	
+ GppNHp	± 0.09	± 20	± 0.13	± 50	± 0.13	± 60		
hsst ₂	9.89	370	9.45	340	9.76	180	9.89	210
	± 0.04	± 60	± 0.09	± 70	± 0.06	± 20	± 0.02	± 10
hsst ₂	10.21	160	9.93	140	9.53	130	9.93	170
+ GppNHp	± 0.06	± 20	± 0.13	± 30	± 0.13	± 10	± 0.23	± 40
hsst ₃	10.28	560	10.06	340	9.76	270	-	
	± 0.06	± 60	± 0.11	± 50	± 0.05	± 40		
hsst ₃	10.41	220	9.68	360	9.54	110	-	
+ GppNHp	± 0.06	± 20	± 0.08	± 70	± 0.06	± 10		
$hsst_4$	9.64	440	9.67	340	9.35	690	-	-
	± 0.03	± 50	± 0.14	± 110	± 0.03	± 50		
hsst ₄	9.51	520	9.62	450	9.56	790		544
+ GppNHp	± 0.03	± 20	± 0.08	± 60	± 0.07	± 100		
hsst ₅	10.48	6950	$10.33 \pm$	5630	9.52	3530	9.64	920
	± 0.04	± 220	0.03	± 330	± 0.08	± 50	± 0.04	± 170
$hsst_5$	10.18	6560	10.48	6960	9.82	930	9.80	270
+ GppNHp	± 0.11	± 560	± 0.14	± 760	± 0.08	± 270	± 0.25	± 90

The data are expressed as the mean of $pK_d\text{-values}$ (-log M) or $B_{max}\text{-values}\pm$ SEM of 3 different experiments.

In a second series of experiments, a range of increasing GppNHp concentrations were used to inhibit the binding of the radioligands to human sst_{1-5} receptors (table 2; figure 2). Overall, at sst_1 and especially sst_4 receptors, radioligand binding was relatively little affected by GppNHp (see figure 2, table 2). At sst_3 and especially sst_2 receptors (E_{max} -values = 82- 89 %, pEC₅₀'s = 6.76- 7.32), the effects were rather similar independently of the radioligand tested.

Figure 1: Guanine nucleotide sensitivity of $[^{125}I]LTT-SRIF_{28}$, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 or $[^{125}I][Tyr^3]$ octreotide binding to membranes prepared from CCL39 cells stably expressing sst₅ receptors.



Crude membrane preparations (2 µg per assay) were incubated with increasing concentrations of the radioligand in the absence (\blacksquare) or presence (\blacktriangle) of GppNHp (10⁻⁵ M; final concentration), and assayed for receptor binding. The plots depict specific binding expressed as amount of radioligand bound (fmol/mg) versus free radioligand concentration (pM). The figures show one representative example of three different experiments.

By contrast, at sst₅ receptors, whereas [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ binding was only moderately inhibited ($E_{max} = 47 \pm 6$ % and 31 ± 6 %, pEC₅₀ = 5.87 ± 0.30 and 4.81 ± 0.36, respectively), [¹²⁵I]CGP 23996 binding, and especially [¹²⁵I][Tyr³]octreotide binding were almost entirely blocked ($E_{max} = 76 \pm 1$ % and 88 ± 1 %, pEC₅₀ = 6.89 ± 0.20 and 7.77 ± 0.14 respectively) by GppNHp.

The pharmacological profiles of the five SRIF receptors were determined in classical competition assays. SRIF₁₄, SRIF₂₈ and CST₁₇ and their analogues bound nanomolar affinity to hsst_{1.5} receptors (pK_d's = 8.39 - 10.21) (tables 3(A)-(E); figure 4). The rank order of affinity at sst₁ sites was similar for all three radioligands: $CST_{17} \ge SRIF_{28} \approx$ LTT-SRIF₂₈ \approx SRIF₁₄ \approx CST₁₄ > [Tyr¹⁰]CST₁₄ \approx CGP 23996 \approx BIM 23052 >> octreotide > seglitide. Also at sst₄ sites the affinity profiles were comparable for the three radioligands: $CST_{17} \approx$ LTT-SRIF₂₈ \geq SRIF₂₈ \approx SRIF₁₄ \approx CGP 23996 > SRIF₁₄ \approx CGP 23996 > ITyr¹⁰]CST₁₄ \approx BIM 23052 >> octreotide > seglitide. Also at sst₄ sites the affinity profiles were comparable for the three radioligands: $CST_{17} \approx$ LTT-SRIF₂₈ \geq SRIF₂₈ \approx SRIF₁₄ \approx CGP 23996 > ITyr¹⁰]CST₁₄ \approx BIM 23052 >> octreotide > seglitide.

The SRIF₁ receptors revealed different types of behaviour, with affinity values almost identical whichever radioligand used at sst, receptors: $SRIF_{28} \approx SRIF_{14} \approx seglitide \approx$ LTT-SRIF₂₈ > RC160 \approx BIM 23014 \geq CST₁₇ \approx octreotide > CST₁₄ \approx [Tyr¹⁰]CST₁₄. At sst₃ binding was also largely comparable although [¹²⁵I]LTT-SRIF₂₈ labelled sites tended to show somewhat lower affinity for the synthetic analogues: $SRIF_{28} \approx SRIF_{14} \approx LTT$ - $SRIF_{28} \approx CST_{17} \geq BIM \ 23052 \geq CST_{14} \approx [Tyr^{10}]CST_{14} \approx CGP \ 23996 > octreotide >$ seglitide. At sst₅ sites, virtually every radioligand showed a separate profile; especially the two natural ligands defined very low affinity values for the synthetic peptides with CGP23996 and octreotide having only micromolar affinity, although their radioactive analogues labelled these sites with sub-nanomolar affinity: (a) $\begin{bmatrix} 125 \\ I \end{bmatrix} LTT-SRIF_{28}$ and $[^{125}I][Tyr^{10}]CST_{14}: CST_{17} \geq SRIF_{14} \approx SRIF_{28} > seglitide \approx LTT-SRIF_{28} \approx CST_{14} \approx$ $[Tyr^{10}]CST_{14} >> BIM 23052 \approx BIM 23014 > octreotide, (b) [^{125}I]CGP 23996: SRIF_{28} \approx$ $\text{CST}_{17} \approx \text{seglitide} > \text{SRIF}_{14} \approx \text{LTT-SRIF}_{28} \approx [\text{Tyr}^{10}] \text{CST}_{14} \approx \text{BIM } 23052 > \text{CST}_{14} > \text{BIM}$ 23014 \approx octreotide, (c) [¹²⁵I][Tyr³]octreotide: SRIF₂₈ \approx seglitide \geq SRIF₁₄ \approx CST₁₇ > $LTT-SRIF_{28} \approx [Tyr^{10}]CST_{14} > L363,301 \approx octreotide \approx CST_{14} \approx BIM 23052 \approx BIM$ 23014.

	[¹²⁵ I]LT	T-SRIF ₂₈	[¹²⁵ I][Ty	r ¹⁰]CST ₁₄	[¹²⁵ I]CC	GP 23996	[¹²⁵ I] octro	[Tyr ³] eotide
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
CCL39/	39	6.67	63	6.62	34	6.24		
$hsst_1$	± 0	± 0.28	± 3	± 0.23	± 4	± 0.07		
CCL39/	82	6.97	83	7.32	82	6.76	89	7.07
$hsst_2$	± 1	± 0.05	± 4	± 0.16	± 3	± 0.10	± 3	± 0.17
CCL39/	68	6.91	83	7.74	76	7.64		
$hsst_3$	± 3	± 0.21	± 1	± 0.12	± 6	± 0.23		
CCL39/	44	6.89	36	6.17	8	(-)	-	-
$hsst_4$	± 2	± 0.08	± 7	± 0.04	± 2			
CCL39/	47	5.87	31	4.81	76	6.89	88	7.77
$hsst_5$	± 6	± 0.30	± 6	± 0.36	± 1	± 0.20	± 1	± 0.14

Table 2: Effects of GppNHp (max. 10^{-4} M) on $[^{125}I]LTT-SRIF_{28}$, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide binding to human sst₁₋₅ receptors: comparison of pEC₅₀-values (-log M) or E_{max}-values [% inhibition] ± SEM of three experiments

At SRIF₂ - sst₁ and sst₄ - receptors all affinity profiles highly significantly correlated (correlation coefficients r = 0.926- 0.987) (table 4). At SRIF₁ receptors, the situation was less clear cut. Interestingly, at human sst₅ receptors the affinity profiles of the pairs [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, or [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide correlated highly significantly (r = 0.942 and 0.916, respectively), whereas the pharmacological profiles of [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide revealed lower correlations with those of the other two radioligands (r = 0.767- 0.898).

5.3. Discussion

The purpose of this study was to compare agonist-receptor interactions at various human somatostatin receptors using classical radioligand binding studies.

Table 3: Comparison of the pharmacological profiles of human sst_{1-5} receptors defined with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 or [¹²⁵I][Tyr³]octreotide. The affinity values are expressed as pK_d-values (-log M) ± SEM of 3 determinations

	[¹²⁵ I]LTT-	$[^{125}I][Tyr^{10}]$	[¹²⁵ I]CGP
	SRIF_{28}	CST_{14}	23996
$SRIF_{14}$	9.12 ± 0.05	9.08 ± 0.07	8.95 ± 0.11
SRIF ₂₈	9.22 ± 0.02	9.26 ± 0.07	9.38 ± 0.06
LTT-SRIF ₂₈	9.22 ± 0.11	9.28 ± 0.01	9.13 ± 0.13
CST ₁₇	9.61 ± 0.04	9.61 ± 0.17	9.48 ± 0.08
CST_{14}	8.76 ± 0.06	7.74 ± 0.09	9.07 ± 0.29
[Tyr ¹⁰]CST ₁₄	8.56 ± 0.08	9.04 ± 0.13	8.32 ± 0.06
seglitide	4.50 ± 0.04	4.32 ± 0.06	4.87 ± 0.03
CGP 23996	8.33 ± 0.06	8.31 ± 0.04	8.45 ± 0.09
octreotide	6.65 ± 0.05	6.41 ± 0.04	6.23 ± 0.08
[Tyr ³]octreotide	5.57 ± 0.07	5.82 ± 0.10	5.69 ± 0.13
L362,855	6.25 ± 0.07	6.30 ± 0.07	6.08 ± 0.16
L363,301	5.32 ± 0.08	5.38 ± 0.15	5.66 ± 0.15
RC 160	7.08 ± 0.08	6.96 ± 0.24	6.65 ± 0.24
BIM 23030	5.06 ± 0.04	4.85 ± 0.02	5.17 ± 0.06
BIM 23014	6.75 ± 0.04	6.66 ± 0.18	6.41 ± 0.24
BIM 23056	6.61 ± 0.10	6.46 ± 0.07	6.56 ± 0.25
BIM 23052	8.37 ± 0.04	8.62 ± 0.05	8.17 ± 0.07
cycloantagonist SA	7.02 ± 0.00	6.80 ± 0.17	6.48 ± 0.25

Table 3(A) CCL39/hsst₁

Table 3(B) CCL39/hsst₄

	[¹²⁵ I]LTT-	[¹²⁵ I][Tyr ¹⁰]	[¹²⁵ I]CGP
	SRIF ₂₈	CST_{14}	23996
SRIF ₁₄	8.91 ± 0.15	8.39 ± 0.28	8.87 ± 0.08
SRIF ₂₈	9.08 ± 0.12	8.44 ± 0.30	9.06 ± 0.09
LTT-SRIF ₂₈	9.16 ± 0.01	9.13 ± 0.02	9.37 ± 0.20
CST ₁₇	9.24 ± 0.02	9.55 ± 0.30	9.26 ± 0.02
CST ₁₄	8.76 ± 0.02	8.75 ± 0.14	8.57 ± 0.03
[Tyr ¹⁰]CST ₁₄	8.44 ± 0.06	8.17 ± 0.09	8.30 ± 0.03
seglitide	5.37 ± 0.08	5.11 ± 0.07	5.04 ± 0.05
CGP 23996	8.77 ± 0.03	8.67 ± 0.14	8.62 ± 0.03
octreotide	6.40 ± 0.09	5.76 ± 0.08	6.02 ± 0.09
[Tyr ³]octreotide	6.29 ± 0.06	6.17 ± 0.08	5.89 ± 0.06
L362,855	7.31 ± 0.07	6.76 ± 0.32	7.08 ± 0.11
L363,301	5.61 ± 0.03	5.06 ± 0.06	5.64 ± 0.40
RC 160	7.25 ± 0.05	6.56 ± 0.44	6.97 ± 0.26
BIM 23030	5.98 ± 0.04	5.56 ± 0.14	5.53 ± 0.11
BIM 23014	6.64 ± 0.07	6.25 ± 0.28	6.52 ± 0.05
BIM 23056	7.17 ± 0.10	6.47 ± 0.35	7.04 ± 0.07
BIM 23052	8.63 ± 0.04	8.20 ± 0.11	8.13 ± 0.06
cycloantagonist SA	6.48 ± 0.13	6.07 ± 0.26	6.29 ± 0.07

The somatostatin field is notorious for rather strong disagreements about the degree of selectivity of various SRIF analogues for one or the other somatostatin receptor reported by some authors which could not be confirmed by others (see discussions in Chadwick et al, 1995, Bruns et al, 1995; Patel, 1997).

Table 3(C) CCL39/hsst₂

	[¹²⁵ I]LTT-	[¹²⁵ I][Tyr ¹⁰]	[¹²⁵ I]CGP	[¹²⁵ I][Tyr ³]
	SRIF_{28}	CST_{14}	23996	octreotide
SRIF ₁₄	10.00 ± 0.01	10.06 ± 0.07	10.10 ± 0.12	10.01 ± 0.04
SRIF ₂₈	9.92 ± 0.03	10.16 ± 0.11	9.99 ± 0.14	9.99 ± 0.08
LTT-SRIF ₂₈	9.70 ± 0.25	8.90 ± 0.29	10.06 ± 0.07	9.17 ± 0.02
CST ₁₇	9.07 ± 0.01	9.29 ± 0.13	9.33 ± 0.15	8.85 ± 0.10
CST ₁₄	8.75 ± 0.20	8.54 ± 0.44	9.04 ± 0.08	8.35 ± 0.11
[Tyr ¹⁰]CST ₁₄	8.77 ± 0.09	8.91 ± 0.21	8.93 ± 0.04	9.00 ± 0.09
seglitide	9.96 ± 0.02	9.62 ± 0.17	9.82 ± 0.07	9.81 ± 0.13
CGP 23996	8.58 ± 0.07	8.94 ± 0.02	9.06 ± 0.05	8.95 ± 0.07
octreotide	9.19 ± 0.03	9.11 ± 0.14	9.16 ± 0.23	9.10 ± 0.07
[Tyr ³]octreotide	8.43 ± 0.23	7.10 ± 0.11	9.48 ± 0.23	8.66 ± 0.10
L362,855	8.36 ± 0.05	8.79 ± 0.19	8.69 ± 0.24	8.79 ± 0.06
L363,301	8.39 ± 0.11	8.47 ± 0.18	8.28 ± 0.61	8.39 ± 0.08
RC 160	9.35 ± 0.09	9.60 ± 0.02	9.56 ± 0.06	9.50 ± 0.16
BIM 23030	7.77 ± 0.07	7.66 ± 0.07	7.88 ± 0.03	7.94 ± 0.22
BIM 23014	9.27 ± 0.06	9.26 ± 0.07	9.43 ± 0.09	9.55 ± 0.03
BIM 23056	6.33 ± 0.10	6.23 ± 0.12	6.33 ± 0.14	6.38 ± 0.11
BIM 23052	8.30 ± 0.14	8.50 ± 0.32	8.76 ± 0.46	8.55 ± 0.01
cycloantagonist SA	5.40 ± 0.06	5.74 ± 0.05	5.80 ± 0.17	5.77 ± 0.05

To avoid problems, which could be generated by species differences and/ or the use of different expression systems and/ or of different radioligands, it was decided to deal only with human recombinant receptors, all expressed in the same cellular system, i.e. stably transfected CCL39 Chinese hamster lung fibroblast cells and with the same radioligands.

Table 3(D) CCL39/hsst₅

	[¹²⁵ I]LTT-	[¹²⁵ I][Tyr ¹⁰]	[¹²⁵ I]CGP	[¹²⁵ I][Tyr ³]
	SRIF_{28}	CST_{14}	23996	octreotide
SRIF ₁₄	9.53 ± 0.13	9.01 ± 0.24	9.82 ± 0.19	9.87 ± 0.24
SRIF ₂₈	9.39 ± 0.22	9.18 ± 0.19	10.15 ± 0.23	10.30 ± 0.25
LTT-SRIF ₂₈	8.47 ± 0.02	8.12 ± 0.01	9.70 ± 0.21	9.60 ± 0.02
CST ₁₇	9.54 ± 0.10	9.37 ± 0.09	10.21 ± 0.16	9.85 ± 0.04
CST ₁₄	8.71 ± 0.02	8.40 ± 0.04	9.24 ± 0.07	9.34 ± 0.23
[Tyr ¹⁰]CST ₁₄	8.67 ± 0.24	8.06 ± 0.40	9.77 ± 0.24	9.65 ± 0.22
seglitide	8.70 ± 0.26	9.14 ± 0.30	10.22 ± 0.35	10.18 ± 0.22
CGP 23996	6.59 ± 0.41	6.67 ± 0.24	8.26 ± 0.08	8.68 ± 0.20
octreotide	7.17 ± 0.30	7.31 ± 0.18	8.96 ± 0.10	9.48 ± 0.11
[Tyr ³]octreotide	6.49 ± 0.01	6.00 ± 0.07	8.03 ± 0.05	8.41 ± 0.06
L362,855	7.17 ± 0.30	7.17 ± 0.12	8.72 ± 0.04	9.17 ± 0.10
L363,301	7.69 ± 0.13	7.17 ± 0.15	8.77 ± 0.09	9.51 ± 0.14
RC 160	7.51 ± 0.06	7.27 ± 0.11	8.72 ± 0.25	9.13 ± 0.35
BIM 23030	6.02 ± 0.09	5.56 ± 0.17	7.09 ± 0.05	7.45 ± 0.18
BIM 23014	7.76 ± 0.13	7.38 ± 0.19	9.07 ± 0.04	9.31 ± 0.10
BIM 23056	7.17 ± 0.05	6.68 ± 0.05	7.77 ± 0.09	8.32 ± 0.17
BIM 23052	7.92 ± 0.19	7.45 ± 0.24	9.59 ± 0.14	9.28 ± 0.35
cycloantagonist SA	6.38 ± 0.23	6.02 ± 0.11	7.77 ± 0.06	8.25 ± 0.17

Further, whenever practical, experiments were run in parallel. In three additional reports (Siehler and Hoyer, submitted (b), (c), (d), we investigate in with the same models, agonist-stimulated GTP γ S binding, inhibition of adenylate cyclase and stimulation of PLC activities.

Table 3(E) CCL39/hsst₃

	[¹²⁵ I]LTT-	$[^{125}I][Tyr^{10}]$	[¹²⁵ I]CGP
	SRIF_{28}	CST_{14}	23996
SRIF ₁₄	9.54 ± 0.05	9.67 ± 0.07	9.71 ± 0.08
SRIF ₂₈	9.65 ± 0.04	9.80 ± 0.08	9.94 ± 0.17
LTT-SRIF ₂₈	9.84 ± 0.12	9.26 ± 0.03	10.09 ± 0.13
CST ₁₇	9.43 ± 0.06	9.52 ± 0.10	9.88 ± 0.04
CST ₁₄	9.06 ± 0.12	9.13 ± 0.09	9.27 ± 0.01
[Tyr ¹⁰]CST ₁₄	8.70 ± 0.18	8.90 ± 0.08	9.02 ± 0.25
seglitide	6.88 ± 0.08	7.89 ± 0.25	7.68 ± 0.15
CGP 23996	8.82 ± 0.05	9.28 ± 0.19	9.15 ± 0.04
octreotide	7.88 ± 0.04	8.60 ± 0.16	8.44 ± 0.01
[Tyr ³]octreotide	6.84 ± 0.25	6.20 ± 0.10	7.90 ± 0.00
L362,855	7.62 ± 0.23	8.25 ± 0.06	8.29 ± 0.04
L363,301	6.34 ± 0.06	6.83 ± 0.08	6.97 ± 0.13
RC 160	7.37 ± 0.15	7.91 ± 0.03	7.82 ± 0.15
BIM 23030	7.17 ± 0.08	7.85 ± 0.11	7.64 ± 0.20
BIM 23014	7.86 ± 0.41	8.02 ± 0.14	7.93 ± 0.11
BIM 23056	6.90 ± 0.04	7.08 ± 0.11	7.20 ± 0.10
BIM 23052	8.42 ± 0.12	9.55 ± 0.12	9.71 ± 0.02
cycloantagonist SA	6.23 ± 0.03	7.08 ± 0.04	6.88 ± 0.13

The radioligands used here, are as far as known, agonists at SRIF receptors or at least closely linked to compounds known as agonists, since the true "cold" iodinated equivalents of the ligands are not available. Thus, [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄ are analogues of the natural somatostatin-28 and cortistatin-14, whereas [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide are analogues of the synthetic peptide agonists CGP 23996 and octreotide.

The four analogues are full or close to full agonists in adenylate cyclase experiments performed in these cells; therefore, it may be anticipated that such compounds determine the same B_{max} -values at a given receptor and share a number of features. All four radioligands showed high affinity and saturable binding, and altogether the levels of non-specific binding and noise were low.

The first surprise of this study comes from saturation experiments: at the five receptors and as may be anticipated, the natural analogues [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ labelled similar receptor densities, although there is somewhat less binding for the cortistatin analogue at sst₁ and sst₃ receptors. By contrast, the synthetic peptide [¹²⁵I]CGP 23996 labelled only about half of the sites recognised by [¹²⁵I]LTT-SRIF₂₈, except at sst₄ receptors. Similarly, [¹²⁵I][Tyr³]octreotide labelled only about half sst₂ and almost 8-fold less sst₅ receptor sites compared to [¹²⁵I]LTT-SRIF₂₈, as if the ligands recognise different states (or combinations thereof) of the receptors.

To further investigate the possibility of multiple agonist receptor states, the effects of the non-hydrolysable GTP-analogue GppNHp on [^{125}I]LTT-SRIF₂₈, [^{125}I]CGP 23996, [^{125}I][Tyr¹⁰]CST₁₄ and [^{125}I][Tyr³]octreotide binding to sst₁₋₅ receptors were investigated in both "competition" and saturation experiments. At sst₁₋₄ receptors, differences in B_{max}-values were rather limited following co-incubation with GppNHp. By contrast, the large differences in B_{max}-values at sst₅ receptors labelled with [^{125}I]LTT-SRIF₂₈, [^{125}I][Tyr¹⁰]CST₁₄, [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide (B_{max} = 6950, 5630, 3530 and 920 fmol/ mg, respectively) were amplified when GppNHp (10 μ M) was added: on the one hand, [^{125}I]LTT-SRIF₂₈ and [^{125}I][Tyr¹⁰]CST₁₄ binding were almost GppNHp-insensitive (6560 and 6960 fmol/ mg, respectively), suggesting the labelling of primarily G-protein uncoupled receptors. On the other hand, B_{max}-values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr¹⁰]CST₁₄ binding were almost GppNHp-insensitive (6560 and 6960 fmol/ mg, respectively), suggesting the labelling of primarily G-protein uncoupled receptors. On the other hand, B_{max}-values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide values for [^{125}I]CGP 23996 and [^{125}I][Tyr³]octreotide were reduced 3- 4 fold (930 and 270 fmol/ mg, respectively), suggesting predominantly binding to G-protein-coupled receptor states.

In "competition" experiments, GppNHp affected radioligand binding to rather different extents even at the same receptor subtype. At $SRIF_2$ (sst₁ and sst₄) receptors, the radioligands appear to bind to a mixture of G-protein-coupled and –uncoupled receptor states.



Figure 2: Competition experiments performed in membranes prepared from CCL39 cells expressing human sst₂ or sst₃ receptors.

Crude membrane preparations from sst₂ or sst₅ receptor transfected cells were incubated with [125I]LTT-SRIF₂₈, $[125I][Tyr^{10}]CST_{14}$, [125I]CGP 23996 or $[125I][Tyr^3]$ octreotide and the indicated concentrations of SRIF₁₄ (\blacksquare), CST₁₇ (\blacktriangledown), octreotide (\blacktriangle), seglitide (\diamondsuit) and BIM 23056 (\bullet). Data are expressed as percentage of specific binding. The graphs show one example of at least 3 different experiments.

In particular, [¹²⁵I]CGP 23996 seemed to recognise only uncoupled sst₄ receptors, since its binding was not significantly affected by GppNHp, whereas it was reduced by 30-60 % with the other ligands. Of notice, the little effect produced by GppNHp on [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ binding, illustrating that natural ligands do not necessarily recognise receptors in a high affinity (G-protein-coupled) state only or primarily. At SRIF, receptors, the situations were quite variable. Thus, sst, and sst, receptors seem to be essentially recognised in a coupled state by all tested radioligands, since the effects of GppNHp rather marked, > 80 % inhibition for all four ligands at sst, receptors, and 70-80 % inhibition at sst₃ receptors. In marked contrast, the sst₅ receptor binding of [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, of which B_{max}-values were high and ligand affinities lower, was only moderately inhibited by GppNHp, suggesting again binding to a mixed population of G-protein-coupled and -uncoupled receptor states. On the other hand, the sst₅ receptor binding of [¹²⁵I]CGP 23996, and especially [¹²⁵I][Tyr³]octreotide, of which B_{max} -values were low and ligand affinities high, was almost entirely inhibited by GppNHp suggesting binding to essentially G-protein-coupled receptor states. Not only were the maximal effects of GppNHp different and dependent on ligand and receptor, but also the potency of GppNHp varied rather markedly, with apparent pEC₅₀values ranging from 4.81 to 7.77 at sst₅ binding, i.e. up to 1000-fold difference.

Subsequently, we compared the binding profiles of the three (or when feasible four) radioligands in competition studies with a number of rather varied structures including analogues of the natural SRIF and CST, as well as cyclic and linear peptides known to have affinity for one or the other member of the SRIF receptor family. In essence, affinities obtained in competition assays were almost superimposable at $sst_{1.4}$ receptors whichever the radioligand used, although this has to be qualified. By contrast, at sst_5 receptors, highest affinity values were determined using [¹²⁵I][Tyr³]octreotide, which defined the lowest B_{max}-values and was most sensitive to GppNHp. Similarly, higher affinities were measured with [¹²⁵I]CGP 23996-labelled sites, which labelled also a relatively low receptor density. Altogether, lower affinities were determined when using the hormone analogues [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, which both labelled high receptor densities.

Table 4: Correlation coefficients (r) of correlation analyses between affinity profiles (pK_d -values) obtained by using [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide at human sst₁₋₅ receptors. Data used for correlation are shown in Tables 4(A)-(E).

Table 4(A) CCL39/hsst₁

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰]CST ₁₄
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.966	**
[¹²⁵ I]CGP 23996	0.971	0.926

Table 4(B) CCL39/hsst₄

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰]CST ₁₄
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.969	-
[¹²⁵ I]CGP 23996	0.987	0.960

Table 4(C) CCL39/hsst₂

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰]CST ₁₄	[¹²⁵ I]CGP 23996
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.874	-	-
[¹²⁵ I]CGP 23996	0.978	0.761	
[¹²⁵ I][Tyr ³]octreotide	0.954	0.888	0.924

Table 4(D) CCL39/hsst₅

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰]CST ₁₄	[¹²⁵ I]CGP 23996
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.942	-	-
[¹²⁵ I]CGP 23996	0.850	0.896	-
[¹²⁵ I][Tyr ³]octreotide	0.767	0.843	0.916

Table 4(E) CCL39/hsst₃

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰]CST ₁₄
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.839	-
[¹²⁵ I]CGP 23996	0.932	0.829

Thus, the affinity profiles of human sst₁₋₄ receptors determined with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide correlated highly significantly. This was much less conspicuous at sst₅ receptors: for instance, the profile of [125I]CGP 23996 and [125I][Tyr3]octreotide correlated significantly, but not when compared to the profiles of $[^{125}I]LTT$ -SRIF₂₈ or $[^{125}I][Tyr^{10}]CST_{14}$. Indeed, the absolute affinity values could easily vary by a factor 100 or higher depending on the radioligand used, but also and more surprisingly the rank order of affinity did also vary rather markedly. A number of discrepancies became apparent when comparing homologous versus heterologous binding. Thus it is not always evident that heterologous displacement studies will predict which ligand may turn into a good radioligand; in other words, affinities may be well underestimated when competing [Tyr³]octreotide or CGP 23996 for sites labelled with [125I]LTT-SRIF28 or [125I][Tyr10]CST14. In several cases, the resulting affinity values would not predict the high affinity that can be obtained with the corresponding radioligands, [¹²⁵I]CGP 23996 and ¹²⁵I][Tyr³]octreotide.

Similar findings have been made at NK receptors, to the extent that it was not expected to label NK1 receptors with either NKA or NKB, since these peptides have low affinity for NK1 receptors labelled with Substance P. Yet contrary to all expectations [³H]NKA or [³H]NKB label NK1 receptors with high affinity, questioning some of the points made about the selectivity of these ligands or senktide (Hastrup and Schwartz, 1996). Similarly, it was not expected that [¹²⁵I][Tyr³]octreotide would label sst₅ receptor based on its affinity for the receptor labelled with [¹²⁵I]LTT-SRIF₂₈ or [¹²⁵I][Tyr¹⁰]CST₁₄. This may be another illustration that each ligand may induce a somewhat different agonist receptor complex.



Figure 3: Effects of GppNHp on radioligand binding at human sst_{1.5} receptors.

Crude membrane preparations from st_{1-5} receptor transfected cells were incubated with [125I]LTT-SRIF₂₈ (\blacksquare), $[125I][Tyr^{10}]CST_{14}$ (\blacktriangledown), [125I]CGP 23996 (\blacktriangle) or $[125I][Tyr^3]$ octreotide (\blacklozenge) and the indicated concentrations of GppNHp. Data are expressed as percentage of specific binding. One representative example of at least 3 different experiments is shown.

Overall it remains to be seen whether the notion of high and low affinity states is useful at all; if two states were to exist and the ligands differentiate between these, one would expect biphasic competition curves, however these were not observed. One may wonder why endogenous peptides such as SRIF₂₈ or CST may bind to G-protein-uncoupled SRIF receptors; to be functionally relevant this suggest G-protein-independent signalling pathways. A Na⁺/H⁺ exchanger regulatory factor (NHERF) binds to the β_2 -adrenergic receptors to mediate inhibition of a Na⁺/H⁺ exchanger without involving any G-protein (Hall et al., 1998). SRIF receptors were found to inhibit Na⁺/H⁺ exchanger activity in a pertussis toxin-insensitive manner (Barber et al., 1989; Hou et al., 1994), an effect, which might also involve NHERF or NHERF-like proteins, in the absence of G-protein coupling.

According to the "ternary complex model", agonists bind with high affinity to Gprotein-coupled receptors, which stabilises the receptor/ G-protein complex, and with low affinity to non-coupled receptors. Antagonists on the other hand, bind with the same affinity to both, G-protein-coupled and non-coupled receptors (De Lean et al., 1980). The ternary complex model was extended to the "allosteric ternary complex model", since mutants of adrenergic and other receptors were shown to be constitutively active and thereby couple to G-proteins even in the absence of any ligand (Samama et al., 1993; Lefkowitz et al., 1993). However, the various versions of these models do not explain the present results, since all four tested radioligands are shown to behave as full agonists in second messenger studies at sst₁₋₅ receptors (De Lecea et al., 1996; Hoyer et al., 1994b), but nevertheless show depending on the radioligand and the SRIF receptor subtype "antagonist" behaviour in binding to receptors coupled and non-coupled to Gproteins. The results may rather be explained by assuming multiple agonist-specific receptor conformations, which have already been suggested for β_2 -adrenergic receptors as in adenylate cyclase assays the G-protein dissociation rate was agonist-specific (Krumins et al., 1997). Another study at Y_4 receptors supports this model: iodinated pancreatic polypeptide, which is an endogenous agonist at rat Y4 receptors as peptide YY is, labelled about 26-fold more rat Y4 receptor sites in COS cells than iodinated peptide YY.

Figure 4: Comparison of affinity profiles defined by $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}, [^{125}I]CGP$ 23996 and $[^{125}I][Tyr^{3}]$ octreotide at human recombinant sst₅ receptors expressed in CCL39 cells.



Data are from tables 3(A)-(E) and compare pK_d-values of human sst5 receptors obtained in radioligand binding assays. Correlation coefficients (r) are indicated in the plots.

Binding of the pancreatic polypeptide was rather insensitive to GppNHp, whereas binding of peptide YY was efficiently inhibited by GppNHp ($E_{max} = 78 \pm 4 \%$) (Walker et al., 1997).

Addition of 20 μ M GTP γ S to rat sst₁ receptors immunoprecipitated in complex with [¹²⁵I][Tyr¹¹]SRIF₁₄ induced dissociation of the iodinated ligand, but roughly 30 % of the ligand/ receptor complex was insensitive to GTP γ S (Gu et al., 1995) suggesting binding of [¹²⁵I][Tyr¹¹]SRIF₁₄ to G-protein-coupled and –uncoupled receptors as observed with [¹²⁵I]LTT-SRIF₂₈ in our study.

In conclusion, our study shows, that different agonists may bind a given receptor with different features; G-protein-coupled receptors therefore might not only exist in a G-protein-coupled state with high affinity for agonists and in a G-protein-uncoupled state with low affinity for agonists, but rather in multiple agonist-specific receptor states. As shown for [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, some agonists seem to bind not only G-protein-coupled receptors, but also G-protein-uncoupled receptors with high affinity as suggested by their low GppNHp-sensitivity, while other agonists like [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide seem to bind mostly the G-protein-coupled receptor conformation. Since the SRIF receptors were overexpressed in CCL39 cells, the receptor level compared to the G-protein level is probably higher and therefore the ratio of G-protein-uncoupled receptors to G-protein-coupled receptors is higher than in vivo, but nevertheless G-protein-coupled and –uncoupled receptors in an equilibrium are also existent in vivo.

Ultimately, the data also show that depending on the radioligand used, large differences in affinity can be determined and thus it is not surprising that the so-called selectivity ratios reported from one or another group may be entirely different; for instance, seglitide shows the rank order $sst_2 > sst_5 > sst_3$ when defined with [¹²⁵I]LTT-SRIF₂₈ but the rank order $sst_5 > sst_2 > sst_3$ when determined with [¹²⁵I]CGP 23996, and if one starts comparing different radioligand the situation is even more complex.

Chapter 6

Characterisation of human recombinant somatostatin receptors: 2) modulation of GTPγS binding

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6.1. Abstract

G-protein activation by somatostatin (SRIF), cortistatin (CST) and analogues of these neuropeptides was investigated at human somatostatin receptor subtypes 1-5 (sst_{1-5}) stably expressed in CCL39 Chinese hamster lung fibroblast cells by measuring agonist-stimulated [${}^{35}S$]GTP γ S binding.

 $[^{35}S]GTP\gamma S$ binding was performed in the presence of 100 mM NaCl and 1 μ M GDP, although higher E_{max} and/ or pEC₅₀ values may have been obtained under other conditions, but at the expense of lower absolute stimulation or signal/ noise ratio.

SRIF₁₄ stimulated [³⁵S]GTP γ S binding to 162 %, 220 %, 148 % and 266 % of control levels levels via sst₂, sst₃, sst₄ and sst₅ receptors, respectively. At sst₁ receptors, SRIF₁₄ produced only a limited stimulation (E_{max} = 115 %). Hence sst₁ receptors were not subjected to further [³⁵S]GTP γ S binding experiments. [³⁵S]GTP γ S binding assays were then performed with sst_{2.5} receptors.

Most of the peptide analogues stimulated [${}^{35}S$]GTP γS binding in sst₂₋₅ receptor expressing cells. BIM 23056 behaved as an antagonist on SRIF₁₄-induced [${}^{35}S$]GTP γS binding with apparent pK_B-value of 6.33 and 5.84 at hsst₃ and hsst₅ receptors, respectively, whereas neither agonism nor antagonism could be shown (at 1 μ M) at sst₂ or sst₄ receptors. The effect at sst₅ receptors was not surmountable and needs further investigations. The so-called "antagonist" SA, was devoid of antagonist activity at sst₂ or sst₃ receptors, whereas it was almost a full agonist at sst₄ and sst₅ receptor mediated [${}^{35}S$]GTP γ S binding.

The [³⁵S]GTP γ S binding profiles of hsst₂₋₅ receptors were compared to their respective radioligand binding profiles. For sst₄ and sst₅ receptors, the rank order of affinity of all tested radioligands correlated highly significantly with [³⁵S]GTP γ S binding (r = 0.814 - 0.897). At sst₃ receptors, [³⁵S]GTP γ S correlated somewhat less with binding profiles obtained with [¹²⁵I][Tyr¹⁰]CST₁₄ and [¹²⁵I]CGP 23996 than with [¹²⁵I]LTT-SRIF₂₈ (r = 0.743, 0.757 and 0.882, respectively).

At sst₂ receptors, [³⁵S]GTP γ S binding correlated with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide binding profiles (r = 0.596- 0.699), but not with [¹²⁵I][Tyr¹⁰]CST₁₄ binding.

The present [³⁵S]GTPγS binding data combined to previous radioligand binding results obtained in cells expressing human SRIF receptors, suggest that at any given receptor, agonists' rank orders of potency (not to mention absolute affinity values which vary profoundly) are not as strictly ordered as may be anticipated. We are investigating these aspects further by analysing additional signalling pathways.

6.2. Results

Assay conditions

The conditions for [³⁵S]GTP γ S binding assays were established at hsst₅ receptors using SRIF₁₄ as the agonist and a Mg²⁺-concentration of 5 mM. Initially, 100 mM NaCl were added to determine the optimal GDP-concentration (table 1(A); figure 1). SRIF₁₄ did not stimulate [³⁵S]GTP γ S binding in the absence of GDP. Basal levels of specifically bound [³⁵S]GTP γ S decreased with increasing GDP concentrations (from 0.1 to 30 μ M), whereas the agonist-stimulated [³⁵S]GTP γ S binding increased to reach a maximum at 30 μ M GDP (E_{max} = 475 ± 54 %). In parallel, an increase of the GDP-concentration was accompanied by a decrease of the pEC₅₀-value of SRIF₁₄ (from 8.82 to 8.06, see table 1 and figure 1). Therefore, a GDP-concentration of 1 μ M was considered as optimal with respect to absolute stimulation but also signal to noise ratio and apparent potency (E_{max} = 266 ± 19 %; pEC₅₀ = 8.39 ± 0.12). This set-up was used to determine the optimal NaCl-concentration (table 1(B); figure 2). The maximal stimulation of [³⁵S]GTP γ S binding increased with increasing NaCl concentrations (E_{max} = 339 ± 50 %), whereas specific bound [³⁵S]GTP γ S decreased in parallel.

Table 1: Stimulation of $[{}^{35}S]GTP\gamma S$ binding by $SRIF_{14}$ at human sst₅ receptors: influence of different GDP or NaCl concentrations on the pEC₅₀-value and the maximal stimulation. pEC₅₀'s (-log M) and E_{max}-values [% stimulation over basal level (= 100 %)] ± SEM of three experiments are shown

GDP [µM]	pEC ₅₀	E _{max}
0	(-)	101 ± 2
0.1	8.82 ± 0.05	167 ± 5
0.3	8.80 ± 0.07	178 ± 7
1	8.39 ± 0.12	266 ± 19
5	8.43 ± 0.07	371 ± 48
10	8.38 ± 0.01	430 ± 68
30	8.29 ± 0.04	475 ± 54
100	8.06 ± 0.08	308 ± 24

Table 1(A)

Variation of the GDP concentration (100 mM NaCl)

NaCl [mM]	pEC ₅₀	E _{max}
10	9.18 ± 0.08	138 ± 11
25	9.09 ± 0.11	152 ± 4
50	8.92 ± 0.05	203 ± 8
100	8.39 ± 0.12	266 ± 19
150	8.08 ± 0.21	304 ± 20
200	7.90 ± 0.16	339 ± 50
300	7.39 ± 0.17	336 ± 68

Table 1(B)

Variation of the NaCl concentration $(1 \mu M \text{ GDP})$

In addition, an increase in the sodium chloride level (from 10 to 300 mM) markedly reduced the potency of SRIF₁₄ to stimulate [35 S]GTP γ S binding (pEC₅₀ = 9.18 to 7.39). Therefore, 100 mM NaCl was considered as optimal, although higher E_{max} and/ or lower EC₅₀-values may have been obtained under other conditions, but at the expense of lesser absolute agonist-induced stimulation or signal/ noise.



Figure 1: Effect of GDP concentration on [35 S]GTP γ S binding to microsome preparations from CCL39 cells expressing human sst₅ receptors using 100 mM NaCl.

(A) Microsomes (2 µg per assay) were incubated with [35 S]GTP γ S (0.2 nM), the indicated concentrations of SRIF₁₄ and a fixed GDP concentration. Each curve represents a different GDP concentration: 0.1 µM (\blacksquare), 0.3 µM (\blacktriangle), 1 µM (\blacktriangledown), 5 µM (\blacklozenge), 10 µM (\bullet), 30 µM (\square), or 100 µM (Δ).

(B) Microsomes were incubated with $[^{35}S]GTP\gamma S$, the indicated concentrations of SRIF₁₄, and in the absence of GDP (\blacksquare).

(C) % stimulation of $[^{35}S]$ GTP γ S binding by 1 μ M SRIF₁₄ with the indicated GDP concentrations. Data represent the percentage of basal $[^{35}S]$ GTP γ S binding at each GDP concentration.

(D) Specific [35 S]GTP γ S binding in the absence (\blacksquare) or presence (\blacktriangle) of 1 μ M SRIF₁₄ using the indicated GDP concentrations.

The data points show one representative example of 3 independent determinations.

Figure 2: Effect of sodium chloride concentration on [35 S]GTP γ S binding to microsome preparations from sst₅ receptor expressing CCL39 cells using 1 μ M GDP.



(A) Microsomes (2 µg per assay) were incubated with $[^{35}S]GTP\gamma S$ (0.2 nM), the indicated concentrations of SRIF₁₄ and a fixed NaCl concentration. Each curve represents a different NaCl concentration: 10 mM (\blacksquare), 25 mM (\blacktriangle), 50 mM (\triangledown), 100 mM (\diamondsuit), 150 mM (\bullet), 200 mM (\square), or 300 mM (Δ).

(B) % stimulation of $[^{35}S]$ GTP γ S binding by 1 μ M SRIF $_{14}$ with the indicated NaCl concentrations. Data represent the percentage of basal $[^{35}S]$ GTP γ S binding at each NaCl concentration.

(C) Specific [35 S]GTP γ S binding in the absence (\blacksquare) or presence (\blacktriangle) of 1 μ M SRIF₁₄ using the indicated NaCl concentrations.

The data points represent one representative example of 3 different experiments.

Table 2: Stimulation of $[{}^{35}S]GTP\gamma S$ binding by SRIF, CST, and various analogues at human sst₂₋₅ receptors: comparison of pEC₅₀ values (-log M) and E_{max}-values [% stimulation] ± SEM of 3 independent determinations

Table 2(A)	CCL	39/hsst ₂	CCL39/hsst ₃		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	162 ± 3	6.95 ± 0.05	220 ± 8	7.32 ± 0.11	
$SRIF_{28}$	172 ± 7	6.14 ± 0.03	225 ± 6	6.96 ± 0.06	
LTT-SRIF ₂₈	168 ± 9	6.78 ± 0.20	243 ± 5	7.44 ± 0.19	
CST ₁₇	137 ± 5	5.83 ± 0.15	188 ± 12	6.59 ± 0.15	
[Tyr ¹⁰]CST ₁₄	124 ± 4	6.28 ± 0.27	151 ± 10	6.83 ± 0.27	
seglitide	185 ± 5	7.39 ± 0.09	159 ± 2	5.78 ± 0.02	
CGP 23996	159 ± 8	6.06 ± 0.09	197 ± 18	7.14 ± 0.08	
octreotide	158 ± 11	6.52 ± 0.34	150 ± 19	6.70 ± 0.30	
[Tyr ³]octreotide	181 ± 3	6.57 ± 0.14	156 ± 4	5.76 ± 0.07	
L362,855	132 ± 1	5.65 ± 0.03	128 ± 2	6.27 ± 0.29	
BIM 23056	78 ± 1	(-)	88 ± 2	(-)	
BIM 23052	133 ± 5	5.91 ± 0.27	212 ± 5	6.29 ± 0.04	
cycloantagonist SA	102 ± 2	(-)	116 ± 6	(-)	

These optimised conditions were used in [35 S]GTP γ S binding assays performed with sst₂₋₅ receptors. SRIF₁₄ stimulated [35 S]GTP γ S binding at sst₂, sst₃, sst₄ and sst₅ receptors to 162 %, 220 %, 148 % and 266 % respectively, of control levels (table 2; figure 3). At sst₁ receptors SRIF₁₄ produced only a slight stimulation (E_{max} = 115 %), which was not increased by using 5 μ M GDP (data not shown); hence sst₁ receptors were not subjected to further [35 S]GTP γ S binding experiments.

Table 2(B)	CCL	.39/hsst ₄	CCL39/hsst ₅		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	148 ± 3	8.05 ± 0.17	266 ± 19	8.39 ± 0.12	
SRIF ₂₈	145 ± 8	7.58 ± 0.13	268 ± 14 7.65 ± 0.0		
LTT-SRIF ₂₈	149 ± 3	7.12 ± 0.26	278 ± 6	7.63 ± 0.09	
CST ₁₇	146 ± 12	7.66 ± 0.07	231 ± 7	7.94 ± 0.09	
[Tyr ¹⁰]CST ₁₄	142 ± 3	7.02 ± 0.22	215 ± 19	7.43 ± 0.08	
seglitide	N.D.	N.D.	240 ± 18	7.89 ± 0.10	
CGP 23996	151 ± 4	8.12 ± 0.07	211 ± 9	7.12 ± 0.31	
octreotide	126 ± 2	5.67 ± 0.21	278 ± 13	6.89 ± 0.09	
[Tyr ³]octreotide	131 ± 10	5.49 ± 0.03	220 ± 1	6.56 ± 0.17	
L362,855	N.D.	N.D.	231 ± 16	6.29 ± 0.02	
BIM 23056	98 ± 3	(-)	100 ± 12	(-)	
BIM 23052	154 ± 1	6.42 ± 0.11	266 ± 12	6.80 ± 0.14	
cycloantagonist SA	126 ± 5	5.57 ± 0.05	222 ± 5	5.82 ± 0.08	

Hsst₂ receptors

Interestingly, $SRIF_{14}$ revealed higher potencies than $SRIF_{28}$ in stimulating [³⁵S]GTP γ S binding at sst₂₋₅ receptors, although their affinities determined in radioligand binding studies are not distinguishable (Siehler et al., submitted (a)). $SRIF_{14}$ showed an E_{nax} of 162 % at sst₂ receptors. Most of the compounds tested had similar efficacy to $SRIF_{14}$, except cortistatin analogues, L362,855 and BIM 23052, which acted as partial agonists.

BIM 23056 did not stimulate [³⁵S]GTP γ S binding at any of the receptor subtypes, and the cycloantagonist SA was also devoid of activity at sst₂ and sst₃ receptors. Since BIM 23056 and the SA compound revealed no or only very low agonist activities at [³⁵S]GTP γ S binding, both peptides were tested for their potential antagonist activity on SRIF₁₄-stimulated [³⁵S]GTP γ S binding (table 3; figure 4).



Figure 3: Stimulation of specific [35 S]GTP γ S binding to microsome preparations from CCL39 cells expressing human sst₂₋₅ receptors by SRIF analogues.

Microsomes of transfected cells (sst₂, sst₃, sst₄: 4 µg protein; sst₅: 2 µg protein) were incubated with [³⁵S]GTP γ S (0.2 nM), the indicated concentrations of SRIF₁₄ (**■**),SRIF₂₈ (**▲**), CST₁₇ (**▼**), CGP 23996 (**♦**), seglitide (**●**), or octreotide (Δ) in the presence of 5 mM MgCl₂, 1 µM GDP, and 100 mM NaCl. Graphs represent the percentage of specific [³⁵S]GTP γ S binding stimulated by 10 µM SRIF₁₄, which was included in each experiment. The data points show one representative example of 3 different experiments performed in triplicates.

No antagonist activity could be measured for the "cycloantagonist" SA at sst_{2-5} receptors, but rather a slightly increased pEC₅₀ of SRIF₁₄ when tested in the presence of SA (1 μ M final concentration). BIM 23056 (1 μ M) was devoid of effect and may have to be tested at higher concentrations.

The following rank order of potency in stimulating [³⁵S]GTP γ S binding at sst₂ receptors was observed: seglitide > SRIF₁₄ > LTT-SRIF₂₈ > octreotide \approx [Tyr³]octreotide > [Tyr¹⁰]CST₁₄ > SRIF₂₈ > CGP 23996 > BIM 23052 \approx CST₁₇ > L362,855. The [³⁵S]GTP γ S binding profiles of human sst₂ receptors were correlated to their pharmacological profiles determined in radioligand binding experiments (tables 4 and 5; figure 5).

The [³⁵S]GTP γ S binding profile correlated modestly with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide binding profiles (r = 0.596- 0.699), and not at all with [¹²⁵I][Tyr¹⁰]CST₁₄ binding.

Hsst₃ receptors

SRIF₁₄ displayed an E_{max} of 220 % at sst₃ receptors. The somatostatin analogues, CGP 23996 and BIM 23052 had similar efficacy to SRIF₁₄. The cortistatin and octreotide analogues, seglitide, and L362,855 acted as partial agonists whereas BIM 23056 and SA were virtually devoid of activity. BIM 23056 (1 µM final concentration) behaved as an antagonist on SRIF₁₄-stimulated [³⁵S]GTPγS binding (pK_B = 6.33 ± 0.24) whereas SA at 1 µM showed no antagonism. The following rank order of potency in stimulating [³⁵S]GTPγS binding was observed at sst₃ receptors: LTT-SRIF₂₈ ≈ SRIF₁₄ > CGP 23996 > SRIF₂₈ > [Tyr¹⁰]CST₁₄ ≈ octreotide ≈ CST₁₇ > BIM 23052 ≈ L362,855 > seglitide > [Tyr³]octreotide. The [³⁵S]GTPγS binding profile of human sst₃ receptors was compared to their pharmacological profiles determined in radioligand binding experiments (tables 4 and 5; figure 5). The affinities obtained with [¹²⁵I][Tyr¹⁰]CST₁₄ and [¹²⁵I]CGP 23996 correlated somewhat less with [³⁵S]GTPγS binding than affinities obtained with [¹²⁵I]LTT-SRIF₂₈ (r = 0.743, 0.757 and 0.882, respectively).

Hsst₄ receptors

SRIF₁₄ displayed an E_{max} of 148 % at sst₄ receptors. Most of the compounds tested had similar efficacy to SRIF₁₄, except octreotide analogues, and SA which acted as partial agonists. BIM 23056, at 1µM, did not stimulate [³⁵S]GTPγS binding, but was also devoid of antagonist activity. The following rank order of potency in stimulating [³⁵S]GTPγS binding was observed at sst₄ receptors: CGP 23996 > SRIF₁₄ > CST₁₇ ≈ SRIF₂₈ > LTT-SRIF₂₈ ≈ [Tyr¹⁰]CST₁₄ > BIM 23052 > octreotide ≈ [Tyr³]octreotide ≈ cycloantagonist SA. The [³⁵S]GTPγS binding profile of human sst₄ receptors was correlated to the pharmacological profiles determined in radioligand binding experiments (tables 4 and 5; figure 5). The radioligand binding profiles of all tested radioligands correlated well with corresponding [³⁵S]GTPγS binding profile (r = 0.867 -0.897).

Table 3: Antagonistic activity of BIM 23056 and cycloantagonist SA (10⁻⁶ M final concentration) on SRIF₁₄-stimulated [³⁵S]GTP γ S binding at human sst₂₋₅ receptors: comparison of pEC₅₀-values (-log M), E_{max}-values [% stimulation], and pK_B-values \pm SEM of 3 independent determinations

	SF	RIF ₁₄	SRIF ₁₄		SRIF ₁₄			
			+ cycloantagonist SA			+BIM 23056		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	рК _в	E _{max}	pEC ₅₀	pК _в
CCL39/	162	6.95	171	7.53	-	169	7.74	
hsst ₂	± 3	± 0.05	± 6	± 0.06		± 5	± 0.04	
CCL39/	220	7.32	161	7.38	-	153	6.72	6.33
hsst ₃	± 8	± 0.11	± 8	± 0.06		± 8	± 0.17	± 0.24
CCL39/	148	8.05	126	8.67	-	126	8.73	
$hsst_4$	± 3	± 0.17	± 4	± 0.09		± 1	± 0.13	
CCL39	266	8.39	158	8.85	box.	137	8.19	5.84
hsst ₅	±19	± 0.12	± 5	± 0.03		± 7	± 0.04	± 0.17

SRIF₁₄ displayed an E_{max} of 255 % at sst₅ receptors. All compounds tested were close to full agonists compared to SRIF₁₄, the least efficacious compounds showing about 70 % intrinsic activity. Only BIM 23056 was devoid of agonist activity. When tested as an antagonist, an apparent pK_B of 5.84 was determined, but the antagonism appeared to be non competitive. The following rank order of potency in stimulating [³⁵S]GTPγS binding at sst₅ receptors was observed: SRIF₁₄ > CST₁₇ \approx seglitide > SRIF₂₈ \approx LTT-SRIF₂₈ > [Tyr¹⁰]CST₁₄ > CGP 23996 > octreotide \approx BIM 23052 > [Tyr³]octreotide > L362,855 > SA. [³⁵S]GTPγS binding profiles of human sst₅ receptors were correlated to their pharmacological profiles determined in radioligand binding experiments (tables 4 and 5; figure 5). At sst₅ receptors, the binding profiles of all tested radioligands correlated highly with their corresponding [³⁵S]GTPγS binding profile (r = 0.814 -0.874).

6.3. Discussion

We have reported previously some rather marked differences in B_{max} -values and ligand affinities at human sst₅ receptors stably expressed in CCL39 cells using the four agonist radioligands [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide. On the other hand, such differences were not observed at human sst₁₋₄ receptors expressed in the same cells (Siehler et al., 1998a, submitted (a)), although a similar situation was noticed with the fish sst₃ receptor (Siehler et al, 1999). The nonhydrolysable GTP-analogue guanylylimidodiphospate (GppNHp) inhibited radioligand binding to various degrees even at a single receptor subtype.



Figure 4: Antagonist activity of BIM 23056 on SRIF₁₄-stimulated [35 S]GTP γ S binding at human SRIF receptor subtypes.

Microsomes of SRIF receptor transfected CCL39 cells were incubated with $[^{35}S]GTP\gamma S$ (0.2 nM), the indicated concentrations of SRIF₁₄ and either without (\blacksquare) or with BIM 23056 (\blacktriangle)(1 μ M final concentration), in the presence of 5 mM MgCl₂, 1 μ M GDP, and 100 mM NaCl. Graphs show the percentage of specific $[^{35}S]GTP\gamma S$ binding stimulated by 10 μ M SRIF₁₄, which was included in each experiment. The curves represent one example of 3 different experiments performed in triplicates. pK_B-values ± SEM are shown in the graphs.

The data suggested, that $[^{125}I][Tyr^{3}]$ octreotide and $[^{125}I]CGP$ 23996, which defined higher ligand affinities, label predominantly a G-protein-coupled sst₅ receptor population, and therefore lower receptor densities; whereas the agonists $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I][Tyr^{10}]CST_{14}$ seemed to label G-protein-coupled and -uncoupled sst₅ receptors i.e. higher receptor densities (Siehler et al., submitted (a)), in spite of the fact, that the non-iodinated ligands behave as full agonists in second messenger experiments (De Lecea et al., 1996; Hoyer et al., 1994b). In addition, we noticed that rank orders of affinity defined with the different radioligands at the same receptors may vary to a significant extent. These data do not fit to the allosteric ternary complex model (De Lean et al., 1980; Lefkowitz et al., 1993; Samama et al., 1993), but rather suggest various agonist-specific receptor states.

Therefore, [³⁵S]GTP γ S binding was established at sst₅ receptors. Increasing GDP or NaCl concentrations lead to decreased pEC₅₀'s for SRIF₁₄, whereas E_{max} was increased. GTP γ S has a higher affinity than GDP for the agonist/ receptor/ G-protein complex, but high GDP concentrations will inhibit GTP γ S binding (Gilman, 1987). Hence, higher agonist concentrations might be needed to stimulate [³⁵S]GTP γ S binding in the presence of high GDP; on the other hand, such conditions allow a better gain in the system (signal/ noise).

Sodium ions are thought to increase the receptor/ G-protein interactions (Costa et al., 1990), and thereby might increase ligand-stimulated [35 S]GTP γ S binding. On the other hand, agonist binding to SRIF receptors is regulated by sodium binding to an allosteric receptor site: while receptors of the SRIF₂-family (sst₁, sst₄) are less sodium-sensitive, sodium ions inhibit agonist binding to SRIF₁-family members (sst₂, sst₃, sst₅) (Horstman et al., 1990; Raynor et al., 1993a; 1993b; Reubi and Maurer, 1986). All five SRIF receptor subtypes reveal a conserved aspartate residue in the second or third transmembrane domain; upon exchange of this residue at sst₂ and sst₃ receptors, the inhibition of agonist binding by sodium was abolished (Nehring et al., 1995; Kong et al., 1993). Eventually, 1 μ M GDP and 100 mM NaCl were considered to be optimal for the study of agonist-stimulated [35 S]GTP γ S binding via SRIF receptors.

SRIF₁₄ stimulated [³⁵S]GTP γ S binding to 162 %, 220 %, 148 % and 266 % respectively of control levels at sst₂, sst₃, sst₄ and sst₅ receptors. By contrast, although coupling of sst₁ receptors to inhibition of adenylate cyclase activity is reported (Hoyer et al., 1994b; Patel et al., 1994), stimulation of [³⁵S]GTP γ S binding was almost not detectable at sst₁ receptors. The expression levels of the diverse G-protein subunits vary between different cell lines, and might be partially responsible for apparently deficient G-proteincoupling as has been reported for sst₁ receptors (see Hoyer et al, 1995a, 1995b). **Table 4:** Human sst₂₋₅ receptors: comparison of affinities $(pK_d)s$ of the receptors labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 or [¹²⁵I][Tyr³]octreotide (Siehler et al., submitted (a)), and potencies $(pEC_{50})s$ in stimulation of [³⁵S]GTP γ S binding (table 2); data are expressed as pK_d 's or pEC_{50} 's (log M) or E_{max} -values [% stimulation] of 3 determinations

	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[¹²⁵ I][Tyr ³] octreotide	[³⁵ S]GTPγS	
	pK _d	рК _d	pK _d	pK _d	E _{max}	pEC ₅₀
SRIF ₁₄	10.00	10.06	10.10	10.01	162	6.95
SRIF ₂₈	9.92	10.16	9.99	9.99	172	6.14
LTT-SRIF ₂₈	9.70	8.90	10.06	9.17	168	6.78
CST ₁₇	9.07	9.29	9.33	8.85	137	5.83
[Tyr ¹⁰]CST ₁₄	8.77	8.91	8.93	9.00	124	6.28
seglitide	9.96	9.62	9.82	9.81	185	7.39
CGP 23996	8.58	8.94	9.06	8.95	159	6.06
octreotide	9.19	9.11	9.16	9.10	158	6.52
[Tyr ³]octreotide	8.43	7.10	9.48	8.66	181	6.57
L362,855	8.36	8.79	8.69	8.79	132	5.65
BIM 23056	6.33	6.23	6.33	6.38	78	(-)
BIM 23052	8.30	8.50	8.76	8.55	133	5.91
cycloantagonist SA	5.40	5.74	5.80	5.77	102	(-)

Table 4(A) CCL39/hsst₂

However, negative coupling of sst₁ receptors to adenylate cyclase activity could be measured in CCL39 cells (Siehler and Hoyer, submitted (c)), which might be explained by an amplification effect in the signalling cascade, since a single G-protein may activate or inhibit many effector molecules such as adenylate cyclase (Birnbaumer and Birnbaumer, 1995).
	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[³⁵ S]	GTPγS
	pK_d	pK_d	pK _d	E _{max}	pEC ₅₀
$SRIF_{14}$	9.54	9.67	9.71	220	7.32
SRIF ₂₈	9.65	9.80	9.94	225	6.96
LTT-SRIF ₂₈	9.84	9.26	10.09	243	7.44
CST ₁₇	9.43	9.52	9.88	188	6.59
[Tyr ¹⁰]CST ₁₄	8.70	8.90	9.02	151	6.83
seglitide	6.88	7.89	7.68	159	5.78
CGP 23996	8.82	9.28	9.15	197	7.14
octreotide	7.88	8.60	8.44	150	6.70
[Tyr ³]octreotide	6.84	6.20	7.90	156	5.76
L362,855	7.62	8.25	8.29	128	6.27
BIM 23056	6.90	7.08	7.20	88	(-)
BIM 23052	8.42	9.55	9.71	212	6.29
cycloantagonist SA	6.23	7.08	6.88	116	(-)

Table 4(B) CCL39/hsst₃

The pEC₅₀-values determined in [³⁵S]GTP γ S binding are obviously much lower than the respective pK_d-values determined in radioligand binding assays, especially for sst₂ and sst₃ receptors. This may be due to the rather low density of receptors expressed in the CCL39 cells used here.

SRIF₁₄ stimulates [³⁵S]GTP γ S binding with a higher potency than SRIF₂₈, at all four receptors. In CCL39 cells, SRIF₁₄ and SRIF₂₈ bind with similar high affinity to human sst₅ receptors (Siehler et al., 1998a, 1998b). In other studies, SRIF₂₈ shows higher affinity than SRIF₁₄ in radioligand and [³⁵S]GTP γ S binding assays at human sst₅ receptors expressed in CHO (e.g. Williams et al., 1997).

	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[³⁵ S]	GTPγS
	pK_d	pK _d	рК _d	E _{max}	pEC ₅₀
$SRIF_{14}$	8.91	8.39	8.87	148	8.05
SRIF ₂₈	9.08	8.44	9.06	145	7.58
LTT-SRIF ₂₈	9.16	9.13	9.37	149	7.12
CST ₁₇	9.24	9.55	9.26	146	7.66
[Tyr ¹⁰]CST ₁₄	8.44	8.17	8.30	142	7.02
CGP 23996	8.77	8.67	8.62	151	8.12
octreotide	6.40	5.76	6.02	126	5.67
[Tyr ³]octreotide	6.29	6.17	5.89	131	5.49
BIM 23056	7.17	6.47	7.04	98	(-)
BIM 23052	8.63	8.20	8.13	154	6.42
cycloantagonist SA	6.48	6.07	6.29	126	5.57

Table 4(C) CCL39/hsst₄

The relative potency of CST_{17} in stimulating [³⁵S]GTP γ S binding is equivalent to that of SRIF₂₈ and moderately lower than that of SRIF₁₄ at the receptors investigated here. Similarly, CST_{17} has been reported to bind with similar high affinity to all SRIF receptor subtypes (Siehler et al., 1998a). Therefore, it cannot be decided which receptor subtype(s) may mediate the cortistatin-specific effects on neuronal depression and sleep modulation (De Lecea et al., 1996; Fukusumi et al., 1997). Although octreotide and seglitide show high affinity for sst₅ receptors (Siehler et al, 1998a), the relative potency of the two compounds compared to somatostatins in [³⁵S]GTP γ S binding, suggest octreotide and seglitide to be relatively more selective for sst₂ receptors. Nevertheless, octreotide, when used to inhibit growth of hormone-secreting tumours (Lamberts et al., 1991), might activate sst₂ and sst₅ receptors when both receptor subtypes are expressed.

	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[¹²⁵ I][Tyr ³] octreotide	[³⁵ S]GTPγS	
	pK _d	pK _d	рК _d	pK _d	E _{max}	pEC ₅₀
SRIF ₁₄	9.53	9.01	9.82	9.87	255	8.39
SRIF ₂₈	9.39	9.18	10.15	10.30	268	7.65
LTT-SRIF ₂₈	8.47	8.12	9.70	9.60	278	7.63
CST ₁₇	9.54	9.37	10.21	9.85	231	7.94
[Tyr ¹⁰]CST ₁₄	8.67	8.06	9.77	9.65	215	7.43
seglitide	8.70	9.14	10.22	10.18	240	7.89
CGP 23996	6.59	6.67	8.26	8.68	211	7.12
octreotide	7.17	7.31	8.96	9.48	278	6.89
[Tyr ³]octreotide	6.49	6.00	8.03	8.41	220	6.56
L362,855	7.17	7.17	8.72	9.17	231	6.29
BIM 23056	7.17	6.68	7.77	8.32	100	(-)
BIM 23052	7.92	7.45	9.59	9.28	266	6.80
cycloantagonist SA	6.38	6.02	7.77	8.25	222	5.82

Table 4(D) CCL39/hsst₅

BIM 23056 behaves as an antagonist on SRIF₁₄-induced [³⁵S]GTPγS binding with apparent pK_B-value of 6.33 at hsst₃ receptors and 5.84 at hsst₅ receptors; whereas neither agonism nor antagonism could be shown (at 1 µM) at sst₂ or sst₄ receptors. The antagonism at sst₅ receptors is not surmountable and needs further investigations. The so-called antagonist SA, is devoid of antagonist activity at sst₂ or sst₃ receptors, whereas it is almost a full agonist at sst₄ and sst₅ receptors. BIM 23056 was previously described as sst₃-selective agonist (Patel & Srikant, 1994), but this is not replicated here. BIM 23056 was already reported as a competitive hsst₅ receptor-antagonist on [³⁵S]GTPγS binding in CHO-K1 cells, with a higher pK_B (= 7.44) (Williams et al., 1997). In the same sst₅ receptor-expressing cells BIM 23056 was described to potently antagonise SRIF₁₄-induced phosphoinositide stimulation as well as SRIF₁₄-induced increase of intracellular Ca²⁺ (pK_B = 7.4 and 8.0, respectively) (Wilkinson et al., 1996; 1997). **Table 5:** Correlation coefficients (r) of correlation analyses between $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 or $[^{125}I][Tyr^3]$ octreotide binding (pK_d) and stimulation of $[^{35}S]GTP\gamma S$ binding (pEC₅₀) at human sst₂₋₅ receptors. Data used for correlation are shown in table 4(A)-(D).

	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[¹²⁵ I][Tyr ³] octreotide
CCL39/ hsst ₂	0.682	0.189	0.699	0.596
CCL39/ hsst ₃	0.882	0.743	0.757	~ 1
CCL39/ hsst ₄	0.892	0.867	0.897	-
CCL39/ hsst ₅	0.874	0.882	0.831	0.814

Evidently, G-protein coupling as measured in radioligand binding or second messenger experiments and G-protein activation measured by [${}^{35}S$]GTP γS binding may be rather divergent at times. The two GTP-analogues GppNHp and GTP γS have different Gprotein binding properties: GTP γS binds to recombinant G_o or G_{i1} with higher affinity than GppNHp; in line with the present data, GTP γS activates G_o more potently than does GppNHp. In addition, when compared to GTP both non-hydrolysable GTPanalogues tend to hyperactivate G-proteins, and therefore are different from the naturally occurring and hydrolysable GTP (Rebois et al., 1997; Remmers and Neubig, 1996). The correlation between radioligand and [${}^{35}S$]GTP γS binding is reasonably good at sst₃, sst₄ and sst₅ receptors, which may be surprising in the latter case, since radioligand binding has shown some rather marked differences when the profiles determined by the different radioligands are compared at hsst₅. Also rather surprising, is the fact that at sst₂ receptors, the correlations are not particularly impressive (especially with [125 I][Tyr 10] CST₁₄ binding), although it should be kept in mind that the ranges were rather narrow between the most and least potent compounds.

Figure 5: Human recombinant sst_{2-5} receptors expressed in CCL39 cells: correlation between [¹²⁵I]LTT-SRIF₂₈ (left column) or [¹²⁵I][Tyr¹⁰]CST₁₄ (right column) binding and agonist-stimulated [³⁵S]GTP γ S binding.



Data are from table 4(A)-(D), and represent pK_d -values derived from radioligand binding of human sst₂₋₅ receptors and pEC_{50} -values obtained from [³⁵S]GTP γ S binding assays. Correlation coefficients (r) are indicated in all plots.

However, what appears to be clear is that the individual rank orders of potency determined using either method do not fit very well, and correlations are only obtained because altogether there is a general agreement at a given receptor more than an exact replication from one test to another. This suggests that at any given receptor, agonists' rank orders of potency (not to mention absolute affinity values which vary profoundly) are not as well defined as may be anticipated. We are investigating these aspects further by analysing additional signalling pathways.

7.1. Abstract

The five human somatostatin receptor subtypes (hsst₁₋₅) were stably expressed in CCL39 cells (Chinese hamster lung fibroblast cells) to study the inhibition of forskolinstimulated adenylate cyclase (FSAC) activity induced by somatostatin (SRIF), cortistatin (CST) and SRIF peptide analogues. Inhibition of FSAC was observed with all five receptors, although the maximal effects produced by SRIF₁₄ varied from around 40 (sst₁, sst₂, sst₄) to 67 % (sst₃, sst₅) reflecting to some extent differences in receptor density. SRIF₂₈ was slightly more potent than SRIF₁₄ to inhibit FSAC at all five receptors, although the potency of the natural peptides SRIF₁₄, SRIF₂₈ and CST₁₇ was generally similar with pEC₅₀-values ranging from 7.5 to 8.7 depending on receptor and ligand.

At SRIF₁ receptors (sst₂, sst₃, sst₅) most of the peptide analogues displayed full agonism (with some exceptions e.g. BIM 23056 at sst₁₋₃ and sst₅ receptors, and L362,855 and cycloantagonist SA at sst₃ receptors), whereas at SRIF₂ receptors these analogues tended to behave as partial agonists. BIM 23056 was an antagonist at sst₃ receptors ($pK_B = 6.33$), but not at other receptors.

The AC inhibition profiles of sst_{1-5} receptors were compared with the different radioligand binding profiles as well as with [³⁵S]GTP γ S binding profile for sst_{2-5} receptors. High correlations were observed between FSAC inhibition, radioligand binding and [³⁵S]GTP γ S binding profiles at sst_3 , sst_4 and sst_5 receptors; by contrast, correlation coefficients at sst_1 and sst_2 receptors were low, and the binding profiles of [¹²⁵I][Tyr¹⁰]CST₁₄ correlated poorly. In line with these findings, the FSAC inhibition and [³⁵S]GTP γ S binding correlated poorly at sst_2 receptors (sst_1 receptors show no significant induction of [³⁵S]GTP γ S binding). The apparent lack of or weak relationship between FSAC, radioligand or [³⁵S]GTP γ S binding observed for some SRIF receptors, suggest that different active states may exist for these receptors, which may favour one of transduction cascade over others.

Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity was determined using a radioimmunoassay measuring intracellular cyclic adenosine monophosphate (cAMP) levels in cells expressing one of the five SRIF receptors (tables 1A & 1B; figure 1).

SRIF₁ receptors

Sst₂ receptors:

The most potent agonist at sst₂ receptors was seglitide (pEC₅₀ = 10.03) and the rank order of potencies was: seglitide > [Tyr³]octreotide > SRIF₂₈ > octreotide ≈ LTT-SRIF₂₈ > SRIF₁₄ ≈ CST₁₇ > CGP 23996 > L362,855 ≈ [Tyr¹⁰]CST₁₄ ≈ BIM 23052. Most of the peptides showed full or close to full agonism with intrinsic activities of 85- 110 % compared to that of SRIF₁₄, which inhibited FSAC by 33 ± 1 %. Interestingly, CST₁₇ had only low efficacy (44 % of SRIF₁₄), whereas BIM 23056 and the "cycloantagonist" were almost devoid of agonism. These two compounds however did not produce significant antagonism when tested at 1 µM against SRIF₁₄ (not shown).

Sst₅ receptors:

At sst₅ receptors, the most potent agonist was again seglitide (pEC₅₀ = 9.33). The rank order of potency was: seglitide > SRIF₂₈ \approx CST₁₇ > SRIF₁₄ > LTT-SRIF₂₈ > [Tyr¹⁰]CST₁₄ \approx octreotide > BIM 23052 \approx [Tyr³]octreotide > CGP 23996 > L362,855 > BIM 23056 > cycloantagonist SA. Similarly to sst₂ receptors, most compounds displayed full agonism with intrinsic activities in the range 80- 120 % of SRIF₁₄, which inhibited FSAC by 62 ± 2 %. Octreotide was less potent at sst₅ than at sst₂ receptors. BIM 23056 displayed partial agonism (47 %). Neither, BIM 23056 nor SA did produce significant antagonism when tested at 1 µM against SRIF₁₄ (not shown).

Table 1(A)	CCL	39/hsst ₁	CCL39/hsst ₄		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	100 ± 7	8.21 ± 0.09	100 ± 5	8.53 ± 0.21	
SRIF ₂₈	114 ± 10	8.29 ± 0.12	100 ± 5	8.53 ± 0.16	
LTT-SRIF ₂₈	100 ± 7	7.18 ± 0.02	78 ± 11	7.85 ± 0.08	
CST ₁₇	62 ± 3	8.13 ± 0.14	65 ± 5	8.30 ± 0.17	
$[Tyr^{10}]CST_{14}$	100 ± 3	6.82 ± 0.05	86 ± 5	7.61 ± 0.13	
CGP 23996	97 ± 17	7.18 ± 0.20	95 ± 5	8.27 ± 0.20	
octreotide	38 ± 0	(-)	78 ± 3	6.00 ± 0.25	
[Tyr ³]octreotide	14 ± 7	(-)	81 ± 5	5.79 ± 0.19	
BIM 23056	55 ± 17	(-)	86 ± 3	7.06 ± 0.08	
BIM 23052	104 ± 7	6.69 ± 0.03	105 ± 3	7.20 ± 0.23	
cycloantagonist SA	79 ± 7	6.48 ± 0.05	73 ± 0	6.03 ± 0.07	

Table 1: Inhibition of forskolin-stimulated adenylate cyclase activity by human sst_{1-5} receptors

Sst₃ receptors:

The most potent antagonist to inhibit forskolin-stimulated cAMP production in sst₃ receptor-expressing cells was LTT-SRIF₂₈ (pEC₅₀ = 8.40). The rank order was: LTT-SRIF₂₈ > SRIF₂₈ > CGP 23996 \approx SRIF₁₄ > CST₁₇ \approx BIM 23052 > octreotide > [Tyr¹⁰]CST₁₄ \approx L362,855 \approx seglitide > cycloantagonist SA \approx [Tyr³]octreotide. Similarly to the activities measured at the other two SRIF₁ receptors, most of the compounds displayed full agonism when compared to SRIF₁₄ (67 ± 8 % inhibition of FSAC), in the range 80- 100 %. There were two noticeable exceptions, BIM 23056 and the cycloantagonist SA with values around 30 %. SA did not produce significant antagonism when tested at 1 μ M against SRIF₁₄, whereas BIM 23056 at 1 μ M produced a shift in the CRC with an apparent pK_B of 6.33 ± 10 (figure 2).

Table 1(B)	CCL39/hsst ₂		CCL	.39/hsst ₅	CCL39/hsst ₃		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	100 ± 11	8.36 ± 0.22	100 ± 10	8.33 ± 0.24	100 ± 14	7.76 ± 0.17	
SRIF ₂₈	111 ± 7	8.72 ± 0.12	109 ± 4	8.45 ± 0.12	94 ± 11	8.19 ± 0.20	
LTT-SRIF ₂₈	111 ± 7	8.33 ± 0.05	106 ± 4	7.84 ± 0.17	97 ± 5	8.40 ± 0.20	
CST ₁₇	44 ± 11	8.15 ± 0.10	92 ± 0	8.38 ± 0.26	75 ± 3	7.47 ± 0.07	
[Tyr ¹⁰]CST ₁₄	107 ± 7	6.80 ± 0.19	109 ± 10	7.69 ± 0.10	84 ± 3	6.80 ± 0.16	
seglitide	107 ± 15	10.03 ± 0.13	119 ± 12	9.33 ± 0.25	89 ± 11	6.68 ± 0.12	
CGP 23996	100 ± 7	7.79 ± 0.07	112 ± 6	7.07 ± 0.04	89 ± 3	7.84 ± 0.16	
octreotide	104 ± 4	8.44 ± 0.21	123 ± 4	7.68 ± 0.17	97 ± 2	7.01 ± 0.01	
[Tyr ³]octreotide	115 ± 7	9.70 ± 0.16	118 ± 4	7.30 ± 0.04	81 ± 2	6.31 ± 0.01	
L362,855	137 ± 4	6.87 ± 0.04	143 ± 4	6.81 ± 0.17	58 ± 17	6.70 ± 0.05	
BIM 23056	22 ± 7	(-)	47 ± 8	6.60 ± 0.04	26 ± 2	(-)	
BIM 23052	122 ± 29	6.74 ± 0.13	125 ± 10	7.40 ± 0.11	104 ± 2	7.43 ± 0.17	
cycloantagonist SA	37 ± 4	(-)	100 ± 6	5.69 ± 0.04	32 ± 8	6.38 ± 0.08	

Comparison of pEC₅₀ values (-log M) or E_{max} -values [% inhibition] ± SEM of three or more experiments; E_{max} -values were normalized to the maximal inhibition reached by SRIF₁₄ ($E_{max} = 100$ % inhibition).

SRIF₂ receptors

Sst₁ receptors:

The most potent agonist to inhibit cAMP production via sst_1 receptors was $SRIF_{28}$ (pEC₅₀ = 8.33) and the rank order of potency was: $SRIF_{28} > CST_{17} > SRIF_{14} > LTT$ - $SRIF_{28} \approx CGP \ 23996 > [Tyr^{10}]CST_{14} \approx BIM \ 23052 > cycloantagonist SA.$ When taking $SRIF_{14}$ as the reference full agonist (39 ± 4 % inhibition of FSAC), most other analogues acted as partial agonists (including CST_{17}) with efficacy values ranging from 14 to 80 % the least efficacious being octreotide and [Tyr³]octreotide. BIM 23056 and SA did not produce significant antagonism when tested at 1 μ M against SRIF₁₄ (not shown).

Sst₄ receptors:

Inhibition of cAMP production in sst₄ receptor-expressing CCL39 cells showed SRIF₂₈ to be the most potent agonist ($pEC_{50} = 8.45$) and was characterised by the rank order of potency: SRIF₂₈ > CST₁₇ \approx CGP 23996 > SRIF₁₄ > LTT-SRIF₂₈ > [Tyr¹⁰]CST₁₄ > BIM 23052 > BIM 23056 > cycloantagonist SA \approx octreotide > [Tyr³]octreotide. None of the compounds tested had an intrinsic activity lower than 65 % of that of SRIF₁₄ (37 ± 3 %), thus all compounds were very efficacious partial or full agonists.

Comparison of inhibition of FSAC at sst₁₋₅ with radioligand binding

The pharmacological profiles determined in radioligand binding and inhibition of FSAC assays were compared for all five SRIF receptors (table 2; figure 3). At hsst₅ receptors, the binding profiles of all four radioligands correlated highly significantly with the FSAC profile, although somewhat less for [¹²⁵I]LTT-SRIF₂₈ binding. Similarly, at sst₃ and sst₄ receptors, the binding profiles of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄ and [¹²⁵I]CGP 23996 correlated highly significantly with the inhibition of FSAC (correlation coefficient r = 0.83 -0.95, table 3). At hsst₁ receptors, binding and inhibition of FSAC were statistically significant, although the correlation coefficients were rather modest (0.67- 0.80). The least convincing comparisons were established with the hsst₂ receptor: thus, [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide binding correlated modestly with sst₂ receptor mediated inhibition of FSAC (r = 0.43- 0.67), whereas the [¹²⁵I][Tyr¹⁰]CST₁₄ profile showed no correlation at all. The very poor correlation stems actually from [Tyr³]octreotide, which behaved as a rather weak ligand at [¹²⁵I]LTT-SRIF₂₈ and especially [¹²⁵I][Tyr¹⁰]CST₁₄ labelled sites, yet was one of the most potent agonists at FSAC.



Figure 1: Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity by SRIF peptides in CCL39 cells expressing human sst_{1-5} receptors.

100

75

100

75

50.

25.

100

75

50.

25.

sst₅

10-10 10-9

10-8 10-7

ligand (M)

10-6

10-5

% FSAC activity

% FSAC activity

% FSAC activity

Transfected cells were treated with forskolin (10 µM) and the indicated concentrations of SRIF₂₈ (), $[Tyr^{10}]CST_{14}$ (**A**), seglitide (**V**), CGP 23996 (\diamondsuit) , octreotide (•) or cycloantagonist SA (\Box) , and cAMP levels determined by radioimmunassay using [125I]cAMP. Graphs represent the percentage of inhibition of forskolin-stimulated adenylate cyclase activity. The data points represent one representative example of 3 different experiments. The mean of the pEC50values \pm SEM of 3 determinations are shown in table 1.

Comparison of inhibition of FSAC at sst₁₋₅ with [³⁵S]GTPγS binding

Inhibition of FSAC profiles and [${}^{35}S$]GTP γS binding profiles at human sst₂₋₅ receptors (table 2; figure 4) revealed statistically significant correlations at sst₄ receptors (r = 0.98, table 3) > sst₅ and sst₃ receptors (r = 0.88 and 0.83, respectively) > sst₂ receptors (r = 0.72). [${}^{35}S$]GTP γS binding did not produce robust data with hsst₁ receptors. It can also be seen form table 2 that the rank orders of efficacy were more or less divergent depending on the receptor type.

7.3. Discussion

There are three main signalling pathways known so far to be modulated by somatostatin receptors: the adenylate cyclase/ protein kinase A-pathway, the phospholipase C/ IP₃-pathway, and the Ras/ Raf/ MAP kinase (mitogen-activated protein kinase)-pathway. In the present study, we measured the inhibition of forskolin-stimulated AC activity; forskolin stimulates directly and non selectively adenylate cyclases, although it is not established, whether all known AC isoforms are affected (Seamon et al., 1986). Thus, inhibition of forskolin-stimulated adenylate cyclase activity (FSAC) was determined in CCL39 cells expressing one of the five SRIF receptors. The maximal inhibition of cAMP production obtained via sst₃ and sst₅ receptors (e.g. for SRIF₁₄: $E_{max} = 67$ and 62 %, respectively) was larger than that produced by sst₁, sst₂ and sst₄ receptors (SRIF₁₄: $E_{max} = 39$, 33 and 37 %, respectively). The natural peptides SRIF₁₄, SRIF₂₈ and CST₁₇ were similarly potent to inhibit FSAC activity at human sst₁₋₅ receptors (pEC₅₀'s = 8.11-8.72), although SRIF₁₄ and CST₁₇ were less potent at sst₁ receptors (pEC₅₀ = 7.41) and sst₃ receptors respectively (pEC₅₀ = 7.47).

Overall, $SRIF_{28}$ seems to be slightly more potent and efficacious than $SRIF_{14}$ to inhibit cAMP production at the human SRIF receptor subtypes, whereas CST_{17} tended to show only partial agonism.

Figure 2: Antagonistic activity of BIM 23056 on $SRIF_{14}$ -inhibited forskolin-stimulated adenylate cyclase (FSAC) activity at human sst receptor subtypes.



CCL39 cells transfected with sst3 or sst5 receptors were treated with forskolin (10 μ M), the indicated concentrations of SRIF₁₄, and either without (**I**) or with BIM 23056 (**A**)(1 μ M final concentration), and cAMP levels measured as described. Graphs show the percentage of inhibition of forskolin-stimulated adenylate cyclase activity. The data points represent one representative example of 3 different experiments. pK_B-values ± SEM are shown in the graphs.

BIM 23056 and the peptide SA inhibited FSAC with low efficacy; the E_{max} -values of these peptides especially at SRIF₁ receptors (sst₂, sst₃, sst₅) were very low. Therefore, the possible antagonism by both peptides on SRIF₁₄-inhibited FSAC was studied. SA did not antagonise the effect of SRIF₁₄ at a concentration of 1 μ M, whereas BIM 23056 showed sst₃ receptor antagonism (pK_B = 6.33), but not at the other four SRIF receptor subtypes.

In previous studies, $SRIF_{28}$, CGP 23996, octreotide, and cycloantagonist SA revealed a similar cAMP inhibition profile at hsst₁ receptors expressed in HEK293 cells (Hoyer et al., 1995b); similarly for $SRIF_{14}$, $SRIF_{28}$, seglitide, CGP 23996, octreotide, BIM 23052 and cycloantagonist SA at hsst₂ receptors expressed in CHO cells (Schoeffter et al., 1995), although all pEC₅₀'s were somewhat higher compared to the present study carried out in CCL39 cells.

Table 2: Human sst₁₋₅ receptors: comparison of affinities (pK_d) 's of the receptors labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 or [¹²⁵I][Tyr³]octreotide, efficacies (pEC_{50}) 's in stimulation of [³⁵S]GTP γ S specific binding, and efficacies in inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity (table 1).

	[¹²⁵ I]	[¹²⁵ I]	$[^{125}I]$	inhib	ition of
	LTT-	$[Tyr^{10}]$	CGP	FSAC	activity
	SRIF ₂₈	CST_{14}	23996		
	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀
SRIF ₁₄	9.12	9.08	8.95	100	8.21
SRIF ₂₈	9.22	9.26	9.38	114	8.29
LTT-SRIF ₂₈	9.22	9.28	9.13	100	7.18
CST ₁₇	9.61	9.61	9.48	62	8.13
[Tyr ¹⁰]CST ₁₄	8.56	9.04	8.32	100	6.82
CGP 23996	8.33	8.31	8.45	97	7.18
octreotide	6.65	6.41	6.23	38	(-)
[Tyr ³]octreotide	5.57	5.82	5.69	14	(-)
BIM 23056	6.61	6.46	6.56	55	(-)
BIM 23052	8.37	8.62	8.17	104	6.69
cycloantagonist SA	7.02	6.80	6.48	79	6.48

Table 2(A) CCL39/hsst₁

This difference may be due to methodology, since here cAMP levels were determined indirectly in a radioimmunoassay, while in previous studies formation of [³H]cAMP was measured directly; when the latter method was applied to hsst₅ receptors expressed in CCL39 cells, SRIF₂₈, seglitide and octreotide produced pEC₅₀-values of 9.15 \pm 0.08, 9.66 \pm 0.09 and 8.46 \pm 0.11, respectively (data not shown).

	$\begin{bmatrix} 125 \\ I \end{bmatrix}$	$[^{125}I]$	$[^{125}I]$	stimulation of		inhibition of	
	LTT-	$[Tyr^{10}]$	CGP	[³⁵ S](GTPγS	FSAC activity	
	SRIF ₂₈	CST ₁₄	23996	bin	ding		
	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	8.91	8.39	8.87	100	8.05	100	8.53
SRIF ₂₈	9.08	8.44	9.06	94	7.58	100	8.53
LTT-SRIF ₂₈	9.16	9.13	9.37	102	7.12	78	7.85
CST ₁₇	9.24	9.55	9.26	96	7.66	65	8.30
[Tyr ¹⁰]CST ₁₄	8.44	8.17	8.30	88	7.02	86	7.61
CGP 23996	8.77	8.67	8.62	106	8.12	95	8.27
octreotide	6.40	5.76	6.02	54	5.67	78	6.00
[Tyr ³]octreotide	6.29	6.17	5.89	65	5.49	81	5.79
BIM 23056	7.17	6.47	7.04	-4	(-)	86	7.06
BIM 23052	8.63	8.20	8.13	113	6.42	105	7.20
cycloantagonist SA	6.48	6.07	6.29	54	5.57	73	6.03

Table 2(B) CCL39/hsst₄

The ability of a ligand-receptor complex to inhibit AC activity may vary with cell typespecific expression of G-protein isoforms and AC isoforms. Sst₁ receptors expressed in CHO cells are reported to inhibit AC activity by coupling to G_{i3} ; by contrast, according to some authors (Kagimoto et al., 1994; Kubota et al., 1994), sst₂ receptors did not couple to AC inhibition in CHO cells; only after co-transfection of G_{i1} , which is not endogenously expressed in CHO cells, inhibition of FSAC was observed. In HEK293 cells, in which G_{i1} is endogenously expressed, sst₂ receptors did not couple to AC (Law et al., 1993), although they activate G_{i3} ; in these cells, as well as in CHO cells, sst₃ receptors couple via G_{i1} proteins to AC inhibition (Law et al., 1994). Sst₂ receptors expressed in GH₄C₁ cells couple via G_{i2} and G_{i3} proteins to AC (Tallent and Reisine, 1992), but when expressed in AtT20 cells they mediate AC inhibition via G_{i1} like in CHO cells (Yajima et al., 1993).

	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	stimul	ation of	inhibition of	
	LTT-	$[Tyr^{10}]$	CGP	[Tyr ³]	$[^{35}S]GTP\gamma S$		FSAC activity	
	SRIF ₂₈	CST ₁₄	23996	octreo	bin	ding		
				tide				
	pK _d	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	10.00	10.06	10.10	10.01	100	6.95	100	8.36
SRIF ₂₈	9.92	10.16	9.99	9.99	116	6.14	111	8.72
LTT-SRIF ₂₈	9.70	8.90	10.06	9.17	110	6.78	111	8.33
CST ₁₇	9.07	9.29	9.33	8.85	60	5.83	44	8.15
[Tyr ¹⁰]CST ₁₄	8.77	8.91	8.93	9.00	39	6.28	107	6.80
seglitide	9.96	9.62	9.82	9.81	137	7.39	107	10.03
CGP 23996	8.58	8.94	9.06	8.95	95	6.06	100	7.79
octreotide	9.19	9.11	9.16	9.10	94	6.52	104	8.44
[Tyr ³]octreotide	8.43	7.10	9.48	8.66	131	6.57	115	9.70
L362,855	8.36	8.79	8.69	8.79	52	5.65	137	6.87
BIM 23056	6.33	6.23	6.33	6.38	-35	(-)	22	(-)
BIM 23052	8.30	8.50	8.76	8.55	53	5.91	122	6.74
cycloantagonist SA	5.40	5.74	5.80	5.77	3	(-)	37	(-)

Table 2(C) CCL39/hsst₂

More surprisingly perhaps, hsst₅ receptors expressed in CHO cells were found to <u>inhibit</u> FSAC at low concentrations, but to <u>stimulate</u> AC activity via G_s at high agonist concentrations (Carruthers et al., 1999); this stimulatory effect on AC activity at high agonist concentrations was not obvious at human sst₅ receptors expressed in CCL39 cells. The differential expression of the nine types of AC's has not been studied in cell lines, and it may vary from one clone to another.

G_i is known to inhibit mainly AC types I, V and VI. In vivo, AC type I is specifically expressed in neurones, whereas type V and VI are ubiquitous (for review, Birnbaumer and Birnbaumer, 1995; Taussig et al., 1993; 1994). Thus, AC type V and VI might be the isoforms inhibited by somatostatin receptors in CCL39 cells.

	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	stimulation of		inhibition of	
	LTT-	[[Tyr ¹⁰]	CGP	[Tyr ³]	$\begin{bmatrix} 1^{3}S\end{bmatrix}$	JTPγS	FSAC activity	
	SRIF ₂₈	CS1 ₁₄	23996	octreo	bin bin	ding		
	TZ	17	T7			- FA		TO
	рК _d	рк _d	pK _d	рК _d	E _{max}	pec ₅₀	E _{max}	pEC_{50}
SRIF_{14}	9.53	9.01	9.82	9.87	100	8.39	100	8.33
SRIF ₂₈	9.39	9.18	10.15	10.30	101	7.65	109	8.45
LTT-SRIF ₂₈	8.47	8.12	9.70	9.60	107	7.63	106	7.84
CST ₁₇	9.54	9.37	10.21	9.85	79	7.94	92	8.38
[Tyr ¹⁰]CST ₁₄	8.67	8.06	9.77	9.65	69	7.43	109	7.69
seglitide	8.70	9.14	10.22	10.18	84	7.89	119	9.33
CGP 23996	6.59	6.67	8.26	8.68	67	7.12	112	7.07
octreotide	7.17	7.31	8.96	9.48	107	6.89	123	7.68
[Tyr ³]octreotide	6.49	6.00	8.03	8.41	72	6.56	118	7.30
L362,855	7.17	7.17	8.72	9.17	79	6.29	143	6.81
BIM 23056	7.17	6.68	7.77	8.32	0	(-)	47	6.60
BIM 23052	7.92	7.45	9.59	9.28	100	6.80	125	7.40
cycloantagonist SA	6.38	6.02	7.77	8.25	74	5.82	100	5.69

Table 2(D) CCL39/hsst₅

Inhibition of AC in CCL39 cells was more pronounced via $hsst_3$ and sst_5 than by sst_1 , sst_2 and sst_4 receptors. In contrast, in CHO cells expressing the human sst_{1-5} receptors, the AC inhibition was highest with sst_1 receptors, and lowest at sst_3 receptors (Patel et al., 1994). Thus, it cannot be concluded, that one or the other SRIF receptor shows higher ability to inhibit FSAC, as this varies with cell lines, receptor density, and presumably G_i and/ or AC subtype expression.

We have previously reported differences in B_{max} - and affinity values at human sst₅ receptors labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide. In addition, the binding of the radioligands to the same receptor subtype was differently sensitive to GppNHp (Siehler et al., 1998a; 1998b; 1999; submitted (a)).

	[¹²⁵ I]	$\left[^{125}I \right]$	[¹²⁵ I]	stimul	ation of	inhibition of	
	LTT-	$[Tyr^{10}]$	CGP	[³⁵ S](GTPγS	FSAC activity	
	SRIF_{28}	CST ₁₄	23996	bin	ding		
	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	9.54	9.67	9.71	100	7.32	100	7.76
SRIF ₂₈	9.65	9.80	9.94	104	6.96	94	8.19
LTT-SRIF ₂₈	9.84	9.26	10.09	119	7.44	97	8.40
CST ₁₇	9.43	9.52	9.88	73	6.59	75	7.47
[Tyr ¹⁰]CST ₁₄	8.70	8.90	9.02	43	6.83	84	6.80
seglitide	6.88	7.89	7.68	49	5.78	89	6.68
CGP 23996	8.82	9.28	9.15	81	7.14	89	7.84
octreotide	7.88	8.60	8.44	42	6.70	97	7.01
[Tyr ³]octreotide	6.84	6.20	7.90	47	5.76	81	6.31
L362,855	7.62	8.25	8.29	23	6.27	58	6.70
BIM 23056	6.90	7.08	7.20	-10	(-)	26	(-)
BIM 23052	8.42	9.55	9.71	93	6.29	104	7.43
cycloantagonist SA	6.23	7.08	6.88	13	(-)	32	6.38

Table 2(E) CCL39/hsst₃

The data are expressed as pK_d 's or pEC_{50} 's (-log M), or E_{max} -values values [% stimulation or inhibition, normalized to the E_{max} of $SRIF_{14} = 100$ %] of at least 3 determinations.

These differences could not be explained by the agonist or antagonist nature of the ligands, since all four "cold" ligands displayed nearly full agonism at inhibiting FSAC activity. However, the more surprising findings may come from the comparison between FSAC, radioligand and [35 S]GTP γ S binding.

SRIF₂ receptors: Sst₁ receptors reveal a good agreement between FSAC and radioligand binding, although the three radioligands were not affected profoundly by GppNHp and no robust [35 S]GTP γ S binding could be documented. Thus, EC₅₀-values were 25 to 100 fold lower than K_d's, but overall there was a similar rank order of potency; and most compounds display partial agonism.

Table 3: Correlation coefficients (r) of linear regression analyses between the pharmacological profile of inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity and either the affinity profiles of $[^{125}I]LTT-SRIF_{28}, [^{125}I][Tyr^{10}]CST_{14}, [^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide, or the pharmacological profile of stimulation of $[^{35}S]GTP\gamma S$ binding for human sst₁₋₅ receptors

	[¹²⁵ I]LTT- SRIF ₂₈	[¹²⁵ I][Tyr ¹⁰] CST ₁₄	[¹²⁵ I]CGP 23996	[¹²⁵ I][Tyr ³] octreotide	[³⁵ S]GTPγS binding
CCL39/ hsst ₁	0.789	0.671	0.795	-	Nak
CCL39/ hsst ₂	0.548	0.007	0.669	0.428	0.716
CCL39/ hsst ₃	0.901	0.833	0.874		0.827
CCL39/ hsst ₄	0.944	0.894	0.951		0.976
CCL39/ hsst ₅	0.796	0.874	0.871	0.888	0.876

Data used for correlation analyses are presented in tables 2(A)-(E).

Sst₄ receptors: although at sst₄, like at sst₁ receptors, binding was not much affected by GppNHp, there is almost a perfect agreement between inhibition of FSAC and radioligand binding data, which show about 10 fold higher affinity. Thus at SRIF₂ receptors, values determined in radioligand binding studies, [³⁵S]GTP γ S binding and inhibition of FSAC appear to be rather predictive. **SRIF₁ receptors**: Sst₂ receptors showed a perfect agreement between the profiles defined by the four radioligands [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide, [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, which were all markedly GppNHp sensitive. However, both [³⁵S]GTP γ S binding and inhibition of FSAC are only rather modestly stimulated via sst₂ receptors in these cells. EC₅₀-values obtained in the two tests do not compare well, differences range from 25 to 1300 fold in favour of FSAC (see [Tyr³]octreotide, CST₁₇, seglitide or even SRIF₂₈ which are markedly less potent in [³⁵S]GTP γ S binding). Surprisingly, the intrinsic activities are comparable and many compounds display full agonism except BIM23056 and SA.

Figure 3: Human recombinant sst_{1-5} receptors expressed in CCL39 cells: correlation analyses between [¹²⁵I]LTT-SRIF₂₈ (left column) or [¹²⁵I][Tyr¹⁰]CST₁₄ binding (right column) and inhibition of forskolin-stimulated adenylate cyclase activity.



Data are from tables 2(A)-(E) and represent pK_d-values obtained with radioligand labeling of human sst₁₋₅ receptors and pEC₅₀-values obtained with adenylate cyclase activity assays. Correlation coefficients (r) are indicated in all plots.

The comparison with radioligand binding is even less convincing: K_d 's are about 10 to 100 fold higher than EC₅₀'s in FSAC, with marked exception: [Tyr³]octreotide and seglitide are more potent at FSAC than at any binding sites. Sst₃ receptors: pEC₅₀-values determined at [35]GTPyS binding and inhibition of FSAC are very similar although somewhat higher at FSAC. In both cases, the efficacy of the compounds is very significant (up to 250 % stimulation of [35S]GTPyS binding and 70 % inhibition of FSAC), although full agonism is more common at the latter. There is a reasonably good correlation with binding although the cortistatin analogues, for instance, show very high affinity in binding when their effect on FSAC is about 100- 400 fold lower, especially when considering [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr¹⁰]CST₁₄ binding data. Sst₅ receptors: the same comments can be made for sst, receptors; the peptides show good overall efficacy in stimulating [³⁵S]GTPyS binding and in inhibiting FSAC, many compounds display full agonism, the intrinsic activity of the peptides are similar in both tests as well as their absolute pEC_{50} -values, and therefore a good correlation is seen between the two tests. [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide were strongly GppNHp sensitive and affinity values are about 80- 120 fold higher than effects at FSAC. In both cases rank orders of affinity correlate well. [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄, which were much less GppNHp sensitive and labelled 8 and 2 fold more sites than [125I]CGP 23996 and [125][Tyr3]octreotide, show absolute affinity values which are in rather good agreement with FSAC data with differences of 10 or less. However, seglitide by far the most potent in FSAC ranks 4th -6th in binding. Thus, at SRIF₁ receptors, radioligand binding data tends to overestimate affinities systematically at sst₂, and to a significant extent at sst₃ and sst₅; in the case of the two latter receptors, there are good to very significant correlations between FSAC activity, [³⁵S]GTP_YS, and radioligand binding.

Figure 4: Human sst₂₋₅ receptors stably expressed in CCL39 cells: linear regression analyses between the pharmacological profiles of inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity and of stimulation of $[^{35}S]GTP\gamma S$ specific binding.



Data are from tables 2(A)-(E) and represent pEC₅₀-values obtained from adenylate cyclase activity assays and $[^{35}S]$ GTP γ S binding assays with sst₂₋₅ receptors. Correlation coefficients (r) are indicated in all plots.

However for all three receptors, there are manifest discrepancies between one or the other test such as with seglitide and octreotide analogues, which are very potent in second messengers, but less so in binding or with cortistatin, for which depending on the receptor the reverse is true.

Altogether, it should be clear, that neither radioligand nor [35 S]GTP γ S binding provide an absolute predictor for the pharmacological profile of a receptor as determined in adenylate cyclase experiments, be it absolute or relative potency and/ or efficacy. The affinity values are often very high compared to more "functional" values, and neither the rank orders of affinities nor the intrinsic activities are entirely superimposable.

This varies obviously with ligand, receptor, second messenger and there might be many reasons, even technical, since all tests are not performed under identical conditions; however, one may suggest that such diversity may be linked to the existence of multiple agonist-specific receptor conformations, each of which may couple preferentially to one or the other intracellular pathways within the signal transduction network. The switch of the G-protein coupled receptors from one signalling pathway to another might be regulated by receptor phosphorylation: phosphorylation of the β_3 -adrenergic receptor by protein kinase A couples the receptor to the MAPK-pathway via G_i proteins, whereas the nonphosphorylated receptor is coupled to the AC/ protein kinase A-pathway via G_s proteins (Daaka et al., 1997). It remains to be seen, whether the coupling of somatostatin receptors to signal transduction cascades is regulated by similar phosphorylation mechanisms. However, one cannot rule out, that ligands may lead to receptor trafficking simply because the conformation of the ligand-receptor-complex may show preference for one or the other G-proteins, and subsequently messenger cascades (see Berg et al., 1998a, 1998b, 1998c ; Leff et al., 1997, 1998; Scaramellini et al., 1998). If so, a number of discrepancies that have been reported between recombinant and native systems may be partly explained.

8.1. Abstract

[³H]-total phosphoinositide (IP_x) accumulation, a measure of phospholipase C (PLC) activity, induced by somatostatin (SRIF)- and cortistatin (CST)-analogues was studied at human somatostatin receptor subtypes 1-5 (hsst₁₋₅) recombinantly expressed in CCL39 (Chinese hamster lung fibroblast) cells.

SRIF₁₄ (10 μ M) stimulated total [³H]-IP_x production 200 % and 1070 % over basal levels, and increased intracellular Ca²⁺ ([Ca²⁺]_i) 1600 % and 2790 %, in cells expressing hsst₃ and hsst₅ receptors, respectively. The SRIF₁₄-stimulated IP_x production was partly blocked by 100 ng/ ml pertussis toxin (PTX) (30 % and 15 % inhibition, respectively). At hsst₁, hsst₂, and hsst₄ receptors, only weak or no stimulation of PLC activity was found (E_{max} = 114 %, 122 %, and 102 %, respectively). Consequently, hsst₃ and hsst₅ receptors were subjected to more detailed studies to establish pharmacological profiles of PLC stimulation.

At hsst₃ receptors, the efficacies of most ligands were in the same range ($E_{max} = 218-267$ %). At hsst₅ receptors E_{max} -values varied over a broad range, seglitide, CST_{17} , $SRIF_{28}$ displaying almost full agonism compared to $SRIF_{14}$, whereas octreotide and BIM 23052 showed very low partial agonism. BIM 23056 behaved as an antagonist on $SRIF_{14}$ -induced total [³H]-IP_x accumulation with a pK_B-value of 6.74 at hsst₃ receptors, and of 6.94 at hsst₅ receptors. The putative cycloantagonist SA showed weak antagonist activity on $SRIF_{14}$ -induced total [³H]-IP_x levels at hsst₃ (pK_B = 5.85), but not at hsst₅ receptors.

The $[{}^{3}\text{H}]$ -IP_x accumulation profiles at sst₃/ sst₅ receptors were compared to their respective radioligand binding ($[{}^{125}\text{I}]$ LTT-SRIF₂₈, $[{}^{125}\text{I}]$ [Tyr¹⁰]CST₁₄, $[{}^{125}\text{I}]$ CGP 23996, $[{}^{125}\text{I}]$ [Tyr³]octreotide binding), to $[{}^{35}\text{S}]$ GTP γ S binding, and to forskolin-stimulated adenylate cyclase (FSAC) inhibition profiles determined previously in CCL39 cells (Siehler et al., submitted (a); Siehler and Hoyer, submitted (b), (c)).

The different affinity profiles correlated relatively well at both receptor subtypes with PLC activation (sst₃: r = 0.90- 0.97; sst₅: r = 0.80- 0.87). However, [³⁵S]GTP γ S binding correlated only minimally with stimulation of [³H]-IP_x levels at sst₅ receptors (r = 0.59), but rather well at sst₃ receptors (r = 0.80). A moderate correlation was also observed between inhibition of FSAC activity and stimulation of PLC activity for hsst₃ and hsst₅ receptors with correlation coefficients of 0.85 and 0.70, respectively.

In summary, most SRIF analogues behave as full agonists at hsst₃ receptors and agonistinduced phosphoinositide turnover correlates well with radioligand binding, [³⁵S]GTP γ S binding and inhibition of adenylate cyclase activity, all measured in CCL39 cells. By contrast, at hsst₅ receptors, most SRIF analogues behave as intermediate or very low partial agonists (although receptor levels are very high) and the agonist-induced phosphoinositide turnover correlates rather poorly with radioligand binding, [³⁵S]GTP γ S binding or inhibition of adenylate cyclase activity, all measured in the same cell line, suggesting either that PLC activity is irrelevant at the sst₅ receptor or that receptor trafficking may have taken place.

8.2. Results

To study the activation of phospholipase C (PLC) activity via human sst₁₋₅ receptors stably expressed in CCL39 cells, total [³H]-IP_x accumulation was determined using an anion exchange column assay. The assay was performed in the presence of 20 mM LiC1 to block inositolmonophosphate phosphatase activity. Therefore, total [³H]-IP_x accumulation measures predominantly inositolmonophosphate and only trace amounts of di- or triphosphorylated inositol, which are dephosphorylated to IP₁ by their specific phosphatases. 10 μ M SRIF₁₄ induced a time-dependent increase of total [³H]-IP_x for up to 60 min at human sst₅ receptors. The stimulation over basal level (100 %) reached 427 \pm 45 % after 10 min and 1408 \pm 119 % after 60 min (table 1; figure 1).





Transfected cells were treated for 10, 20, 30, 40, 50 or 60 min with 10 μ M SRIF₁₄ in HBS buffer containing 20 mM LiCl, or with the buffer alone (control). Bars represent E_{max}-values ± SEM, which were calculated as percentage stimulation over the control level (= 100 %) of 3 independent experiments.

Since the maximal effect was reached after 50 minutes, all subsequent experiments were performed with a 50 min treatment time.

SRIF₁₄-stimulated [³H]-IP_x accumulation via hsst₃ and hsst₅ receptors (200 ± 10 % and 1069 ± 134 %, respectively) was only partially affected by the addition of 100 ng/ ml pertussis toxin (30 ± 6 % and 15 ± 7 % inhibition, respectively). Cells were preincubated with pertussis toxin 3- 5 hrs prior to the experiment, since longer treatment times with PTX inhibited cell proliferation to various degrees at the different cell clones. By contrast, SRIF₁₄-induced total [³H]-IP_x accumulation was not significant at human sst₄ receptors (102 ± 5 %), and only marginal at sst₁ and sst₂ receptors (114 ± 8 % and 122 ± 4 %, respectively), which were therefore not subjected to further studies (table 2; figure 2).

The pharmacological profiles of total $[^{3}H]$ -IP_x accumulation were established at human sst₃ and sst₅ receptors using a number of SRIF and CST analogues (table 3; figure 3).



Figure 2: Stimulation of total [3 H]-IP_x accumulation via recombinant human sst₁₋₅.

10 µM SRIF₁₄

were incubated in HBS buffer alone (control) either with or without 20 mM LiCl, or treated with 10 µM SRIF14 (in HBS/ Li⁺) either without or with PTX (100 ng/ ml). Bars represent Emax-values \pm SEM as percentage of stimulation over the non stimulated level (HBS/ $Li^+ = 100$ %) of at least 3 independent experiments.

At sst₃ receptors, the E_{max} -values were about in the same range (218- 267 %) with the exception of [Tyr3]octreotide, L362,855, and BIM 23056, which revealed lower efficacy; the so-called cycloantagonist SA displayed no significant agonist activity. In comparison, at human sst5 receptors, Emax-values ranged from full agonism to low partial agonism: 1141 % (SRIF₁₄), followed by 788-862 % (seglitide, CST₁₇, SRIF₂₈), down to 289 % (octreotide), 191 % (BIM 23052) and 123 % (BIM 23056); the cycloantagonist SA had no agonist activity.

The pEC₅₀-values were intermediate to low compared to radioligand binding at both receptor subtypes (pEC₅₀ = 5.53- 7.90). The rank order of ligand potency for sst₃ was: LTT-SRIF₂₈ > SRIF₁₄ > BIM 23052 \approx CST₁₇ \approx SRIF₂₈ > [Tyr¹⁰]CST₁₄ \approx CGP 23996 > L362,855 > octreotide > seglitide > [Tyr³]octreotide > BIM 23056. The rank order of ligand potency for sst₅ was: CST₁₇ > seglitide \approx SRIF₁₄ > SRIF₂₈ > BIM 23052 \approx L362,855 > LTT-SRIF₂₈ > [Tyr¹⁰]CST₁₄ \approx CGP 23996 > CGP 23996.

SRIF₁₄ induced via human sst₃ and sst₅ receptors a maximal increase of intracellular Ca²⁺ ([Ca²⁺]_i) of 1603 ± 217 % and 2792 ± 709 % over the basal level, with pEC₅₀-values of 6.87 ± 0.22 and 6.27 ± 0.04, respectively (figure 4). As in total [³H]-IP_x accumulation measurements, SRIF₁₄ induced [Ca²⁺]_i was not significant at sst₄ receptors (97 ± 3 % of controls), and rather moderate at sst₁ and sst₂ receptors (123 ± 5 % and 502 ± 10 %, respectively).

BIM 23056 and SA were examined for antagonism, since their efficacy was very low at both receptor subtypes. BIM 23056 antagonised SRIF₁₄-stimulated total [³H]-IP_x levels at sst₃ and sst₅ receptors with an apparent pK_B of 6.74 \pm 0.10 and 6.94 \pm 0.19, respectively (table 4; figure 5). Cyloantagonist SA showed antagonist activity on SRIF₁₄-induced IP_x levels only at sst₃ receptors (pK_B = 5.85 \pm 0.07), but not at sst₅ receptors (final concentration of 1 μ M).

Sst₃/ sst₅ receptor-modulated PLC activity was compared to data obtained previously in radioligand binding assays using different radioligands ([¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide), in [³⁵S]GTPγS binding experiments, and in adenylate cyclase activity (FSAC) (Siehler et al., submitted (a); Siehler and Hoyer, submitted (b), (c)) (table 5), and correlated to each other (table 6; figure 6; figure 7; figure 8). Overall, pEC₅₀-values determined at PLC activity were lower compared to affinity values of the ligands at sst₃/ sst₅ receptors, and lower or comparable to pEC₅₀-values obtained in GTPγS binding or FSAC experiments.

	CCI	L39/hsst ₃	CCL39/hsst ₅		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	100 ± 26	7.71 ± 0.18	100 ± 20	7.22 ± 0.10	
SRIF_{28}	98 ± 10	7.36 ± 0.22	66 ± 13	6.90 ± 0.20	
LTT-SRIF ₂₈	87 ± 18	7.90 ± 0.08	21 ± 6	6.45 ± 0.11	
CST ₁₇	89 ± 15	7.38 ± 0.09	71 ± 7	7.39 ± 0.00	
[Tyr ¹⁰]CST ₁₄	78 ± 16	7.05 ± 0.05	46 ± 3	6.31 ± 0.05	
seglitide	77 ± 6	6.01 ± 0.12	73 ± 8	7.27 ± 0.04	
CGP 23996	87 ± 10	7.05 ± 0.14	16 ± 2	5.53 ± 0.02	
octreotide	71 ± 17	6.27 ± 0.09	18 ± 2	6.00 ± 0.12	
[Tyr ³]octreotide	47 ± 5	5.79 ± 0.14	11 ± 3	5.76 ± 0.10	
L362,855	31 ± 4	6.61 ± 0.08	3 ± 0	6.78 ± 0.08	
BIM 23056	21 ± 5	5.62 ± 0.22	2 ± 0	5.81 ± 0.06	
BIM 23052	81 ± 18	7.44 ± 0.04	9 ± 1	6.80 ± 0.08	
cycloantagonist SA	7 ± 2	(-)	2 ± 0	(-)	

Table 1: Activation of total $[{}^{3}H]$ -IP_x accumulation by SRIF, CST, and analogues by human sst₃ and sst₅ receptors

Comparison of pEC₅₀-values (-log M) and E_{max} -values [% activation] ± SEM of 3 different determinations; E_{max} -values were normalised to the maximal stimulation reached by SRIF₁₄ ($E_{max} = 100$ % stimulation).



CCL39 cells were incubated with 2 μ Ci myo-[2-³H(N)]-inositol, treated with the indicated concentrations of SRIF₁₄ (**■**), SRIF₂₈ (**▲**), CST₁₇ (**▼**), seglitide (**♦**) or octreotide (**●**), and total [³H]-IP_X levels determined by anion exchange chromatography. Graphs represent the percentage of activation over the control level, and one representative example of at least 3 different determinations; the mean of the pEC₅₀-values ± are shown in table 3.

The various radioligand affinity profiles correlated at both studied receptor subtypes highly significantly, with their respective PLC activation profile although the correlation coefficients were higher for sst₃ than for sst₅ (sst₃: r = 0.90- 0.97; sst₅: r = 0.80- 0.87) (figure 6). In general, all correlation coefficients were lower at human sst₅ receptors compared to human sst₃ receptors. Thus, [³⁵S]GTPγS binding correlated weakly with stimulation of total [³H]-IP_x levels at sst₅ receptors (r = 0.59), but well at sst₃ receptors (figure 7). A significant correlation was observed between inhibition of forskolinstimulated AC activity and stimulation of PLC activity for both receptors (figure 8). Further, whereas the rank order of efficacy was rather comparable at hsst₃ receptor mediated effects, this was not the case at hsst₅ receptors.



Figure 4: SRIF₁₄-induced increase of intracellular Ca^{2+} at human sst₃ and sst₅ receptors expressed in CCL39 cells.

CCL39 cells were loaded with 5 μ M Fluo-4 dye, treated with the indicated SRIF₁₄ concentrations, and emitted fluorescence was kinetically monitored using the FLIPRTM II system. Graphs show the percentage of $[Ca^{2+}]_i$ increase over the control level, and one representative example of 3 different experiments.

8.3. Discussion

We have stably expressed the five human SRIF receptors in CCL39 cells (Siehler et al, 1998a, 1998b). These clones have been used previously to characterise radioligand binding, agonist-stimulated [35 S]GTP γ S binding and inhibition of forskolin-stimulated adenylate cyclase activity. Similar studies were performed with a fish sst₃ receptor also expressed in CCL39 cells (Siehler et al, 1999). These studies revealed some atypical features of the pharmacological profiles of some of the receptors examined, especially hsst₅ and fsst₃. Thus, affinity and B_{max}-values appeared to depend on the radioligand used ([125 I]LTT-SRIF₂₈, [125 I][Tyr¹⁰]CST₁₄, [125 I]CGP 23996, [125 I][Tyr³] octreotide, Siehler et al., 1998a; 1998b, 1999, submitted (a)), although the non-iodinated analogue of all radioligands showed full agonism in second messenger assays (De Lecea et al., 1996; Hoyer et al., 1995b; Siehler and Hoyer, submitted (b), (c)).

	SRIF ₁₄			SRIF ₁₄		SRIF ₁₄			
			+]	BIM 230	56	+ cycloantagonist SA			
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	pK _B	E _{max}	pEC ₅₀	рК _в	
CCL39/	100	7.71	113	6.70	6.74	87	7.37	5.85	
hsst ₃	± 16	± 0.18	±15	± 0.12	± 0.10	±16	± 0.07	± 0.07	
CCL39/	100	7.22	43	6.28	6.94	76	7.15	**	
$hsst_5$	± 20	± 0.10	± 8	± 0.09	± 0.19	±13	± 0.02		

Table 2: Antagonist activity of BIM 23056 (10^{-6} M) and cycloantagonist SA (10^{-6} M) on stimulation of total [³H]-IP_x accumulation by human sst₃ and sst₅ receptors

Comparison of pEC₅₀-values (-log M), E_{max} -values [% stimulation], and pK_B-values ± SEM of 3 independent determinations; E_{max} -values were normalised to the stimulation reached by SRIF₁₄ (= 100 %).

Similarly, the rank orders of potency and/ or efficacy determined in [35 S]GTP γ S binding and adenylate cyclase activation were not entirely consistent for a given receptor (Siehler and Hoyer, submitted (b), (c)). Thus, the data indicated quite some variability in the "pharmacological profile" of a given receptor depending on the agonist used and/ or the system studied (radioligand binding or second messenger).

In contrast to the predictions made by the allosteric ternary complex model (De Lean et al., 1980; Lefkowitz et al., 1993; Samama et al., 1993), these data suggested agonists to label G-protein-coupled or G-protein-coupled/ and –uncoupled receptor states, and that each agonist-specific receptor conformation triggers specifically the linked signalling cascades as may be suggested by Berg et al., 1998a, 1998b, 1998c, Leff et al., 1997, 1998 and Scaramellini et al., 1998.





CCL39 cells were incubated with myo- $[2-^{3}H(N)]$ -inositol, treated with the indicated concentrations of SRIF₁₄, and either without (**I**) or with BIM 23056 or cycloantagonist SA (**(**) (1 μ M f. c.), and total $[^{3}H]$ -IP_x levels measured as described. Graphs show the % of induction of total $[^{3}H]$ -IP_x accumulation over the control level. The data points represent one example of 3 different experiments. pK_B-values ± SEM are shown in the graphs.

To further examine these aspects, inositol phosphate accumulation measurements were established at human SRIF receptors to determine phospholipase C (PLC) activity at the five human SRIF receptors expressed in CCL39 cells. At hsst₅ receptors, SRIF₁₄ produced a maximal 11 to 14 fold stimulation of PLC activity after 50 min at 37° C, conditions which were used in all further experiments.

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By comparison, Wilkinson et al., (1997) reported a 2-fold induction by $SRIF_{14}$ of IP_x levels via hsst₅ receptors expressed in CHO cells.

Under the conditions used, $SRIF_{14}$ induced a stimulation of total [³H]-IP_x accumulation via hsst, and hsst, receptors of 200 % and 1069 %, respectively. By contrast SRIF₁₄ increased only minimally IP, levels in CCL39 cells expressing hsst, and sst, receptors (114 % and 122 %). These results were confirmed by measurement of $[Ca^{2+}]_i$, which is increased by PLC-induced IP₃ molecules: SRIF₁₄ induced an $[Ca^{2+}]_i$ increase via sst₃ and sst₅ receptors of 1600 % and 2790 %, but only of 120 % and 500 % via sst₁ and sst₂ receptors, respectively. It has been reported that SRIF₁₄ induced about 130 % stimulation of [³H]-IP_x in COS-7 cells expressing hsst₁ receptors (Akbar et al., 1994; Tomura et al., 1994), but no stimulation in F_4C_1 rat pituitary cells expressing rodent sst receptors (Chen et al., 1997). On the other hand, SRIF₁₄ has been reported to produce almost a 6-fold activation of PLC activity at mouse sst₂ receptors, and SRIF₁₄ produced even a 10-fold stimulation of PLC activity at human sst, receptors when expressed COS cells (Akbar et al., 1994; Chen et al., 1997; Tomura et al., 1994). In our hands, human sst₄ receptors failed to mediate significant IP_x production and $[Ca^{2+}]_i$ increase in CCL39 cells. This may not be surprising, since stimulation of rat sst₄ receptors also failed to induce IP₃ synthesis or Ca²⁺ mobilisation (Bito et al., 1994); on the other hand, human sst₄ receptors were reported to induce IP₃ synthesis 1.7-fold by SRIF₁₄ when expressed in COS-7 cells (Akbar et al., 1994). Such rather drastic differences are probably explained by the use of different cell lines, in which a number of mechanisms are cellspecific such as: (a) the receptor may post-translationally modified, e.g. glycosylated or phosphorylated, (b) the expression and respective levels of G-protein isoforms; (c) the expression of the four PLC_{β} -isoenzymes (Exton et al., 1996), (d) the presence or absence of different RGS proteins (regulators of G-protein signalling), e.g. RGS2 selectively blocks $G_0\alpha$ -mediated activation of PLC_{B1}, (e) expression and levels of RAMPs (receptor-activity-modifying proteins), which modulate receptor activity by regulation of the receptor glycosylation pattern, (f) receptor activity might be cellspecifically modulated by receptor heterodimerisation (Heximer et al., 1997; Kaupmann et al., 1998; Lefkowitz et al., 1993; McLatchie et al., 1998; Roush et al., 1996).

Table 3: Human sst₃ and sst₅ receptors: comparison of ligand potencies (pEC₅₀-values) to activate total [³H]-IP_x accumulation (a) with affinities (pK_d's) of the receptors labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 or [¹²⁵I][Tyr³]octreotide, (b) with potencies (pEC₅₀'s) to stimulate [³⁵S]GTPγS specific binding, and (c) potencies to inhibit forskolin-stimulated adenylate cyclase (FSAC) activity.

	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	[³⁵ S]	GTPγS	FSAC activity		total [³ H]IP _x	
	LTT- SRIF ₂₈	$\begin{bmatrix} Tyr^{10} \\ CST_{14} \end{bmatrix}$	CGP 23996						
	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	9.54	9.67	9.71	100	7.32	100	7.76	100	7.71
SRIF ₂₈	9.65	9.80	9.94	104	6.96	94	8.19	98	7.36
LTT-SRIF ₂₈	9.84	9.26	10.09	119	7.44	97	8.40	87	7.90
CST ₁₇	9.43	9.52	9.88	73	6.59	75	7.47	89	7.38
[Tyr ¹⁰]CST ₁₄	8.70	8.90	9.02	43	6.83	84	6.80	78	7.05
seglitide	6.88	7.89	7.68	49	5.78	89	6.68	77	6.01
CGP 23996	8.82	9.28	9.15	81	7.14	89	7.84	87	7.05
octreotide	7.88	8.60	8.44	42	6.70	97	7.01	71	6.27
[Tyr ³]octreotide	6.84	6.20	7.90	47	5.76	81	6.31	47	5.79
L362,855	7.62	8.25	8.29	23	6.27	58	6.70	31	6.61
BIM 23056	6.90	7.08	7.20	-10	(-)	26	(-)	21	5.62
BIM 23052	8.42	9.55	9.71	93	6.29	104	7.43	81	7.44
cycloantagonist SA	6.23	7.08	6.88	13	(-)	32	6.38	7	(-)

Table 3(A) CCL39/hsst₃

Obviously, neither the effects of RAMPs, nor receptor dimerisation have been documented for any of the SRIF receptors, but this may only be a matter of time.
Table 3(B) CCL39/hsst₅

	[¹²⁵ I] LTT- SRIF ₂₈	[¹²⁵ I] [Tyr ¹⁰] CST ₁₄	[¹²⁵ I] CGP 23996	[¹²⁵ I] [Tyr ³] octreo tide	[³⁵ S](GTPγS	FSAC activity		total [³ H]IP _x	
	pK _d	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	9.53	9.01	9.82	9.87	100	8.39	100	8.33	100	7.22
SRIF ₂₈	9.39	9.18	10.15	10.30	101	7.65	109	8.45	66	6.90
LTT-SRIF ₂₈	8.47	8.12	9.70	9.60	107	7.63	106	7.84	21	6.45
CST ₁₇	9.54	9.37	10.21	9.85	79	7.94	92	8.38	71	7.39
[Tyr ¹⁰]CST ₁₄	8.67	8.06	9.77	9.65	69	7.43	109	7.69	46	6.31
seglitide	8.70	9.14	10.22	10.18	84	7.89	119	9.33	73	7.27
CGP 23996	6.59	6.67	8.26	8.68	67	7.12	112	7.07	16	5.53
octreotide	7.17	7.31	8.96	9.48	107	6.89	123	7.68	18	6.00
[Tyr ³]octreotide	6.49	6.00	8.03	8.41	72	6.56	118	7.30	11	5.76
L362,855	7.17	7.17	8.72	9.17	79	6.29	143	6.81	3	6.78
BIM 23056	7.17	6.68	7.77	8.32	0	(-)	47	6.60	2	5.81
BIM 23052	7.92	7.45	9.59	9.28	100	6.80	125	7.40	9	6.80
cycloantagonist SA	6.38	6.02	7.77	8.25	74	5.82	100	5.69	2	(-)

The data are expressed as pK_d 's or pEC_{50} 's (-log M), or E_{max} -values [% stimulation or inhibition, respectively; normalised to E_{max} of $SRIF_{14} = 100$ %] of at least 3 determinations.

The hsst₃ and hsst₅ receptors mediated stimulation of total [³H]-IP_x accumulation was partially blocked by PTX treatment (30 % and 15 %, respectively) suggesting that G_i/G_o proteins are only marginally involved in the response measured, especially at sst₅ receptors. Along these lines, Akbar et al. (1994) reported a 2.7-fold increase of total IP_x levels at hsst₃ receptors and a 12-fold increase at hsst₅ receptors in COS cells, which were blocked via PTX by 70 % and 35 %.

Table 4: Human sst₃ and sst₅ receptors expressed in CCL39 cells: correlation coefficients (r) and P-values from linear regression analyses between the pharmacological profile of stimulation of total [³H]-IP_x accumulation and (a) the affinity profiles of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide, or (b) the profile of stimulation of [³⁵S]GTPγS binding, or (c) the profile of inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity

	CCL3	9/ hsst ₃	CCL39/ hsst ₅			
	r	Р	r	Р		
[¹²⁵ I]LTT-SRIF ₂₈	0.946	< 0.0001	0.833	0.0008		
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.896	< 0.0001	0.867	0.0003		
[¹²⁵ I]CGP 23996	0.967	< 0.0001	0.842	0.0006		
[¹²⁵ I][Tyr ³]octreotide		-	0.803	0.0017		
[³⁵ S]GTPγS binding	0.799	0.0032	0.585	0.0589		
inhibition of FSAC activity	0.849	0.0010	0.717	0.0087		

Data used for correlation analyses are presented in tables 3(A)+(B).

Similarly, Murthy et al. (1996) reported a 2.4-fold increase of $PLC_{\beta 3}$ activity at guinea pig sst₃ receptors, which was inhibited via PTX by 86 %. At hsst₅ receptors expressed in CHO cells, PTX treatment resulted in 92 % inhibition IP_x levels (Wilkinson et al., 1997). The marked inhibition of PLC activation by PTX described in some instances may be due to the prolonged PTX treatment of the cells (\geq 18 hrs). Such conditions however, inhibited cell proliferation of CCL39 cells and we limited pre-treatment time to 3 hours. At both hsst₃ and hsst₅ receptors, SRIF₁₄ (pEC₅₀ = 7.71 and 7.22) was somewhat more potent in stimulating total [³H]-IP_x production than SRIF₂₈ (7.36 and 6.90). A lower potency of SRIF₁₄ compared to that of SRIF₂₈ was reported at hsst₅ receptors expressed in CHO cells (pEC₅₀ = 6.48 and 6.83, Wilkinson et al., 1997), but overall it still remains to be seen whether sst₅ receptors show indeed some selectivity for SRIF₂₈ over SRIF₁₄ as initially claimed. Potencies of SRIF₁₄ to induce $[Ca^{2+}]_i$ increase via hsst₃ and hsst₅ receptors were lower than those obtained measuring PLC activity (pEC₅₀ = 6.87 and 6.27).

In CCL39 cells expressing hsst₃ receptors, most agonists stimulated [³H]-IP_x production to a similar extent (218- 267 % of basal), in other words most compounds acted as full or nearly full agonists, except BIM 23056 or cycloantagonist SA, which had essentially antagonist activity. By contrast, at hsst₅ receptors, the efficacy of the studied ligands varied over a broad range (1141 % for SRIF₁₄ to 118 % = cycloantagonist SA). Thus, whereas SRIF₁₄ was a full agonist on total [³H]-IP_x accumulation, the other peptides behaved as partial agonists. Less extreme variations were also observed at the human sst₅ receptor in [³⁵S]GTPγS binding and adenylate cyclase inhibition (Siehler and Hoyer, submitted (b), (c)).

BIM 23056 antagonised SRIF₁₄-stimulated accumulation of phosphoinositide levels with an apparent pK_B of 6.74 at hsst₃, and 6.94 at hsst₅ receptors. Wilkinson et al. (1996; 1997) found for BIM 23056 a similar pK_B of 7.4 at hsst₅ receptors on SRIF₁₄-induced phosphoinositide turnover, and a pK_B of 8.0 on SRIF₁₄-induced increase of intracellular Ca²⁺. In addition, in previous studies we found BIM 23056 to antagonise SRIF₁₄induced [³⁵S]GTPγS binding at hsst₃ and hsst₅ receptors (6.33 and 5.84, respectively), as well as SRIF₁₄-induced inhibition of forskolin-stimulated adenylate cyclase activity at hsst₃ (pK_B = 6.33), but not at hsst₅ receptors (Siehler and Hoyer, submitted (b), (c)). Cycloantagonist SA, which revealed no significant activity on stimulation of PLC at both receptor subtypes, showed antagonism on SRIF₁₄-stimulated phosphoinositide turnover at hsst₃ receptors (pK_B = 5.85), but not at hsst₅ receptors in this assay, nor in [³⁵S]GTPγS binding or adenylate cyclase at both receptor subtypes.



Figure 6: Human recombinant sst, and sst, receptors expressed in CCL39 cells.

 pEC_{50} ([³H]-IP_x accumulation)

sst5 receptors. Correlation coefficients (r) are indicated in all plots.



Figure 7: Human sst₃ and sst₅ receptors stably expressed in CCL39 cells.

Linear regression analysis between the pharmacological profiles of total $[^{3}H]$ -IP_x measurements and of $[^{35}S]$ GTP_yS specific binding experiments. Data are from tables 3(A)+(B) and represent pEC₅₀-values. Correlation coefficients (r) are given in all plots.

However, these values have to be taken with care as the antagonism produced does not seem to be competitive in nature.

A comparison between the rank orders of potency determined at hsst₃ and hsst₅ receptors for [³H]-IP_x accumulation on the one hand, and radioligand binding profiles, [³⁵S]GTP₇S binding and adenylate cyclase activity on the other (Siehler et al., submitted (a); Siehler and Hoyer, submitted (b), (c)) resulted in correlation coefficients, which were high for hsst₃ receptors (r = 0.799- 0.967), and lower for hsst₅ receptors (r = 0.585- 0.867). This may have been expected, since radioligand binding studies performed with various agonists resulted in more homogeneous results at sst₃ receptors compared to sst₅ receptors. Thus, when comparing [³⁵S]GTP₇S binding and phosphoinositide turnover, the low correlation (r = 0.585) might suggest either 1) that some signalling pathways are preferred with respect to others (e.g.[³⁵S]GTP₇S binding and inhibition of adenylate cyclase activity correlated much better, r = 0.856), or 2) that different signal transduction pathways activated by the same somatostatin receptor may apparently display a different recognition profile, e.g. some agonists may induce preferential coupling to one or another pathway/ G-protein. Figure 8: CCL39 cells expressing human sst, and sst, receptors.



Correlation analysis between the pharmacological profiles of total $[^{3}H]$ -IP_X accumulation and of adenylate cyclase activity measurements. Data (pEC₅₀-values) used for analyses are from tables 3(A)+(B). Correlation coefficients (r) are shown in both graphs.

This cannot be demonstrated here since the incubation conditions are not identical in the different test systems, but is suggested (see also Berg et al, 1998a, 1998b; Leff et al., 1997, 1998).

On the other hand, it cannot be excluded, that coupling of sst₃/sst₅ receptors to the phosphoinositide/ PLC pathway might be due to receptor overexpression as reported for other recombinantly expressed receptors (Cotecchia et al., 1990), and coupling to PLC might not play a role in a normal physiological environment for SRIF receptors. This may hold true for sst₅ receptors which in these cells are expressed at high levels (up to 7000 fmol/ mg) whereas the other four receptors are expressed at similar levels (between 300- 400 fmol/ mg); however, of the "low" expressors, sst₃ was able to couple efficiently to PLC activity.

The expression of PLC_{β} isoenzymes has not been studied in CCL39 cells, but since somatostatin receptors couple efficiently to $G_{i/o}$ proteins (for review: Meyerhof, 1998), they probably activate $PLC_{\beta 2}$ and/or $PLC_{\beta 3}$.

Further, since the response mediated by sst_3/sst_5 receptors was in both cases only partially affected by addition of PTX, which blocks G_{i}/G_{o} signalling, coupling to G_{q} protein family members may also be anticipated: $G_{q}\alpha$ mediates activation of PLC_{β1}, PLC_{β3}, and PLC_{β4}, while $G_{11}\alpha$ mediates activation of PLC_{β1} and PLC_{β3} (Berridge, 1993; for review: Exton, 1996). The phosphoinositide/ PLC pathway is an important Ca²⁺ signalling machinery triggered by G-protein-coupled receptors, although another pathway independent of PLC, and involving sphingosine kinase activation is described for muscarinic acetylcholine receptors (Meyer zu Heringhof et al., 1998). Thus, in rat AR42J pancreas cells endogenously expressing sst_2 receptors SRIF₁₄ induced increases of intracellular calcium levels, but no stimulation of IP₃ production (Taylor, 1995), meaning that modulation of intracellular calcium levels by somatostatin receptors not only involves PLC activation, but also modulation of cell-surface Ca²⁺ channels (Meyerhof, 1998), and/ or might also involve stimulation of the sphingosine kinase pathway.

In summary, hsst₃ and hsst₅ receptors appear to be able to couple rather efficiently to PLC activity and $[Ca^{2+}]_i$ increase in CCL39 cells. The effect on PLC activity is only marginally affected by PTX, i.e. the G-proteins involved are not primarily G₀/G_i, suggesting that G_q may play a major role. This is important since the other parameters measured previously, [35S]GTPyS binding (presumably) and inhibition of adenylate cyclase activity are essentially the result of coupling to G_i-proteins. It appears, that at sst₃ receptors most SRIF analogues behave as full agonists and that the agonist-induced phosphoinositide turnover correlates well with radioligand binding, [35S]GTPyS binding and inhibition of adenylate cyclase activity, all measured in the same cell line. Pretty much the opposite statement can be made about sst, receptors: at sst, receptors, most SRIF analogues behave as moderate or very low partial agonists (although the expression levels are very high) and the agonist-induced phosphoinositide turnover correlates rather poorly with radioligand binding, [³⁵S]GTPyS binding or inhibition of adenylate cyclase activity all measured in the same cell line, suggesting either that PLC activity is irrelevant at the sst, receptor or that receptor trafficking may have taken place.

If so, this would explain difference in both rank orders of potency and rank orders of efficacy observed when comparing data obtained at the same receptor, but using different tests.

9.1. Abstract

The actions of the various forms of somatostatin (SRIF), including those of the tetradecapeptide SRIF₁₄, are mediated by specific receptors. In mammals, five subtypes of SRIF receptors, termed sst₁₋₅, have been cloned. By using a combination of reverse transcriptase polymerase chain reaction and genomic library screening in the gymnotiform fish Apteronotus albifrons, we have isolated a gene encoding the firstknown non-mammalian SRIF receptor. The deduced amino acid sequence displays 59 % identity with the human sst, receptor protein; hence, we have called the gene 'Apteronotus sst₃'. The predicted protein consists of 494 amino-acid residues exhibiting a putative seven-transmembrane domain topology typical of G-protein-coupled receptors. A signal corresponding to the Apteronotus sst₃ receptor was detected in brain after amplification of $poly(A)^+$ -RNA by reverse transcriptase-polymerase chain reaction, but not by Northern Blot analysis or *in situ* hybridization, thus suggesting a low level of expression. Membranes prepared from CCL39 cells stably expressing the Apteronotus sst₃ receptor gene bound [¹²⁵I][Leu⁸,D-Trp²²,¹²⁵I-Tyr²⁵]SRIF₂₈ with high affinity and in a saturable manner ($B_{\text{max}} = 4470 \text{ fmol/ mg protein; } pK_d = 10.5$). SRIF₁₄ and various synthetic SRIF receptor agonists produced a dose-dependent inhibition of radioligand binding, with the following rank order of potency: $SRIF_{14} \approx SRIF_{28} > BIM 23052 >$ octreotide > BIM 23056. Under low stringent conditions, an Apteronotus sst, probe hybridized to multiple DNA fragments in HindIII or EcoRI digests of A. albifrons DNA, indicating that the Apteronotus sst₃ receptor is a member of a larger family of Apteronotus SRIF receptors.

Standard procedures were carried out as described in Sambrook et al. (1989). Subsequent to subcloning of appropriate DNA fragments into pGEM-3Z vector (Promega Biotec, Madison, Wisconsin), DNA sequencing was performed by the dideoxynucleotide chain termination procedure, using Sequenase® Version 2.0 DNA Sequencing Kit (United States Biochemical, Cleveland, Ohio). Both strands were sequenced.

9.2.1. Cloning of A. albifrons sst, receptor

DNA was extracted from liver tissue of adult A. albifrons (Teleostei, Gymnotiformes) obtained from a tropical fish importer (Aquarium Glaser, Rodgau, Germany). Total RNA was isolated from brain tissue using TRIzol® Reagent (Gibco BRL, Gaithersburg, Maryland). For reverse transcriptase-polymerase chain reaction (RT-PCR), cDNA was prepared from total RNA by means of mouse Moloney leukemia virus reverse transcriptase (Gibco BRL) and random hexamer oligonucleotide primers (Perkin-Elmer Corp., Norwalk, Connecticut). sst receptor-related sequences in the cDNA were amplified through PCR (Saiki et al., 1985) with the degenerate primers 5'-GACCGCTA(C/T)(G/C)TGGC(C/T)GTGGT(G/A)CA(T/C)C-3' 5'and ATGGGGTT(T/G)GC(A/G)CAGCTGTT(A/G/C/T)GCATA-3'. The following temperature profile was employed: an initial denaturating step at 94°C for 5 min, and then 35 cycles consisting of 1 min each at 94°C for denaturating, 55°C for annealing, and 72°C for extension.

A resulting 504 basepair PCR product was subcloned into the *Hin*dII site of pGEM-3Z and sequenced. Analysis of this sequence showed that it was most similar to that of the human sst₃ receptor. Mammalian sst receptor genes lack introns, at least in their protein coding regions, and we assumed that the organization of the *A. albifrons* sst₃ receptor gene would be similar. Thus, the remainder of the *A. albifrons* sst₃ receptor sequence was determined by the analysis of genomic clones.

Fragments of the *A. albifrons* sst₃ receptor gene were isolated through inverse PCR technique using *Pst*I-digested *A. albifrons* genomic DNA and the primers 5'– GTGTAGACGATGAACGCTGC–3' and 5'–CCATTCTACATACTCAACAT–3' which generated a 513 basepair PCR product. The two overlapping PCR products obtained by cDNA amplification and inverse PCR were ligated together to generate a fragment of 860 basepairs. This fragment was ³²P-labeled by nick translation and used as a probe to perform a Southern blotting using *Bgl*II digested genomic DNA. A 2.8 kb band was positive. It is likely that this band contained two kinds of fragments, because there was a *Bgl*II site in the probe. An *A. albifrons* genomic DNA library with inserts of size-selected 2.8 kb fragments digested with *Bgl*II was made and screened with the same probe by a plaque hybridization technique. DNA was prepared from plaque-purified clones and sequenced.

A construct encoding *A. albifrons* sst₃ receptor suitable for expression studies was generated by PCR amplification. A 1523 basepair fragment (nucleotides 107-1629) was amplified using specific primers with a *Hin*dIII linker sequence on the forward primer and *Xba*I linker sequence on the reverse primer. The PCR product was subcloned into the *Hin*dIII-*Xba*I sites of pcDNA3.1 (+) (Invitrogen, San Diego, California). The sequence of the insert in this clone, pAa-sst₃, was confirmed.

9.2.2. Fish tissues

Black ghosts (*Apteronotus albifrons*), teleost fish of the order Gymnotiformes, were obtained from local pet shops. The fish were sacrificed with a lethal dose of MS-222 (3-aminobenzoic acid ethyl ester; Sigma Chemical Company) dissolved in aquarium water; brain, liver, heart, spleen, stomach and gut were rapidly removed and snap-frozen in isopentane at -45°C. The organs of individual animals were pooled and kept frozen until further use.

9.3. Results

Isolation of *Apteronotus* sst₃ receptor gene

SRIF receptor clones were isolated from adult *A. albifrons* total brain RNA by RT-PCR (Higuchi, 1990) using degenerate primers based on regions of sequence homology amongst mouse sst_{1-3} receptors. The upstream and downstream primers corresponded to conserved regions between the third and fourth putative transmembrane domains, and in the seventh transmembrane domain, respectively. An amplified band was subcloned and sequenced. Sequence analysis of one clone revealed a 504 basepair insert that was similar to mammalian sst receptors, and less similar to other G-protein-coupled receptors.

Through inverse PCR (Innis et al., 1990; Ochman et al., 1988, 1990), an additional 357 basepair sequence was obtained, and the overlapping PCR products were ligated together to generate an 860 basepair fragment. This fragment was ³²P labeled and used in Southern blot analysis as a probe for *Bgl*II digested genomic DNA. A 2.8 kb band was revealed (data not shown). 5×10^5 plaques of a size-selected library of *A. albifrons* genomic DNA which contained 2.8 kb *Bgl*II fragments were screened. Two clones, λ fsst3-A and λ fsst3-B, obtained from 21 positive plaques, were sequenced.

Amino acid sequence of *Apteronotus* sst, receptor

The sequence of the inserts of λ fsst3-A and λ fsst3-B displayed an open reading frame of 1482 basepairs, thus predicting the sequence of a protein of 494 amino acids (mol wt, 54,696) (figure 1). Hydropathic analysis of this protein sequence demonstrated seven hydrophobic, putatively membrane-spanning domains separated by stretches of hydrophilic amino acids, a feature characteristic of G-proteins (Dohlman et al., 1991; Probst et al., 1992). Comparison of the sequence of the *A. albifrons* gene with those of other G-protein-coupled receptors showed that it was most similar to mammalian sst₃ receptor genes, hence designated '*Apteronotus* sst₃'. It lacks introns in the protein coding region.

The sequence of the protein encoded by the *Apteronotus* sst₃ receptor gene exhibits 59 % (72 %), 58 % (71 %), and 56 % (69 %) identity (similarity) with the sequences of human (Yamada et al., 1992b), mouse (Yasuda et al., 1992), and rat sst₃ (Meyerhof et al., 1992), respectively (figure 2). The *Apteronotus*-specific peptide sequence diverged most at the amino and carboxyl termini from the corresponding regions of the mammalian receptors. Greatest similarity was found in the region between the amino terminus of the first transmembrane domain and the carboxyl terminus of the seventh transmembrane domain. In this region, the protein sequence showed 71 % (82 %), 70 % (80 %), and 70 % (80 %) identity (similarity) with the corresponding sequences of the human, mouse, and rat sst₃ receptors, respectively. There are several long stretches of sequences in these regions which are completely identical (figure 2).

Analysis of the sequence of *Apteronotus* sst₃ demonstrated many features that are conserved among G-protein-coupled receptors (Dohlmann et al., 1991; Findlay and Eliopoulos, 1990; Probst et al., 1992). This includes several conserved amino acids in the transmembrane segments and the highly conserved sequence Asp^{158} -Arg-Tyr (DRY) at the NH₂-terminal end of the second intracellular loop.

A consensus sequence pointing to a potential site for coupling to G-proteins (Okamoto and Nishimoto, 1992) is located in the 26-residue region of Val²⁴⁸ to Arg²⁷³, which comprises the third cytoplasmic loop; it is composed of two basic residues at the aminoterminal side (K²⁴⁹VR) and the R²⁶⁹KITR motif at the carboxyl-terminal end of the loop. Three consensus sites for serine phosphorylation could be identified in the first (Ser⁹¹) and third intracellular loop (Ser²⁶¹ and Ser²⁶⁷) of the *Apteronotus* sst₃ receptor: The sequences RXS⁹¹X, XRXXS²⁶¹X, and XRRXS²⁶⁷X (the phosphate-accepting serine is indicated by S, whereas the determinant arginine residues are marked by R, and the less essential residues by X) match the recognitions motifs of the multifunctional calmodulin-dependent protein kinase II. In addition, the sequence XRRXS²⁶⁷ matches the recognition sequence of cAMP-dependent protein kinase A (Kemp and Pearson, 1990; Kennelly and Krebs, 1991). Two cysteines located at positions Cys¹³⁴ and Cys²⁰⁸ might form a disulfide bond between the first and second extracellular loop. The presence of such a disulfide bridge has been shown in other G-protein-coupled receptors to be essential for ligand binding activity (Strosberg, 1991).

Figure 1: Nucleotide and predicted amino acid sequences of A. albifrons sst_3 receptor gene and protein.

1	CTT	AAGC	тсаа	CGTT	CTTC	rccc	CTTT	ACAG	TAA	CAAA	CANT	ATTT	CAGC	CAAA	SAGC	CAGG	GCT	ATAA(CAGT	TTCT	CATTO	CGT	rrrr?	ICCA	GCA	CAT	GGC	AGGT	
112	CCT	AAAC	CGGC	CAAG		ATG Met	GAG Glu	GCG Ala	CCC Pro	ATA Ile	ACG Thr	GCT Ala	GCG Ala	GTG Val	T TT Phe	GGA Gly	TAC Tyr	GAG Glu	GАС Азр	CCT Pro	CGT Arg	TCC Ser	TGG Trp	GАС Азр	TCC Ser	AAC <u>Asn</u>	GTT Val	TCT Ser	23
196	TCT Ser	CTC Leu	CCC Pro	GCC Ala	CAC His	CCG Pro	GCC Ala	TTT Phe	CCC Pro	CTC Leu	CCC Pro	CCA Pro	GGC Gly	CAC His	GCC Ala	CTC Leu	CTC Leu	CCC Pro	GAC Asp	GGG Gly	TCT Ser	CCG Pro	CAG Gln	AAC <u>Asn</u>	TGG Trp	ACG Thr	GAG Glu	GGC Gly	51
280	GAT Аяр	GGG Gly	GCG Ala	GGT Gly	TTC Phe	TCT Ser	CCG Pro	AGC Ser	GCC Ala	GCC Ala	GGG Gly	GTG Val	CTC Leu	ATC Ile	CCT Pro	CTT Leu	GTC Val	TAC Tyr	ATC Ile	GCC Ala	GTA Val	TGC Cys	GTC Val	GTA Val	GGC Gly	CTC Leu	GGC Gly	GGG Gly	79
364	AAC Asn	ACG Thr	CTG Leu	GTC Val	ATC 11e	CAC His	ATC 11e	GTC Val	CTG Leu	CGC Arg	TAC Tyr	TCT <u>Ser</u>	CAC His	GTG Val	CAG Gln	TCG Ser	GTC Val	ACT Thr	AAC Asn	ATC Ile	TAC Tyr	ATC Ile	CTG Leu	AAC Asn	CTC Leu	GCC Ala	ATA Ile	GCC Ala	107
448	GAC Авр	GAG Glu	CTC Leu	TTC Phe	ATG Met	CTT Leu	GGC Gly	CTG Leu	CCC Pro	TTC Phe	CTG Leu	GCT Ala	GTA Val	CAG Gln	AAC Asn	GCG Ala	CTC Leu	CTC Leu	TCC Ser	TGG Trp	CCG Pro	TTC Phe	GGC Gly	TCG Ser	CTG Leu	ATG Met	TGC Cys	CGG Arg	135
532	CTG Leu	GTC Val	ATG Met	ACC Thr	GTG Val	дас Ляр	GCC Ala	ATC 11e	AAC Asn	CAG Gla	TTC Phe	ACC Thr	AGC Ser	ATC Ile	TTC Phe	TGC Cys	CTG Leu	ACA Thr	GTG Val	ATG Met	AGC Ser	ATC 11e	GAC Авр	CGC Arg	TAT Tyr	GTG Val	GCC Ala	GTG Val	163
616	GTG Val	CAT His	CCC Pro	TCC Ser	GCT Ala	CCT Pro	CCA Pro	GGT Gly	GGC Gly	GCC Ala	GTC Val	CTC Leu	TGG Trp	TGG Trp	CCA Pro	AAG Lys	CGT Arg	GAA Glu	CGT Arg	CAC His	GTG Val	TGG Trp	GCC Ala	GTC Val	TCC Ser	TTC Phe	GTG Val	GTG Val	191
700	GTC Val	CTG Leu	CCG Pro	GTG Val	GTG Val	GTG Val	TTC Phe	GCC Ala	GAC Asp	GTG Val	CTG Leu	CAG Gln	GAC Авр	GAC Авр	CGG Arg	AAC <u>Asn</u>	TGC Cys	AGC Ser	ATC Ile	GTG Val	TGG Trp	CCC Pro	GAG Glu	CCG Pro	GCG Ala	GAG Glu	GTC Val	TGG Trp	219
784	AAA Lys	GCA Ala	GCG Ala	TTC Phe	ATC Ile	GTC Val	TAC Tyr	ACC Thr	GCC Ala	ACG Thr	GTG Val	GGC Gly	TTC Phe	TTC Phe	TGC Cys	CCC Pro	CTA Leu	CTG Leu	GTG Val	ATC 11e	TGC Cys	CTG Leu	TGT Cys	TAC Tyr	CTG Leu	CTC Lau	ATC 11e	GTG Val	247
868	GTG Val	AAG Lys	GTG Val	CGC Arg	ACG Thr	TCC Ser	GGG Gly	CGC Arg	CGG Arg	GTG Val	CGG Arg	GCC Ala	ACG Thr	TCT <u>Ser</u>	GTG Val	CGA Arg	CGC Arg	CGT Arg	AAG Lys	TCC <u>Ser</u>	GAG Glu	CGA Arg	ААG Lyb	ATC Ile	ACG Thr	CGC Arg	ATG Met	GTG Val	275
952	GTG Val	ATA Ile	GTG Val	GTA Val	GCC Ala	GTG Val	TTC Phe	GTG Val	CTC Leu	TGT Cys	TGG Trp	CTG Leu	CCA Pro	TTC Phe	TAC Tyr	ATA Ile	CTC Leu	AAC Asn	ATT Ile	GTC Val	AAC Asn	CTG Leu	TTG Leu	GTT Val	CTC Leu	CTT Leu	CCT Pro	GGG Gly	303
1036	GAG Glu	TTT Phe	CGT Arg	GGC Gly	CTC Leu	TAT Tyr	TAC Tyr	TTT Phe	GTG Val	GTG Val	GTT Val	CTG Leu	TCT Ser	TAT Tyr	GCC Ala	AAC Asn	AGC Ser	TGT Cys	GCC Ala	AAT Asn	CCC Pro	ATT 11e	TTG Leu	TAT Tyr	GGA Gly	TTC Phe	CTC Leu	TCA Ser	331
1120	GAC Asp	AAC Asn	TTT Phe	AAG Lyb	AGA Arg	GGT Gly	TTC Phe	CGG Arg	AAA Lys	GCA Ala	CTG Leu	ТGC Сув	CGC Arg	TCA Ser	ACC Thr	AGA Arg	CGG Arg	GTA Val	GAC Asp	AAT Asn	C AG Gln	GAA Glu	TTG Leu	CAG Gln	CAG Gln	GGC Gly	ACC Thr	ATG Met	359
1204	GGA Gly	AAC Asn	САТ Нів	ACG Thr	CTG Leu	CCA Pro	CTT Leu	GAG Glu	GAA Glu	ATG Met	AAG Lys	AGA Arg	GAT Авр	CTG Leu	GAA Glu	CCC Pro	AGG Arg	GAG Glu	TGC Cys	CTG Leu	AGA Arg	GAA Glu	ACC Thr	тсс Сув	ACA Thr	GAG Glu	ACG Thr	CAG Gln	387
1288	тст Суз	GAG Glu	AGA Arg	GAT Asp	GAA Glu	GAA Glu	GGA Gly	GAG Glu	GAA Glu	GAG Glu	GAG Glu	GAA Glu	GTA Val	G AA Glu	ATA Ile	GGA Gly	TAT Tyr	ATG Met	GAG Glu	AAC Asn	GCC Ala	ACC Thr	CGG Arg	TTG Leu	AAT Asn	GAA Glu	ATC Ile	TAT Tyr	415
1372	ААG Lyb	TCT Ser	GTG Val	CAG Gln	AAT Asn	GGC Gly	TGC Сув	GGA Gly	AAT Asn	GGG Gly	CAC His	ATG Met	GAG Glu	GGC Gly	ACT Thr	AGG Arg	ACC Thr	ATG Met	TTC Phe	GCA Ala	CAT His	GGG Gly	GCA Ala	GAT Asp	GGT Gly	CAT His	GCT Ala	GCA Ala	443
1456	GGC Gly	CAC His	GGT Gly	AGT Ser	GAA Glu	TCC Ser	AGA Arg	ACT Thr	CAG Gln	GGG Gly	AAC Asn	AGG Arg	GGG Gly	CAT His	ATA Ile	AGT Ser	CCG Pro	ATG Met	ACC Thr	TCT Ser	GGA Gly	CCT Pro	GTT Val	CCT Pro	GCT Ala	CTC Leu	AGT Ser	GGA Gly	471
1540	GCT Ala	CAG Gln	AAG Lys	GAG Glu	AAC Asn	GTC Val	AAA Lys	GCT Ala	CTG Leu	CCA Pro	GAG Glu	GAA Glu	ACA Thr	ACG Thr	GAT Asp	ACA Thr	ATC Ile	CTG Leu	GAA Glu	ATT Ile	AGT Ser	TAC Tyr	TTG Leu		TGAG	CTGC	TAT	AAAC	494
1624	GTA	GAA	CAGA	ACT	ratt?	TAA	ACCTI	rttc <i>i</i>	AAA	CCAT	CAAI	AGTO	SAAAT	GCT/	ATGO	ataj	ATA	meen	rttc <i>i</i>	AGAA1	GTG	ATC?	TCAC	CAGI	TGTO	TTGI	ATG	FTTA	
1735	35 ATATCTGTTCAAATATATATTAATTTGTGTAGGCTTTAAGAGTAAGCTATATATA																												
1846	6 CCAAGTGTTCCCATTAAAGAGTGGTGATAACAGTTTTTGTGACTTAATCAGTTGTAGAAATTCAAATAGATTTTTGACAAAGTTTAAATATTT																												

The nucleotide sequence is numbered on the left; the amino acid sequence is indicated on the right. The seven putative transmembrane domains were assigned on the basis of a Kyte and Doolittle hydrophobicity plot and are shown in bold and underlined. The three potential N-glycosylation sites at positions Asn^{21} , Asn^{47} , and Asn^{207} are underlined. The potential phosphorylation sites at Ser^{91} , Ser^{261} , and Ser^{267} in the first and third cytoplasmic loops are marked by double underlining. Two cysteines located at positions Cys^{134} and Cys^{208} might form a disulfide bond between the first and second extracellular loop; these residues are printed in italics.

The cysteine at position Cys³⁴³ is a potential palmitoylation site. It may attach the receptor's carboxyl terminus to the cell membrane via a palmitoyl anchor, thus producing a fourth cytoplasmic loop.

The extracellular domains contain consensus sequences of the types NXS or NXT (N, asparagine; X, any amino acid except proline and aspartic acid; S, serine; T, threonine) for *N*-glycosylation (Kornfeld and Kornfeld, 1985) at Asn²¹, Asn⁴⁷, and Asn²⁰⁷. Polysaccharides *N*-linked to Asn residues have been shown to play a role in promoting high affinity agonist binding to SRIF receptors (Rens-Domiano and Reisine, 1991).

Southern blotting

Hybridization under a low stringent condition of Southern blots of *Hin*dIII or *Eco*RI digests of genomic DNA of *A. albifrons* with a ³²P-labeled fragment of the *Apteronotus* sst₃ receptor gene showed strongly labeled bands at 12 kb (figure 3). In addition, faintly hybridizing DNA fragments of 5 and 2.3 kb in *Hin*dIII digests as well as of 2.8 and 0.9 kb in *Eco*RI digests were evident. The presence of these weakly hybridizing fragments suggested that there is a family of sst receptors in *A. albifrons*, similar to the mammalian somatostatinergic receptors.

Northern blotting and RT-PCR

To check whether the cloned *Apteronotus* sst₃ receptor is expressed in tissues of *A*. *albifrons*, poly(A)⁺-RNA from brain, liver, heart, spleen, and stomach was prepared and subjected to Northern Blot analysis. No signal could be detected, not even in brain from which the receptor was cloned. Similarly, several attempts to localize the *Apteronotus* sst₃ by *in situ* hybridization failed, although various approaches were employed. Therefore, poly(A)⁺-RNA was used for RT-PCR, which is more sensitive than Northern Blot analysis. After high amplification (40 cycles), a weak signal was observed in brain (figure 4); this was confirmed by Southern Blot hybridization. In the other tissues, the rather high background could not be reduced, although the cDNA was of good quality, as shown by amplification of β -actin (data not shown).

Figure 2: Comparison of the amino acid sequences of *Apteronotus* sst₃ and human sst₃ receptors.

66	199	300	400	494	
81	182	284	356	418	
1 MEAPITAAVFGYEDPRSWDSNVSSLPAHPAFPLPPGHALLPDGSPQNWTEGDGAGFSPSAAGVLIPLVYIAVCVVGLGGNTLVIHIVLRYSHVQSVTNI 1 MDMLHPSSVSTTSEPENASSAWPPD:ATLGNVSA:::::GPSPAGLAVS::GVLIPLVYLVVCVVGLLGNSLVIYVVLRHTASPSVTNV	<pre></pre> <pre></pre> <pre></pre> <pre>TM4 TM2</pre>	> <	<pre></pre> <pre></pre> <pre></pre> <pre>CBC</pre>	EIGYMENATRLNEIYKSVQNGCGNGHMEGTRTMFAHGADGHAAGHGSESRTQGNRGHIS:PMTSGPVPALSGAQKENVKALPEETTDT::::ILEISYL :::::::::::::::::::::::::::::::::::DGEESREGGKGKE::MNGRVSQITQPGTSGQERPPSRVASKEQQLLPQEASTGEKSSTMRISYL	
Fish sst ₃	fish sst ₃	fish sst _j	fish set ₃	fish set ₃	
Human sst ₃	Human sst ₃	Human sst _j	Juman set ₃	Iuman set ₃	

The single-letter code for the amino acids is used. Gaps (represented by colons) have been introduced to maximize alignment. The invariant amino acid residues are shown in boldface type. The seven putative transmembrane domains (TM1- TM7) of the Apteronotus sst3 protein are indicated. Pharmacological properties of Apteronotus sst, receptor

To characterize the protein product encoded by the cloned *Apteronotus* sst₃ receptor gene, the corresponding DNA was transfected and stably expressed in CCL39 cells. Saturation experiments performed with [¹²⁵I]LTT-SRIF₂₈ revealed the presence of a high density of binding sites ($B_{max} = 4470 \pm 130$ fmol/ mg protein, pK_d = 10.51 ± 0.12). Non-specific binding was very low (figure 5). The saturation curve displayed an apparent monophasic course as confirmed by linear Scatchard plot (not shown).

Further characterization of the putative SRIF receptor expressed in CCL39 cells was carried out by radioligand-binding-competition analysis using SRIF₁₄ and SRIF₂₈, as well as the SRIF analogues octreotide, BIM 23052, and BIM 23056 (figure 6; table 1). These peptides exhibited the following rank order of binding potency: SRIF₁₄ \approx SRIF₂₈ > BIM 23052 > octreotide > BIM 23056. Competition curves were monophasic as shown in Figure 6, thus suggesting the presence of a single population of SRIF binding sites. Non-transfected cells did not display significant levels of specific binding.

9.4. Discussion

In this paper, we report, to our knowledge for the first time, the cloning and pharmacological characterization of a non-mammalian SRIF receptor. By using a combination of RT-PCR and genomic library screening, the gene encoding this receptor was isolated from the gymnotiform fish *A. albifrons*. Existence of SRIF receptors in this teleost has been suggested by receptor binding autoradiography using the non-selective ligand [^{125}I]Tyr⁰-D-Trp⁸-SRIF₁₄ (Zupanc et al., 1994). As the structure of the cloned receptor resembles the mammalian sst₃ receptor subtype, we have termed it *'Apteronotus* sst₃ receptor'.



Figure 3: Southern blot analysis of genomic DNA of A. albifrons.

Molecular characterization of the cloned *Apteronotus* sst₃ receptor

Comparison of the fish sst₃ receptor with its mammalian homologues points to many conserved features. Almost 60 % of the amino acid residues are invariant compared to the protein encoded by the human sst₃ receptor gene (cf. Yasuda et al., 1992). An even higher degree of identity is found in the region between the amino terminus of the first transmembrane domain and the carboxyl terminus of the seventh transmembrane domain; within this segment, more than 70 % of the amino acid residues are identical. The same tendency of the sequences to be most similar in the region of the seven alphahelical transmembrane regions and to be most divergent at the amino and carboxyl ends has been found in the three mammalian sst₃ receptors (Meyerhof et al., 1992; Yamada et al., 1992b; Yasuda et al., 1992) and in the other subtypes of SRIF receptors (for reviews, see Hoyer et al., 1994b; Reisine and Bell, 1995).



Figure 4: RT-PCR with Poly(A)⁺RNA prepared from *Apteronotus* brain.

PCR products were separated on a 1% agarose gel and stained with ethidium bromide. M, molecular weight marker (φ -X174 RF DNA/*Hae*III fragments; 1353, 1078, 872, 603, 310, 281, 271, 234, 194, 118, 72 bp); (1) cDNA from *Apteronotus* sst3 expressing CCL39 cells (positive control); (2) cDNA from *Apteronotus* brain; (3) poly(A)⁺RNA from *Apteronotus* brain (negative control); (4) H₂O (negative control); (5) pcDNA3-*Apteronotus* sst3 plasmid DNA (positive control).

The high similarity and identity scores especially in the putative transmembrane regions are good indicators to decide whether receptors are, indeed, homologous subtypes, or whether they are just members of the same subfamily (cf. Hoyer et al., 1994a). In the present case, the *Apteronotus* sst₃ receptor is, based on sequence identity/ similarity, clearly homologous to the sst₃ receptor identified in mammalian species.

The cloning of the *Apteronotus* sst₃ receptor gene provides the opportunity to search for highly conserved structural features of SRIF receptors among a much broader scale of species within the vertebrate phylum than previously available. It is very likely that such structures are also functionally important. A highly conserved amino acid is the tyrosine in position 290 of the *Apteronotus* sst₃ receptor. This residue is also present within the sixth transmembrane domain of the mammalian sst₁₋₄, but not of the mammalian sst₅, where it is exchanged by phenylalanine (for sequence comparison, see Bell and Reisine, 1993; Hoyer et al., 1994b; Patel et al., 1995; Reisine, 1995; Reisine and Bell, 1995; Florio et al., 1996; Patel et al., 1996; Schindler et al., 1996; Patel, 1997).



CCL39 cells stably expressing Apteronotus sst₁.

Crude membrane preparations (4 µg/ assay) were incubated with increasing concentrations ^{[125}I]LTT-SRIF₂₈ of and assayed for receptor binding The figure shows activity. specific (•) and non-specific binding (1) expressed as amount of radioligand bound versus free radioligand concentration. Data represent of triplicate the mean determinations. Note low level of non-specific binding.

The motif NXFTS in the third transmembrane domain is found in all sst receptor subtypes, including *Apteronotus* sst₃, but not in other members of the G-protein-coupled receptor superfamily. Similarly, the putative phosphorylation site RXXSE in the third intracellular loop and the motif YANSCAN in the seventh transmembrane domain are specifically conserved in sst receptors. The presence of such motifs in vertebrate groups as diverse as fish and man should help to design mutant receptors. Such constructs could then be employed to elucidate the role of certain segments and amino acids of the receptor protein in the process of ligand binding and signal transduction.

Although it appears likely that several of the conserved sites in the *Apteronotus* sst₃ receptor exert similar functions as they do in the corresponding mammalian receptors, their exact role remains to be elucidated. For example, three consensus sites for serine phosphorylation could be identified in the first and third intracellular loops of the *Apteronotus* sst₃ receptor. The corresponding sites Ser³⁴¹, Ser³⁴⁶, and Ser³⁵¹ (in addition to Thr³⁵⁷) of the rat sst₃ receptor expressed in HEK293 cells have been shown to be phosphorylated; phosphorylation at these sites is essential for agonist-dependent internalization (Roth et al., 1997). The kinases by which sst receptors are phosphorylated have, however, not yet been identified.

Figure 5: Saturation isotherm of [¹²⁵I]LTT-SRIF₂₈ binding to membranes prepared from

ligand	pK _d
SRIF ₁₄	8.73 ± 0.25
SRIF ₂₈	8.70 ± 0.20
BIM 23052	7.84 ± 0.06
octreotide	7.33 ± 0.10
BIM 23056	6.41 ± 0.05

Table 1: Comparison of potencies of SRIF receptor agonists for binding of $[^{125}I]LTT$ -SRIF₂₈ to *Apteronotus* sst₃ receptor gene expressed in CCL39 cells

The data represent the mean of pK_d -values $(-\log M) \pm \text{standard error of six determinations}$.

In another study, rat sst_{2A} receptors were phosphorylated, primarily at serine residues, following stimulation of protein kinase C (Hipkin et al., 1997). However, protein kinase C may activate another kinase, rather than directly mediating receptor phosphorylation.

Pharmacological properties of the cloned fish sst₃ receptor

In addition to the sequence similarity, the pharmacological properties support the notion that the gene cloned in the present investigation codes for an *Apteronotus* homologue of a mammalian sst receptor. The saturation data indicate that the *Apteronotus* sst₃ receptor stably expressed in CCL39 cells recognizes [¹²⁵I]LTT-SRIF₂₈ with high affinity (pK_d = 10.5), thus being comparable to the pK_d-values observed with mammalian sst₂, sst₃, and sst₅ receptors expressed recombinantly in various cell lines (Bruns et al., 1994, 1995; Siehler et al., 1998b).

Figure 6: Competitive radioligand binding assays on membranes prepared from CCL39 cells expressing *Apteronotus* sst₃ receptors.



Crude membrane preparations (4 μ g/ assay) of CCL39 cells were incubated with 50 μ l [¹²⁵I]LTT-SRIF₂₈ (2175 Ci/ mmol) and the indicated concentrations of SRIF₁₄ (**I**), SRIF₂₈ (**•**), BIM 23052 (*), octreotide (**A**), and BIM 23056 (×). The data are expressed as percentage of specific binding. They are the mean of triplicate determinations.

To further characterize the *Apteronotus* sst₃ receptor expressed in CCL39 cells, three other radioligands have been employed in a concurrent study (Siehler et al., 1999). This investigation has shown that, in addition to $[^{125}I]LTT-SRIF_{28}$, $[^{125}I]Tyr^{10}$ -cortistatin₁₄ (the native peptide is a recently discovered putative member of the SRIF family; see De Lecea et al., 1996), as well as the short cyclic radioactively labelled SRIF analogues $[^{125}I]CGP$ 23996 and $[^{125}I]Tyr^{3}$ -octreotide display high affinity. This result is surprising, since the human sst₃ receptor shows rather low affinity for octreotide (Siehler et al., 1998a, 1998b). Thus, the *Apteronotus* sst₃ receptor, pharmacologically, appears to be more closely related to the human sst₅ receptor than to the human sst₃ receptor.

Apparently, the rather minor differences in the amino acid sequence can result in pronounced differences in the pharmacological profile. A similar effect has been found in serotonin (= 5-hydroxytryptamin, 5-HT) receptors. Despite their marked sequence similarity, the rat and human 5-HT_{1B} receptors express different pharmacological profiles. This is in contrast to the human 5-HT_{1B} and 5-HT_{1D} receptors which, although structurally different, exhibit overlapping pharmacological profiles (Hoyer et al., 1994a).

A second surprising finding made in the detailed analysis of the pharmacological properties of the cloned fish sst₃ receptor was that the affinities for ligands depend on the type of radioligand used (Siehler et al., 1999).

Especially, the profile of $[^{125}I]Tyr^3$ -octreotide does not correlate well with those of $[^{125}I]LTT$ -SRIF, $[^{125}I]Tyr^{10}$ -cortistatin₁₄, and $[^{125}I]CGP$ 23996. This could be explained by assuming that $[^{125}I]Tyr^3$ -octreotide might induce or recognize a distinct receptor conformation which is different from the receptor-ligand conformation present when employing the other three radioligands.

Similarly as reported for the mammalian sst_{1-5} receptor subtypes (Patel et al., 1994), both SRIF₁₄ and SRIF₂₈ inhibit forskolin-stimulated adenylate cyclase activity with high potency and efficacy in CCL39 cells expressing the cloned *Apteronotus* sst₃ receptor (Siehler et al., 1999). The inhibition of forskolin-stimulated adenylate cyclase activity by SRIF₁₄, as measured by cAMP accumulation in intact CCL39 cells, is totally blocked by pertussis toxin. This suggests that the inhibitory effect is mediated by G_i and/or G_o, thus resembling the effect of pertussis toxin on the five cloned mammalian SRIF receptors (Law et al., 1994; Murthy et al., 1996; Tallent and Reisine, 1992). The SRIFinduced second messenger pathway, therefore, appears to be conserved within the vertebrate phylum.

Somatostatin receptors in fish brain

The presence of the *Apteronotus* sst₃ receptor in the brain, as suggested by the initial cloning data obtained after reverse transcription of mRNA from brain tissue, was confirmed by preparation of poly(A)⁺-RNA from brain, followed by high amplification through RT-PCR and subsequent Southern Blot hybridization. On the other hand, the missing signals in Northern Blot analysis using poly(A)⁺-RNA suggest a very low level of expression of the *Apteronotus* sst₃ receptor mRNA *in vivo*. Although the very low level of expression was somewhat unexpected, similar difficulties have been encountered in other cases. When RDC4 (= 5-HT_{1D} receptor) was cloned from dog, the authors were unable to find any transcript in the brain (Libert et al., 1989). Yet, as we know now, this receptor is expressed in the brain, but at very low levels and with a very limited distribution (cf. Hartig et al., 1996). Moreover, the low expression level of the *Apteronotus* sst₃ receptor in the brain may not necessarily correspond to a low level of receptor protein, since for this parameter the stability of the transcript is also of crucial importance.

As attempts to map the expression of the *Apteronotus* sst₃ receptor in the brain using *in situ* hybridization have failed so far, probably due to the very low level of expression, no comparison is possible between the distribution of the corresponding mRNA and that of SRIF binding sites. Such sites have been mapped in detail in the brain of *Apteronotus leptorhynchus* (Zupanc et al., 1994). *In situ*-hybridization studies have suggested a wide distribution of the sst₃ receptor mRNA in the rat (Perez and Hoyer, 1995) and the human (Thoss et al., 1996) brain. However, these data are currently unconfirmed at the protein level, since no selective radioligand is yet available to label sst₃ receptors. A preliminary report points to a wide distribution of sst₃ receptor immunoreactivity in the brain of rats and mice (Schulz et al., 1998b). Interestingly, sst₃-like immunoreactivity was localized to the plasma membrane of neuronal cilia rather than to 'classical' pre- and postsynaptic sites (Händel et al., 1999).

Perspectives

It has been hypothesized that SRIF and its receptors are, in the gymnotiform brain, involved in neuronal control of behaviour (for review, see Zupanc and Maler, 1997) and in regulation of postembryonic neurogenesis (for review, see Zupanc, 1999). Future investigations in this field will greatly benefit from the wealth of molecular data obtained through the cloning, sequencing, and pharmacological characterization of the *Apteronotus* sst₃ receptor. These data, together with the availability of *A. albifrons*-specific probes, now enable researchers to explore the cellular mechanisms underlying the action of SRIF in the teleostean brain in much greater detail than was possible previously.

10.1. Abstract

The first cloned non-mammalian somatostatin (somatostatin release-inhibiting factor = SRIF) receptor previously obtained from the teleost fish Apteronotus albifrons and generically named somatostatin receptor 3 (fsst₃), was stably expressed and characterised in Chinese hamster lung fibroblast (CCL39) cells. Radioligand binding studies were performed with four radioligands selective for SRIF receptors in CCL39 cells expressing fsst₃ receptors: [¹²⁵I]LTT-SRIF₂₈ ([Leu⁸, D-Trp²², ¹²⁵I-Tyr²⁵]-SRIF₂₈), [¹²⁵I]Tyr¹⁰-cortistatin, [¹²⁵I]CGP 23996, and [¹²⁵I]Tyr³-octreotide labelled fsst₃ receptor with high affinity (pK_d -values: 10.47, 10.87, 9.59 and 9.57) and in a saturable manner but defined different B_{max}-values: 4500, 4000, 3400 and 1500 fmol/ mg, respectively. The affinities of SRIF peptides and analogues determined for fsst, receptors displayed the following rank order of potency: seglitide = $SRIF_{25} > SRIF_{14} = SRIF_{28} > cortistatin 14$ > BIM 23014 > RC160 = L361,301 = octreotide ≥ BIM 23052 ≥ L362,855 > $CGP23996 > BIM 23056 > BIM 23030 = cycloantagonist > SRIF_{22}$. The pharmacological profiles determined with [125I]LTT-SRIF₂₈, [125I]CGP 23996 and $[^{125}I]Tyr^{10}$ -cortistatin correlated highly significantly (r = 0.96- 0.99), whereas $[^{125}I]Tyr^{3}$ octreotide binding was rather divergent (r = 0.78- 0.81). Further, $[^{125}I]Tyr^{3}$ -octreotideand [¹²⁵I]CGP 23996-labelled sites showed higher affinity for the various peptides than [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I]Tyr¹⁰-cortistatin-labelled sites, although there were exceptions. [^{125}I]LTT-SRIF $_{28}$ -binding to fsst₃ receptors and human sst₁₋₅ receptors was compared; the fsst₃ binding profile correlated better with the hsst₅- than with the hsst₅ receptor profile. SRIF inhibited potently forskolin-stimulated adenylate cyclase activity in fsst, transfected CCL39 cells; this effect was blocked by pertussis toxin, suggesting coupling of the fsst₃ receptor to $G_{i\alpha}$ and/ or $G_{0\alpha}$. [¹²⁵I]LTT-SRIF₂₈ binding was detected in fish brain, liver, heart, spleen, and stomach, but not in gut. The pharmacological profile of [¹²⁵I]LTT-SRIF₂₈-labelled sites in brain, but not in liver, correlated significantly with the recombinant fsst, receptor, in agreement with expression of fsst, receptor gene found by RT-PCR in brain. However, biphasic binding curves obtained with two SRIF-analogues in brain, as well as the distinct pharmacological profile of the liver SRIF receptor, suggest the existence of several yet to be defined SRIF receptor subtypes in fish.

The present data demonstrate that the recombinantly expressed fsst₃ receptor has a pharmacological profile compatible with that of a SRIF₁ receptor, although the rank order of affinity of fsst₃ is closer to that of hsst₅ than hsst₃ receptors, as may be found when comparing very distantly related species. The fsst₃ receptor expressed in CCL39 cells, is negatively coupled to adenylate cyclase activity via pertussis toxin-sensitive G-proteins, like mammalian sst₃ receptors. Radioligand binding performed with fish tissue suggests the presence of a native sst₃ receptor in brain as well as other yet to be defined SRIF receptor subtypes.

10.2. Results

Radioligand binding in CCL39 cells expressing fsst, receptors

[¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996, [¹²⁵I]Tyr¹⁰-CST and [¹²⁵I]Tyr³-octreotide labelled the cloned fsst₃ receptor stably expressed in CCL39 cells with high affinity; the levels of non-specific binding were low for all four radioligands. [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I]Tyr¹⁰-CST (pK_d = 10.47 ± 0.12 and 10.87 ± 0.34, respectively) displayed somewhat higher affinity than [¹²⁵I]CGP 23996 and [¹²⁵I]Tyr³-octreotide (pK_d = 9.59 ± 0.04 and 9.57 ± 0.04) (table 1). All saturation curves were monophasic and compatible with the labelling of a single population of receptor sites (figure 1). However, whereas [¹²⁵I]LTT SRIF₂₈, [¹²⁵I]Tyr¹⁰-CST and [¹²⁵I]CGP 23996 labelled similar densities of receptor sites (between 3000 and 4400 fmol/ mg), [¹²⁵I]Tyr³-octreotide - surprisingly - labelled only about 1500 fmol/ mg (see discussion). No specific binding was detected with any of the four radioligands in non-transfected CCL39 cells (data not shown).

The pharmacological profiles of $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I]Tyr^{10}CST$, $[^{125}I]CGP$ 23996 and $[^{125}I]Tyr^{3}$ -octreotide-labelled sites were established in membranes of CCL39 cells expressing fsst₃ receptors using a number of analogues of somatostatin including the native peptides SRIF₁₄, SRIF₂₂, SRIF₂₅, SRIF₂₈ and CST. The peptides tested showed very high affinity (in the range 30 pM to 100 nM). There were, however, disparities as listed in table 2.

In general, the peptides showed somewhat higher affinity for sites labelled with [¹²⁵I]Tyr³-octreotide when compared to [¹²⁵I]CGP 23996, whereas sites labelled with [¹²⁵I]LTT-SRIF₂₈ or [¹²⁵I]Tyr¹⁰-CST displayed significantly lower affinity. Thus, the differences between [¹²⁵I]Tyr¹⁰-CST and [¹²⁵I]Tyr³-octreotide ranged from 13 to 160 fold, with two exceptions; there was no difference for BIM 23056, whereas that for BIM 23056 was 8900 fold. The differences tended to be larger for the synthetic analogues, about 40-160 fold (except BIM 23052 and BIM 23056), whereas the "natural" peptides showed only 13-51 times higher affinity for [¹²⁵I]Tyr³-octreotide binding (figure 2). Nevertheless, the overall pharmacological profiles were similar, especially when the sites were labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]Tyr¹⁰-CST, or [¹²⁵I]CGP 23996 (r = 0.96- 0.99, P < 0.0001, see figure 3). By contrast, the profile defined with [¹²⁵I]Tyr³-octreotide was rather dissimilar from that determined with each of the three other radioligands (r = 0.75- 0.81).

 Table 1: Results of saturation experiments performed with different radioligands at fish

 sst, receptors expressed in CCL39 cells

	pK _d	B _{max} [fmol/mg]
[¹²⁵ I]LTT-SRIF ₂₈	10.47 ± 0.12	4470 ± 240
[¹²⁵ I]CGP 23996	9.59 ± 0.04	3420 ± 190
[¹²⁵ I]Tyr ¹⁰ -CST	10.87 ± 0.34	4030 ± 210
[¹²⁵ I]Tyr ³ -octreotide	9.57 ± 0.04	1520 ± 60

The data are expressed as B_{max} (fmol/ mg) and pK_d-values (-log mol/ l) ± SEM of 3 different experiments. Dunnett's multiple comparison test indicates that the B_{max} -values defined by [125I]LTT-SRIF₂₈ and [125I]Tyr¹⁰-CST are not different (P > 0.05), whereas [125I]CGP 23996 (P < 0.05) and [125I]Tyr³-octreotide (P < 0.01) labelled significantly less sites.

Figure 1: Saturation isotherms of binding of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996, [¹²⁵I]Tyr¹⁰-CST, and [¹²⁵I]Tyr³-octreotide to membranes prepared from CCL39 cells stably expressing fsst₃ receptors.



Crude membrane preparations from fsst3 receptor expressing cells were incubated with increasing concentrations of each radioligand and assayed for receptor binding activity. The plots depict specific (\bullet) and non-specific binding (\blacksquare) expressed as bound (cpm/ assay) versus free radioligand concentration (pM). The data points represent one representative example of 3 different experiments.

Inhibition of forskolin-stimulated cAMP production

Since the mammalian sst_{1-5} receptor subtypes have been reported to couple negatively to adenylate cyclase, we examined whether the fish sst_3 receptor modulates adenylate activity. Both $SRIF_{14}$ and $SRIF_{28}$ inhibited forskolin-stimulated adenylate cyclase activity (figure 4) with high potency and efficacy, as measured by cAMP accumulation in intact CCL39 cells.

	[¹²⁵ I]LTT-SRIF ₂₈	[¹²⁵ I]Tyr ¹⁰ -CST	[¹²⁵ I]CGP 23996	[¹²⁵ I]Tyr ³ -
				octreotide
seglitide	9.15 ± 0.08	8.55 ± 0.11 ^{ns}	$9.83 \pm 0.13*$	$10.53 \pm 0.23 **$
SRIF ₂₅	9.00 ± 0.07	8.85 ± 0.04 ^{ns}	9.93 ± 0.17 **	$10.32 \pm 0.04^{**}$
SRIF_{14}	8.93 ± 0.19	8.87 ± 0.07 ^{ns}	$9.53 \pm 0.28*$	$9.99 \pm 0.12^{**}$
SRIF ₂₈	8.84 ± 0.15	8.61 ± 0.03 ^{ns}	$9.64 \pm 0.19^*$	10.21 ± 0.39**
cortistatin 14	8.82 ± 0.10	8.51 ± 0.16 ^{ns}	9.63 ± 0.01**	9.85 ± 0.05**
Tyr ¹⁰ -cortistatin	8.54 ± 0.08	8.32 ± 0.17 ns	9.37 ± 0.31 ^{ns}	9.98 ± 0.24 **
BIM 23014	8.06 ± 0.08	$7.69 \pm 0.08*$	9.37 ± 0.08**	$9.63 \pm 0.02^{**}$
RC160	7.67 ± 0.05	7.21 ± 0.06 **	8.86 ± 0.08**	$9.29 \pm 0.02^{**}$
L361,301	7.73 ± 0.26	$7.01 \pm 0.15^*$	8.91 ± 0.08**	9.22 ± 0.02 **
octreotide	7.45 ± 0.10	7.28 ± 0.18 ^{ns}	8.72 ± 0.10**	9.29 ± 0.02**
BIM 23052	7.92 ± 0.08	7.68 ± 0.08 ^{ns}	9.15 ± 0.12**	7.90 ± 0.16 ^{ns}
L362,855	7.54 ± 0.05	7.09 ± 0.13**	8.77 ± 0.02**	8.91 ± 0.06**
CGP23996	7.16 ± 0.28	6.78 ± 0.30^{-ns}	8.24 ± 0.03*	8.94 ± 0.03**
BIM 23056	6.32 ± 0.07	$5.88 \pm 0.09^{**}$	6.97 ± 0.07 **	9.83 ± 0.06**
BIM 23030	6.40 ± 0.05	$6.04 \pm 0.02^{**}$	7.46 ± 0.08 **	$7.62 \pm 0.03 **$
cycloantagonist	6.25 ± 0.15	5.94 ± 0.18 ^{ns}	7.17±0.07**	7.95 ± 0.12 **
SRIF ₂₂	5.33 ± 0.08	5.17 ± 0.07 ^{ns}	6.19 ± 0.09**	6.88 ± 0.03**

Table 2: Comparison of affinities of SRIF, various SRIF-analogues and cortistatin for

 fish sst, receptors labelled with different radioligands

The data represent the mean of pK_d-values (-log mol/ l) \pm SEM of at least 3 determinations. Dunnett's multiple comparison test indicates that the profiles defined by the four radioligands differ to various extents: whereas [125I]LTT-SRIF₂₈ and [125I]Tyr¹⁰-CST are not different (P > 0.05), the profiles defined by [125I]CGP 23996 (P < 0.05) and [125I]Tyr³-octreotide (P < 0.01) are different from that defined using [125I]LTT-SRIF₂₈. In addition, individual pK_d-values were compared to those obtained with [125I]LTT-SRIF₂₈ and significance of difference is indicated: ns = non significant, * = P < 0.05, ** = P < 0.01.



Figure 2: Competitive radioligand binding assays on membranes prepared from CCL39 cells expressing fsst₃ receptors.

Crude membrane preparations from fsst3 receptor-transfected cells were incubated with $[125I]LTT-SRIF_{28}$, [125I]CGP 23996, $[125I]Tyr^{10}-CST$ or $[125I]Tyr^{3}$ -octreotide respectively, and the indicated concentrations of SRIF_{14} (\blacksquare), SRIF_{28} (\blacktriangle), SRIF_{22} (\bigtriangledown), seglitide (\blacklozenge), octreotide (\bullet), and RC160 (\square). Data are expressed as percentage of specific binding. The data points represent one representative example of at least 3 different experiments.

The maximal inhibition induced by $SRIF_{14}$ and $SRIF_{28}$ was 87 % and 91 %, with pEC_{50} -values of 9.52 ± 0.01 and 9.19 ± 0.01 respectively (mean \pm SEM, n = 3). The inhibition of forskolin-stimulated adenylate cyclase activity by $SRIF_{14}$ was totally blocked by pertussis toxin (figure 5). Therefore, the negative coupling of fsst₃ to adenylate cyclase is mediated by $G_{i\alpha}$ and/or $G_{0\alpha}$ in CCL39 cells.

Radioligand binding in fish tissues

The presence and nature of somatostatin binding sites was studied in different tissues of *A. albifrons* with [¹²⁵I]LTT-SRIF₂₈ (table 3). High levels of binding were observed in brain and liver, intermediate levels in heart and spleen, and a low level in stomach. No specific [¹²⁵I]LTT-SRIF₂₈ binding was detectable in gut. Brain and liver were therefore used in competition experiments using [¹²⁵I]LTT-SRIF₂₈ (table 4, figure 6), since binding was too low in stomach, whereas heart and spleen were not available in sufficient quantities. In brain, SRIF₁₄ and SRIF₂₈ displayed high affinity, as did the short cyclic SRIF-analogues seglitide and octreotide; however, both analogues produced biphasic competition curves suggesting the presence of two different populations of sites. In liver, SRIF₂₈ bound with somewhat higher affinity than SRIF₁₄; other SRIF analogues displayed intermediate to high affinity except the cycloantagonist SA, which showed low affinity to both brain and liver.

The profile of the recombinant fsst₃ receptor was compared with that of fish brain and liver sites labelled with [¹²⁵I]LTT-SRIF₂₈ (figure 7). Since two binding populations were defined by seglitide and octreotide in brain, only the high affinity values were considered. The brain and fsst₃ profiles correlated highly significantly (r = 0.942, P < 0.001), supporting the presence of fsst₃ receptor protein in fish brain as previously suggested by RT-PCR data (Zupanc et al., 1999). The correlation coefficient obtained with liver and fsst₃ sites was lower (r = 0.826) suggesting the presence of either a mixture of sst₃ and some other site, or that of another SRIF receptor distantly related to fsst₃.

Comparison with human somatostatin receptors

Finally, the pharmacological profile of the fsst₃ receptor was compared with that of the five recombinant human somatostatin receptors; the data were obtained with [¹²⁵I]LTT-SRIF₂₈ in CCL39 cells expressing hsst₁₋₅ receptors (Siehler et al., 1998a; 1998b). The fsst₃ profile did not correlate with those of hsst₁ and hsst₄ receptors, which belong to the SRIF₂ receptor family (r = 0.461 and r = 0.357, respectively; data not shown).

Figure 3: Comparison of $[^{125}I]$ LTT-SRIF₂₈, $[^{125}I]$ CGP 23996, $[^{125}I]$ Tyr¹⁰-CST, and $[^{125}I]$ Tyr³-octreotide defined pharmacological profiles of fish recombinant sst₃ receptor expressed in CCL39 cells.



Data shown in table 2 are depicted as plots with pK_d -values obtained by labelling of fish sst3 receptor with distinct radioligands. Correlation coefficients (r) are indicated in all plots.

Therefore, only binding data of hsst₂, hsst₃, and hsst₅, which belong to the SRIF₁ family, are presented (table 5). The fsst₃ profile correlated best with the hsst₅ receptor (r = 0.920, P < 0.001), whereas lower correlation coefficients were observed with hsst₂ (r = 0.832) or hsst₃ receptor (r = 0.689) (figure 8).

Figure 4: Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity by $SRIF_{14}$ and $SRIF_{28}$ in CCL39 cells expressing fsst₃ receptors.



Fish sst3 receptor transfected cells were incubated with 6 μ Ci [³H]adenine, treated with forskolin (10 μ M) and the indicated concentrations of SRIF₁₄ (**■**) or SRIF₂₈ (**●**), and [³H]cAMP isolated by sequential chromatography. Graphs represent the percentage of inhibition of forskolin-stimulated adenylate cyclase activity. The data points represent one representative example of 3 different experiments. The mean of the pEC₅₀values ± SEM of three determinations for SRIF₁₄ is 9.52 ± 0.01 and for SRIF₂₈ is 9.19 ± 0.01.

Figure 5: Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity by $SRIF_{14}$ in fsst₃ receptor expressing CCL39 cells is inhibited by pertussis toxin.



Fsst3 receptor transfected cells were treated for 24 hours with pertussis toxin (\bullet) or not treated (\blacksquare), incubated with 6 µCi [³H]adenine, stimulated with forskolin (10 µM) and the indicated concentrations of SRIF₁₄; [³H]cAMP was isolated by sequential chromatography. Graphs represent the percentage of inhibition of forskolin-stimulated adenylate cyclase activity. The data points represent one representative example of 3 different experiments. The present paper describes the pharmacological profile and receptor-effector coupling of the putative $fsst_3$ receptor expressed recombinantly in hamster fibroblast CCL39 cells. In addition, the presence of the native sst_3 receptor was investigated in various fish tissues.

The fsst₃ receptor is a member of the SRIF₁ receptor family

 $[^{125}I]LTT-SRIF_{28}, [^{125}I]CGP 23996, [^{125}I]Tyr^{10}-CST and [^{125}I]Tyr^{3}-octreotide were used to$ label fsst₃ receptors expressed in CCL39 cells. SRIF₁₄ (which is found in all vertebrates),SRIF₂₈, and SRIF₂₅ all displayed high affinity for fsst₃ receptors. It may be surprising thatSRIF₂₂, which has been identified in catfish, a teleostean order closely related to thegymnotiform fish, exhibited low affinity for fsst₃.

Table 3: Specific binding of $[^{125}I]LTT$ -SRIF₂₈ to tissue preparations of *Apteronotus* albifrons

	[¹²⁵ I]LTT-SRIF ₂₈
brain	80.0 % ± 0.7
liver	66.1 % ± 4.2
heart	51.8 % ± 0.5
spleen	45.8 % ± 2.4
stomach	29.9 % ± 2.4
gut	0.0 % ± 0.0

The data represent the percentage of specific binding (mean \pm SEM of 3 determinations) determined with a radioligand concentration of 30 pM.

This suggests that $SRIF_{22}$ and its corresponding receptor are either not expressed at all in tissues of *Apteronotus albifrons*, or that at least one other receptor with higher affinity for $SRIF_{22}$ exists in fish. Cortistatin, of which the prepropeptide was cloned from rat, mouse, and human (De Lecea et al., 1996; De Lecea et al., 1997a; Fukusumi et al., 1997), displays similar high affinity for fsst₃ receptors as $SRIF_{14}$, $SRIF_{28}$, and $SRIF_{25}$. CST also binds with high affinity for the hsst₁₋₅ receptors (Fukusumi et al., 1997; Siehler et al., 1998b). Since CST_{14} is highly similar to $SRIF_{14}$ (11 out of 14 amino acids are identical), these findings provide additional support for the peptide to be considered a member of the SRIF family.

Table 4: Affinities of SRIF and various SRIF-analogues for brain and liver membranes

 of Apteronotus albifrons labelled with [¹²⁵I]LTT-SRIF₂₈

	brain	liver
SRIF ₁₄	9.42 ± 0.22	8.94 ± 0.15
SRIF ₂₈	9.58 ± 0.03	9.58 ± 0.06
seglitide	8.85 ± 0.05 / 6.34 ± 0.05	8.47 ± 0.06
octreotide	9.52 ± 0.01 / 7.55 ± 0.02	8.52 ± 0.14
L362,855	7.52 ± 0.06	8.22 ± 0.12
RC160	8.33 ± 0.03	8.44 ± 0.33
BIM 23014	8.09 ± 0.06	8.39 ± 0.24
cycloantagonist SA	6.38 ± 0.29	6.40 ± 0.03

The data represent the mean of pK_d -values (-log mol/l) \pm SEM of 3 different experiments. The competition curves were biphasic for seglitide and octreotide in brain membranes as evaluated by the high and low affinity values.

Figure 6: Competitive radioligand binding assays on membranes prepared from brain of the fish *Apteronotus albifrons*.



Crude membrane preparations from fish brain were incubated with $[125I]LTT-SRIF_{28}$ and the indicated concentrations of seglitide (\blacksquare) or octreotide (\bullet). Data are expressed as percentage of specific binding. The data points represent one representative example of at least 3 different experiments.

The short cyclic SRIF-analogues seglitide, octreotide, RC160, and BIM 23014 display high affinity for the fsst₃ receptor, as is typical of the SRIF₁ receptor family (Hoyer et al., 1994b, 1995b), although these compounds tend to show higher affinity for the fsst₃ compared to the human receptors. These findings are in line with the classification of SRIF receptors (Hoyer et al., 1995a), which considers sst_2 , sst_3 and sst_5 receptors to form the SRIF₁ receptor family.

Atypical pharmacological features

We have compared the binding characteristics of $[^{125}I]LTT-SRIF_{28}$, $[^{125}I]Tyr^{10}-CST$, $[^{125}I]CGP$ 23996, and $[^{125}I]Tyr^{3}$ -octreotide: all four radioligands showed high affinity, including $[^{125}I]Tyr^{10}-CST$ and, unexpectedly, also $[^{125}I]Tyr^{3}$ -octreotide (since the mammalian sst₃ receptor shows rather low affinity for octreotide). The pharmacological profiles determined with $[^{125}I]LTT-SRIF_{28}$, $[^{125}I]CGP$ 23996, $[^{125}I]Tyr^{10}-CST$ and $[^{125}I]Tyr^{3}$ -octreotide were apparently radioligand-dependent.
Figure 7: Correlation analyses between binding affinities of SRIF and various analogues for recombinant fsst₃ receptor expressed in CCL39 cells, and for fish brain and fish liver labelled with [125 I]LTT-SRIF₂₈.



 pK_d -values of SRIF and SRIF-analogues shown in both tables 2 and 4 are depicted as plots. Correlation coefficients (r) are indicated in the plots. With seglitide and octreotide two binding sites in brain were detected; the high affinity value was used for correlation analysis.

With [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I]Tyr¹⁰-CST, affinity values were up to 160-fold lower than with [¹²⁵I]CGP 23996 and [¹²⁵I]Tyr³-octreotide. In extreme cases, the apparent affinity varied up to 250-300 (even 8900 fold) for a single peptide. However, these differences were not systematic and were more limited for the native peptides compared to synthetic ones. The pharmacological profiles obtained with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996, and [¹²⁵I]Tyr¹⁰-CST were similar, whereas the profile obtained with [¹²⁵I]Tyr³-octreotide was somewhat different from the others (correlation coefficient $r \le 0.81$). Differences in profiles have been reported for species variants of the same receptor; for example, the hsst₅ receptor shows a 160-fold lower affinity for octreotide than the rat sst₅ receptor (O'Carroll et al., 1994). Such differences in affinity may relate to changes in the amino acid sequence and/or protein folding, or to cell type-specific post-transcriptional and post-translational modifications, e.g. phosphorylation and glycosylation, or even cell-specific expression of G-protein subsets (Lefkowitz et al., 1993).

Table 5: Comparison of affinities of SRIF and various SRIF-analogues for fish sst₃ receptors and the human somatostatin receptor subtypes of the SRIF₁ receptor family, labelled with [125 I]LTT-SRIF₂₈

	fsst ₃	hsst ₅	hsst ₂	hsst ₃
SRIF ₁₄	8.93 ± 0.19	9.53 ± 0.13	10.00 ± 0.01	9.54 ± 0.05
SRIF ₂₈	8.84 ± 0.15	9.39 ± 0.22	9.92 ± 0.03	9.65 ± 0.04
seglitide	9.15 ± 0.08	8.70 ± 0.26	9.96 ± 0.02	6.88 ± 0.08
CGP23996	7.16 ± 0.28	6.59 ± 0.41	8.58 ± 0.07	8.82 ± 0.05
octreotide	7.45 ± 0.10	7.17 ± 0.30	9.19 ± 0.03	7.88 ± 0.04
L362,855	7.54 ± 0.05	7.17 ± 0.30	8.36 ± 0.05	7.62 ± 0.23
L361,301	7.73 ± 0.26	7.69 ± 0.13	8.39 ± 0.11	6.34 ± 0.06
RC160	7.67 ± 0.05	7.51 ± 0.06	9.35 ± 0.09	7.37 ± 0.15
BIM 23030	6.40 ± 0.05	6.02 ± 0.09	7.77 ± 0.07	7.17 ± 0.08
BIM 23014	8.06 ± 0.08	7.76 ± 0.13	9.27 ± 0.06	7.86 ± 0.41
BIM 23056	6.32 ± 0.07	7.17 ± 0.05	6.33 ± 0.10	6.90 ± 0.04
BIM 23052	7.92 ± 0.08	7.92 ± 0.19	8.30 ± 0.14	8.42 ± 0.12
cycloantagonist	6.25 ± 0.15	6.38 ± 0.23	5.40 ± 0.06	6.23 ± 0.03
Tyr ¹⁰ -cortistatin	8.54 ± 0.08	8.67 ± 0.24	8.77 ± 0.09	8.70 ± 0.18
cortistatin 14	8.82 ± 0.10	8.71 ± 0.02	8.75 ± 0.20	9.06 ± 0.12

The data represent the mean of pK_d-values (-log mol/ l) \pm SEM of at least 3 determinations. [¹²⁵I]LTT-SRIF₂₈ labelled a single population of binding sites in hsst₂, hsst₃, and hsst₅ expressing CCL39 cells (pK_d = 9.89 \pm 0.04 / B_{max} [fmol/ mg] = 370 \pm 60, pK_d = 10.28 \pm 0.06 / B_{max} = 560 \pm 60, pK_d = 10.48 \pm 0.04 / B_{max} = 6950 \pm 220, respectively).

However, in the present study, the fsst₃ receptor was studied throughout in CCL39 cells, and, nevertheless, affinities for ligands appeared to be radioligand-dependent; this could be explained by varying receptor-ligand conformations. Since the profile of [¹²⁵I]Tyr³- octreotide did not correlate well with those of the other radioligands, [¹²⁵I]Tyr³- octreotide might induce/ recognise a distinct receptor conformation.

By inhibition of radioligand binding at the hsst₅ receptor with the GTP-analogue GppNHp (guanylylimidodiphosphate) it could be shown that $[^{125}I]Tyr^3$ -octreotide labels almost exclusively G-protein-coupled receptors, while $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I]CGP$ 23996 labelled coupled and uncoupled receptors, although all radioligands behave as full agonists in functional assays (Siehler et al., 1998a). This might also be the case with the fsst₃ receptor and could explain the different B_{max}-values obtained with these radioligands.

 $[^{125}I]LTT-SRIF_{28}$ and $[^{125}I]Tyr^{10}$ -CST labelled more receptor sites (4470 and 4030 fmol/ mg, respectively) compared to $[^{125}I]CGP$ 23996 (3420 fmol/ mg) and especially $[^{125}I]Tyr^{3}$ -octreotide (1520 fmol/ mg). The data are surprising in that, although experiments were performed largely in parallel using the same batches of membranes, the four radioligands appear to recognise different populations of receptors. Such data have been reported previously when comparing agonist and antagonist binding, as in the case of 5-HT₂ receptors (Teitler et al., 1990); however, this may not apply here, since the equivalent non-radioactive somatostatin analogues have always been described as agonists at SRIF receptors. This cannot be tested formally, because the corresponding cold ligands (i.e. ligands labelled with ¹²⁷I) are not available.

Nevertheless, assuming that the radioligands are agonists in nature, this would suggest that the ligand-receptor complexes defined by each radioligand are conformationally different. This may seem surprising, but appears to be supported by the competition data (see above). The conformation of the ligand-receptor complex may vary markedly depending on the radioligand used; in other words, higher concentrations of octreotide or seglitide are needed to displace [¹²⁵I]LTT-SRIF₂₈ or [¹²⁵I]Tyr¹⁰-CST compared to [¹²⁵I]Tyr³-octreotide or [¹²⁵I]CGP 23996 binding. Based on the affinity values determined by the former two ligands, it could hardly be anticipated that the iodinated forms of CGP 23996 or octreotide (pK_d-values 35- 166 nM) may be used to label the fsst₃ receptor at concentrations as low as 30 pM (those used to perform competition experiments). Thus, depending on the radioligand used, the affinity of a given compound may be underestimated rather dramatically. Similar discrepancies in both affinity and B_{max}-values have been reported at the hsst₅ receptor when comparing profiles obtained with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I]CGP 23996, and [¹²⁵I]Tyr³-octreotide (Siehler et al., 1998a).

Figure 8: Correlation analyses of affinities of SRIF and various SRIF-analogues for $fsst_3$ receptor expressed in CCL39 cells and human SRIF₁ receptor subtypes expressed in CCL39 cells labelled with [¹²⁵I]LTT-SRIF₂₈.



Species variations

Pharmacologically, the fsst₃ receptor is more closely related to the hsst₅ than to the hsst₃ receptor. Indeed, profiles established with [¹²⁵I]LTT-SRIF₂₈ revealed a very high correlation between fsst₃ and hsst₅ receptors (r = 0.920, P < 0.001) and a lower correlation with hsst₃ receptors; this observation cannot be explained by different cell systems, because all receptors were expressed in CCL39 cells and are, therefore, species related. This, however is not unusual, as it is well known that minor changes in the amino acid sequence of a receptor, as observed e.g. between rat and human 5-HT_{1B} receptors, can result in rather marked differences in pharmacological profile.

For instance, the rat 5-HT_{1D} receptor is pharmacologically closer to the human 5-HT_{1B} receptor than the rat 5-HT_{1B} receptor is to its own species variant, i.e. the human 5-HT_{1B} receptor (Hoyer et al., 1994a).

Presence of sst₃ receptors in fish brain

The fsst₃ receptor is apparently expressed at a very low level in fish brain based on mRNA levels (Zupanc et al., 1999). High correlation of fsst₃ receptor binding data with the fish brain binding data suggested significant fsst₃ receptor protein levels in fish brain; the difference in mRNA and protein levels might be explained by high stability of the fsst₃ receptor transcript. The competition curves of seglitide and octreotide for fish brain labelled sites were biphasic, which is compatible with the presence of at least one additional SRIF subtype in fish. In liver, in contrast to brain, binding profiles obtained with [¹²⁵I]LTT-SRIF₂₈ correlated much less with those obtained in the brain or with recombinant fsst₃. Thus, the fsst₃ receptor is either not expressed in liver, or the SRIF binding represents a combination of different sites which may or may not include fsst₃.

Fish liver recognition sites have preferential affinity for $SRIF_{28}$ compared to $SRIF_{14}$, reminiscent of the sst₅ subtype (O'Carroll et al., 1992; Patel and Srikant, 1994; Raynor et al., 1993b). In addition, the intermediate to high affinity of the SRIF analogues seglitide, octreotide, RC160, BIM 23014, and L362,855 suggests that the liver SRIF receptor belongs to the SRIF₁ family which is characterised by this kind of affinity profile (Hoyer et al., 1994b).

Finally, the presence of specific [125 I]LTT-SRIF $_{28}$ binding in fish spleen, heart, and stomach, in addition to brain and liver, agrees with SRIF receptors being widely distributed in fish as already suggested by the wide distribution of the SRIF peptide (Fletcher et al., 1983; Sas and Maler, 1991; Zupanc et al., 1991) and SRIF binding sites (Zupanc et al., 1994). In mammals, sst₃ receptor mRNA is expressed in specific areas of brain, e.g. in cerebellum, but also in stomach, liver, spleen, pancreas, and muscle (Kaupmann et al., 1993; Raulf et al., 1994; Piwko et al., 1997). However, the localisation of the native protein remains elusive.

Second messenger coupling

Inhibition of forskolin-stimulated adenylate cyclase activity has been reported for all five known mammalian SRIF receptors (Patel et al., 1994). Similarly, negative coupling of fsst₃ to adenylate cyclase is produced by SRIF₁₄ and SRIF₂₈ in CCL39 cells; the effect on cAMP production was potent and efficient for both peptides (around 90 % inhibition with EC₅₀ values in the subnanomolar range). The inhibition of forskolin-stimulated adenylate cyclase activity by SRIF₁₄ is completely blocked by pre-treatment of the cells with pertussis toxin, which is in line with a G_i and/or G_o mediated effect, similarly to the five cloned mammalian SRIF receptors (Law et al., 1994; Murthy et al., 1996; Tallent and Reisine, 1992). It seems that both somatostatins at concentrations above 0.1 micromolar produce less inhibition, either because at higher concentrations inhibition is taking place, or that G_s is being activated directly or indirectly. This has not been investigated further but is not uncommon. It has been reported in COS cells, that the C-terminus of G_iα1 and G_iα2 (but not G_oα) is recognised by the hsst₃ receptor (Komatsuzaki et al., 1997). Thus, SRIF-induced cellular signalling pathways might be conserved within the vertebrate phylum.

In conclusion, the present manuscript describes the pharmacological profile of the putative fsst₃ receptor recombinantly expressed in CCL39 cells. The overall pharmacological profile suggests that, indeed, the fsst₃ receptor belongs to the SRIF₁ receptor family characterised by high affinity for small peptide analogues such as octreotide or seglitide. The native receptor can be found in fish brain as suggested from binding studies. The competition curves of seglitide and octreotide in brain are sufficiently shallow to allow delineation into two sites, which is compatible with the existence of multiple SRIF receptors in brain; one of these receptors shows a profile very similar to that of the recombinant fsst₃ receptor. Binding was also found in liver, although the pharmacological profile is somewhat different from the recombinant fsst₃ receptor; nevertheless, the high affinity of small SRIF analogues suggests, again, the presence of an additional member of the SRIF₁ family in liver.

The fsst₃ receptor is apparently functional and couples well to the inhibition of forskolin-stimulated adenylate cyclase activity, similarly to human $SRIF_1$ receptors (see Hoyer et al., 1995b). However, further work is needed to determine whether a `true` pharmacological profile if at all, can be established for the fsst₃ receptor.

Chapter 11

Fish somatostatin sst_3 receptor: comparison of radioligand and GTP γ S binding, adenylate cyclase and phospholipase C activities reveals agonist-dependent pharmacological differences

Sandra Siehler, Günther K. H. Zupanc, Klaus Seuwen and Daniel Hoyer, Neuropharmacology, submitted The fsst₃ receptor is the only somatostatin (SRIF) receptor cloned from a nonmammalian species so far. Here we investigated the guanine nucleotide sensitivity of agonist radioligand binding, agonist-stimulated GTP γ S binding, inhibition of forskolinstimulated adenylate cyclase (FSAC) and stimulation of phospholipase C (PLC) activities, induced by somatostatin (SRIF)- and cortistatin (CST)-analogues, at fish somatostatin receptor 3 (fsst₃) recombinantly expressed in CCL39 (Chinese hamster lung fibroblast) cells.

The GTP-analogue guanylylimidodiphosphate (GppNHp) inhibited binding of [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide by 72 % and 83 % suggesting preferential labelling of G-protein-coupled fsst₃ receptors; by contrast, binding of the ligands [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ was rather GppNHp-insensitive ($E_{max} = 42$ % and 35 %) suggesting labelling of both coupled and non-coupled receptor states. These results might explain the apparent higher receptor densities determined in saturation experiments with the latter two radioligands compared to [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide.

SRIF₁₄ (10 μM) stimulated specific [³⁵S]GTPγS binding by 314 %; SRIF₂₈ and octreotide displayed full agonism, whereas most other ligands reached 63- 81 % intrinsic activity compared to SRIF₁₄. SRIF₁₄ and SRIF₂₈ inhibited forskolin-stimulated AC (FSAC) activity by 58 and 61 %; all tested ligands except of BIM 23056 inhibited FSAC with comparable high intrinsic activities. 10 μM SRIF₁₄ induced stimulation of PLC activity via fsst₃ receptors determined by measuring total [³H]-IP_x accumulation more than 8-fold ($E_{max} = 831$ %); this response was rather insensitive to 100 ng/ ml pertussis toxin (PTX) (21 % inhibition), which suggests the G_q-family proteins couple to PLC activity. SRIF₁₄, SRIF₂₈ and [Tyr¹⁰]CST₁₄ showed full agonism at PLC, whereas all other ligands behaved as partial agonists (17- 72 % intrinsic activity). BIM 23056, which was a weak agonist in all 3 functional assays, antagonised SRIF₁₄-induced total [³H] IP_x production (pK_B = 6.83), but neither agonist-stimulated [³⁵S]GTPγS binding nor FSAC inhibition.

Comparison of the pharmacological profiles of fsst₃ receptors established in GTP γ S binding, FSAC inhibition and PLC stimulation resulted in low correlation coefficients (r = 0.410- 0.594). Higher, although variable correlations were obtained comparing GTP γ S binding and inhibition of AC activity with previously reported affinity profiles of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide (Siehler et al., 1999) (r = 0.749- 0.829; 0.681- 0.888). The PLC stimulation profile did not correlate with the affinity profiles.

Comparison of the functional data (GTP γ S binding, FSAC inhibition, PLC stimulation) of fsst₃ receptors with those of human sst₂, sst₃, sst₅ (hsst_{2,3,5}) receptors expressed in CCL39 cells (Siehler and Hoyer, submitted (b), (c), (d)) resulted in highest correlation with the hsst₅ receptor (r = 0.936, 0.972, 0.489) > hsst₂ (0.800, 0.502, n.d.) > hsst₃ (0.250, 0.190, 0.167).

In summary, fsst₃ receptors expressed in CCL39 cells are involved in signalling cascades, which are also modulated by mammalian SRIF receptors, and therefore might be highly conserved in evolution. Binding and functional data showed highest similarity of fsst₃ receptors with the mammalian sst₅ receptor subtype (at least with hsst₅). Different affinities, receptor densities and GppHNp-sensitivities determined with the four radioligands (agonists) are assumed to result from ligand-specific states of the fsst₃-ligand complex. The differences between the radioligand binding profiles and the various signalling cascades, may be explained by agonist-induced receptor trafficking.

Effect of GppNHp on radioligand binding

As previously described, $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide labelled fsst₃ receptors stably expressed in CCL39 cells with high affinity, in a saturable manner, and with low levels of non-specific binding: $pK_d = 10.47, 10.87, 9.59, and 9.57; B_{max} = 4470, 4030, 3420, and 1520 fmol/mg (Siehler et al., 1999; table 1(A)). [^{125}I][Tyr^3] octreotide labelled significantly less receptor sites (2- 3 fold) compared to the other radioligands.$

To study, whether these apparent differences in receptor densities may be due to labelling of different receptor affinity states, saturation binding experiments were performed in the presence of 10 μ M GppNHp (table 1(B); figure 1). The affinities of [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide were comparable to those measured in the absence of GppNHp (pK_d = 10.37 ± 0.03, 10.23 ± 0.07, 9.71 ± 0.04, 9.81 ± 0.02). However, the B_{max}-values determined with the 4 radioligands were differently affected by GppNHp (B_{max} = 2910 ± 40, 4480 ± 290, 930 ± 70 and 190 ± 20 fmol/mg, respectively). The binding of [¹²⁵I][Tyr¹⁰]CST₁₄ was not modified by GppNHp, that of [¹²⁵I]LTT-SRIF₂₈ was only slightly affected, whereas both [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide were drastically inhibited, almost 4-fold and 8-fold, respectively (figure 1); i.e. in the presence of GppNHp, [¹²⁵I][Tyr¹⁰]CST₁₄.

In another experimental set up, increasing concentrations of GppNHp (up to 100 μ M) were used to inhibit binding of the different radioligands to fsst₃ receptors (table 2; figure 2). Again, [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ binding were only moderately affected (E_{max} = 42 ± 1 % and 35 ± 2 %, pIC₅₀ = 6.10 ± 0.11 and 6.22 ± 0.25, respectively), whereas [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide were almost entirely inhibited at high GppNHp concentrations (E_{max} = 72 ± 1 % and 83 ± 5 %, pIC₅₀ = 6.87 ± 0.14 and 7.70 ± 0.29, respectively).

Table 1: Saturation data obtained with $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide at fish sst₃ receptors expressed in CCL39 cells

Table 1(A)	
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	pK _d	B _{max}
[¹²⁵ I]LTT-SRIF ₂₈	10.47 ± 0.12	4470 ± 240
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	10.87 ± 0.34	4030 ± 210
[¹²⁵ I]CGP 23996	9.59 ± 0.04	3420 ± 190
[¹²⁵ I][Tyr ³]octreotide	9.57 ± 0.04	1520 ± 60

Table 1(B)

+GppNHp	pK _d	B _{max}
[¹²⁵ I]LTT-SRIF ₂₈	10.37 ± 0.03	2910 ± 40
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	10.23 ± 0.07	4480 ± 290
[¹²⁵ I]CGP 23996	9.71 ± 0.04	930 ± 70
[¹²⁵ I][Tyr ³]octreotide	9.81 ± 0.02	190 ± 20

The data are expressed as means of B_{max} -values (fmol/ mg) and pK_d-values (-log M) ± SEM of 3 different experiments; in contrast to table (A), table (B) shows data from saturation experiments performed in the presence of GppNHp (10⁻⁵ M). Paired t-test analysis for individual values indicates that B_{max} -values defined in the absence (table (A)) or the presence (table (B)) of GppNHp are not different (P > 0.05) using [125I][Tyr10]CST14, but significantly differ with [125I]LTT-SRIF28, [125I]CGP 23996, and [125I][Tyr3]octreotide (P < 0.01).

Induction of specific $[^{35}S]$ GTP γ S binding by SRIF analogues

Experimental conditions have been established previously at human sst₅ receptors expressed in CCL39 cells (Siehler and Hoyer, submitted (b)). SRIF₁₄ stimulated [35 S]GTP γ S binding by 314 ± 3 %. E_{max}-values of all studied peptides were 234- 324 %, and thereby close to full agonism, with the exception of BIM 23056, which was almost devoid of agonist activity (table 3; figure 3).

Figure 1: Saturation isotherms using $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 or $[^{125}I][Tyr^3]$ octreotide to membranes prepared from CCL39 cells stably expressing fsst₃ receptors.



Crude membrane preparations (2 µg per assay) were incubated with increasing concentrations of the radioligand in the absence (\blacksquare) or presence (\blacktriangle) of GppNHp (10⁻⁵ M; final concentration), and assayed for receptor binding. The plots represent specific binding expressed as radioligand bound (fmol/mg) versus free radioligand concentration (pM). The figures show one representative example of 3 different experiments.

However, BIM 23056 failed to antagonise SRIF₁₄-stimulated [³⁵S]GTP γ S binding (table 7; figure 7). SRIF₁₄, seglitide and SRIF₂₈ induced [³⁵S]GTP γ S binding with comparable high potency (pEC₅₀ = 8.19, 8.29 and 7.55, respectively). The rank order of potencies in [³⁵S]GTP γ S binding was: seglitide \geq SRIF₁₄ > [Tyr¹⁰]CST₁₄ \geq SRIF₂₈ = LTT-SRIF₂₈ > SRIF₂₅ > octreotide > BIM 23052 \geq CGP 23996 \approx [Tyr³]octreotide > L362,855.

Table 2: Binding inhibition of $[^{125}I]LTT$ -SRIF₂₈, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide at fish sst₃ receptors by increasing concentrations of GppNHp (max. 10⁻⁴ M): comparison of pIC₅₀-values (-log M) or E_{max}-values [% inhibition] ± SEM of three experiments

	E _{max}	pEC ₅₀
[¹²⁵ I]LTT-SRIF ₂₈	42 ± 1	6.10 ± 0.11
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	35 ± 2	6.22 ± 0.25
[¹²⁵ I]CGP 23996	72 ± 1	6.87 ± 0.14
[¹²⁵ I][Tyr ³]octreotide	83 ± 5	7.70 ± 0.29

Figure 2: Inhibition of radioligand binding at $fsst_3$ receptors by different GppNHpconcentrations (max. 10^{-4} M).



Crude membrane preparations from fsst3 receptor transfected cells were incubated with [125I]LTT-SRIF28 (. [125][Tyr10]CST14 (♥). [125]]CGP 23996 (**A**) or [1251][Tyr³]octreotide (\blacklozenge) and the indicated concentrations of GppNHp. Data are expressed as percentage of specific binding. The data points show one representative example of at least three independent experiments.

Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity

Forskolin-stimulated cytosolic cyclic adenosine monophosphate (cAMP) was inhibited by SRIF analogues via fsst₃ receptors as indirectly measured using a radioimmunassay (table 4; figure 4).

Table 3: Stimulation of $[{}^{35}S]GTP\gamma S$ binding by SRIF analogues at recombinantly expressed fish sst₃ receptors: comparison of pEC₅₀ values (-log M) and E_{max}-values [% stimulation] ± SEM of 3 independent determinations.

	E _{max}	pEC ₅₀
SRIF ₁₄	314 ± 3	8.19 ± 0.01
SRIF ₂₈	320 ± 14	7.55 ± 0.14
LTT-SRIF ₂₈	272 ± 5	7.55 ± 0.12
SRIF ₂₅	274 ± 23	7.25 ± 0.07
[Tyr ¹⁰]CST ₁₄	267 ± 2	7.64 ± 0.03
seglitide	264 ± 31	8.29 ± 0.06
CGP 23996	255 ± 30	6.68 ± 0.04
octreotide	324 ± 29	7.12 ± 0.09
[Tyr ³]octreotide	259 ± 6	6.64 ± 0.13
L362,855	234 ± 39	6.29 ± 0.05
BIM 23056	64 ± 1	(-)
BIM 23052	269 ± 6	6.77 ± 0.01

In direct cAMP determinations using a column assay, SRIF₁₄ and SRIF₂₈ inhibited FSAC activity via fsst₃ receptors expressed in CCL39 cells by 87 and 91 %, with pEC₅₀-values of 9.52 and 9.19, respectively, and in a pertussis toxin-sensitive manner (Siehler et al., 1999). In the radioimmunassay, SRIF₁₄ and SRIF₂₈ inhibited the cAMP production by 58 ± 2 % and 61 ± 3 %, and with pEC₅₀'s of 7.71 and 8.24, respectively. Seglitide was the most potent to inhibit FSAC activity (pEC₅₀ = 8.83). All tested compounds behaved as full agonists, except BIM 23056, which showed weak partial agonism (E_{max} = 24 ± 1 %), but failed to antagonise SRIF₁₄-induced inhibition of FSAC activity (table 6; figure 7). The rank order of potencies was: seglitide > SRIF₂₅ ≈ SRIF₂₈ > LTT-SRIF₂₈ ≈ SRIF₁₄ > [Tyr¹⁰]CST₁₄ > octreotide > BIM 23052 > [Tyr³]octreotide > CGP 23996 ≈ L362,855 ≈ BIM 23056.

	E _{max}	pEC ₅₀
SRIF ₁₄	58 ± 2	7.71 ± 0.06
SRIF ₂₈	61 ± 3	8.24 ± 0.18
LTT-SRIF ₂₈	59 ± 1	7.75 ± 0.03
SRIF ₂₅	54 ± 2	8.29 ± 0.10
[Tyr ¹⁰]CST ₁₄	56 ± 3	7.59 ± 0.02
seglitide	63 ± 2	8.83 ± 0.11
CGP 23996	62 ± 1	6.58 ± 0.07
octreotide	66 ± 2	7.37 ± 0.10
[Tyr ³]octreotide	67 ± 3	6.85 ± 0.12
L362,855	65 ± 1	6.56 ± 0.15
BIM 23056	24 ± 1	6.51 ± 0.04
BIM 23052	66 ± 1	7.24 ± 0.10

Induction of total $[^{3}H]$ -IP_x accumulation via fsst₃ receptors

Fsst₃ receptor-stimulated phospholipase C (PLC) activity was studied by measuring total [³H]-IP_x levels in an anion exchange column assay. The maximal [³H]-IP_x levels were measured after 50 min incubation of the cells with SRIF ligands. 10 μ M SRIF₁₄ induced a 8-fold stimulation of PLC activity: E_{max} = 831 ± 165 %, and addition of pertussis toxin (PTX) blocked this effect only by 21 %: E_{max} = 669 ± 218 % (figure 5). The E_{max}-value of control cells in the absence of lithium ions (90 ± 5 %) was below the basal level of 100 %, and therefore suggests some basal activity of the fish sst₃ receptor on induction of PLC enzymes in CCL39 cells.

Figure 3: Stimulation of specific [³⁵S]GTPγS binding to microsome preparations from CCL39 cells expressing fish sst₃ receptors by SRIF analogues:



Microsomes of fsst3 transfected cells (2 µg protein) were incubated with $[^{35}S]GTP\gamma S$ (0.2 nM), the indicated concentrations of SRIF14 (∎), $SRIF_{25}$ (**A**), $SRIF_{28}$ (**V**), CGP23996 (�), seglitide (\bullet) , or octreotide (\Box) in the presence of 5 mM MgCl₂, 1 µM GDP, and 100 mM NaCl. Graphs represent the percentage of stimulated specific $[^{35}S]GTP\gamma S$ binding. The data points depict one representative example of 3 different experiments performed in triplicates.

Figure 4: Inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity by SRIF peptides in CCL39 cells expressing fsst₃ receptors.



Transfected cells were treated with forskolin (10 μ M) and the indicated concentrations of SRIF14 (1), SRIF₂₅ (\blacktriangle), SRIF₂₈ (\triangledown), CGP 23996 (�), seglitide (\bullet) or octreotide (\Box) , and cAMP levels determined by radioimmunassay using [¹²⁵I]cAMP. Graphs represent the percentage of inhibition of FSAC activity. The data points represent example of 3 different one experiments. The mean of pEC50values \pm SEM of 3 determinations are shown in table 4.

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	E _{max}	pEC ₅₀
SRIF ₁₄	463 ± 59	7.21 ± 0.05
SRIF ₂₈	463 ± 45	6.59 ± 0.09
LTT-SRIF ₂₈	289 ± 15	6.16 ± 0.17
SRIF ₂₅	361 ± 69	6.88 ± 0.13
[Tyr ¹⁰]CST ₁₄	578 ± 127	6.17 ± 0.10
seglitide	324 ± 40	7.26 ± 0.18
CGP 23996	246 ± 20	5.73 ± 0.08
octreotide	186 ± 36	6.82 ± 0.22
[Tyr ³]octreotide	161 ± 20	7.43 ± 0.15
L362,855	168 ± 10	6.46 ± 0.21
BIM 23056	194 ± 3	6.02 ± 0.07
BIM 23052	182 ± 23	7.03 ± 0.16

The pharmacological profile of fsst₃ receptor-mediated stimulation of PLC activity was established with a number of SRIF analogues (table 5; figure 6). The intrinsic activity of the ligands varied over a broad range: from 578 % ([Tyr¹⁰]CST₁₄), 463 % (SRIF₁₄, SRIF₂₈), 324 % (seglitide), 246 % (CGP 23996), to 161 % ([Tyr³]octreotide); i.e. most of the tested compounds revealed partial agonism. [Tyr³]octreotide, seglitide and SRIF₁₄ were the most potent ligands in this functional assay (pEC₅₀ = 7.43, 7.26, and 7.21, respectively). The rank order was: [Tyr³]octreotide > seglitide ≈ SRIF₁₄ > BIM 23052 > SRIF₂₅ ≈ octreotide > SRIF₂₈ > L362,855 > [Tyr¹⁰]CST₁₄ ≈ LTT-SRIF₂₈ > BIM 23056 > CGP 23996. BIM 23056 behaved as a competitive antagonist on SRIF₁₄-induced [³H]-IP_x accumulation (table 6; figure 7).

Figure 5: Stimulation of total $[{}^{3}H]$ -IP_x accumulation at fsst₃ receptors.



Fsst3 expressing cells were incubated in HBS buffer (control) either with or without 20 mM LiCl, or stimulated with 10 μ M SRIF₁₄ (in HBS/ Li⁺) either in the absence or presence of PTX (100 ng/ ml). Bars represent E_{max}-values \pm SEM as percentage of stimulation over the basal level (HBS/ Li⁺ = 100 %) of at least 3 experiments.

Figure 6: Induction of total [³H]-IP_x accumulation by SRIF ligands.



Cells were incubated with 2 µCi $myo-[2-^{3}H(N)]$ -inositol, treated with the indicated concentrations of $SRIF_{14}$ (**I**), $SRIF_{25}$ (**A**), $SRIF_{28}$ (**▼**), CGP 23996 (�), seglitide (●), or octreotide (\Box), and total [³H]-IP_x levels were determined by anion exchange chromatography. Graphs represent the percentage of stimulation over the basal level, and one example of at least 3 separate experiments; the mean of pEC50values \pm are given in table 5.

Comparison of radioligand binding, $[^{35}S]GTP\gamma S$ binding, inhibition of FSAC activity, and stimulation of PLC activity

Data obtained in $fsst_3$ -induced GTP γ S binding, inhibition of cAMP production, and stimulation of PLC activity were compared to the pharmacological profiles of radioligand binding determined using [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide (tables 7 and 8; figures 7-9; Siehler et al., 1999).

Table 6: Antagonist activity of BIM 23056 (10^{-6} M final concentration) on SRIF ₁	4
stimulated [35 S]GTP γ S binding, SRIF ₁₄ -inhibited adenylate cyclase (AC) activity, and	ıd
SRIF ₁₄ -stimulated total [³ H]-IP _x accumulation at fish sst ₃ receptors	

	SI	RIF ₁₄	SRIF ₁₄ +BIM 23056			
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	pK _B	
[³⁵ S]GTPγS binding	100 ± 1	8.19 ± 0.01	37 ± 0	8.58 ± 0.05		
AC activity	100 ± 3	7.71 ± 0.06	65 ± 5	8.64 ± 0.17		
total [³ H]-IP _x	100 ± 16	7.21 ± 0.05	94 ± 27	6.38 ± 0.06	6.83 ± 0.06	

Comparison of pEC₅₀-values (-log M), E_{max} -values [% stimulation/ inhibition; normalised to the E_{max} of SRIF₁₄ = 100 %], and pK_B-value ± SEM of 3 independent determinations.

Linear regression analyses revealed intermediate correlation of the [35 S]GTP γ S binding profile with the different affinity profiles (r = 0.749- 0.829). Similarly, [35 S]GTP γ S binding correlated very moderately with FSAC inhibition and PLC activation (r = 0.594 and 0.410, respectively). The pharmacological profile of fsst₃-mediated inhibition of cAMP production correlated significantly with the affinity profiles of [125 I]LTT-SRIF₂₈, [125 I][Tyr¹⁰]CST₁₄, [125 I]CGP 23996 (r = 0.842- 0.888), but less significantly with radioligand binding data obtained with [125 I][Tyr³]octreotide (r = 0.681) as well as with PLC stimulation (r = 0.424). Interestingly, induction of total [3 H]-IP_x accumulation showed very low correlation coefficients with the 4 radioligand binding profiles (r = 0.056- 0.403).

Comparison of functional assay data of fish sst, receptor and of human SRIF₁ receptors

Data from $fsst_3$ receptor-mediated [${}^{35}S$]GTP γS binding, FSAC inhibition, and PLC activation were compared to data obtained using CCL39 cells stably transfected with either human sst₂, sst₃, or sst₅ receptors (tables 9 and 10; figure 11; Siehler and Hoyer, submitted (b), (c), (d)).



Figure 7: Antagonism of BIM 23056 on $SRIF_{14}$ -induced [³⁵S]GTP γ S binding, inhibition of FSAC activity, and total [³H]-IP_x accumulation at fsst₃ receptors.

In all 3 functional assays studied, fsst₃ receptors were more similar to hsst₂ and hsst₅, than to hsst₃ receptors: e.g. seglitide revealed in these experiments relatively high potencies at fsst₃ receptors, which are typical for hsst₂ and hsst₅ receptors, whereas hsst₃ receptors showed only low potencies for seglitide. The [35 S]GTP γ S binding and FSAC inhibition profiles of fsst₃ receptors correlated significantly with those of hsst₅ receptors (r = 0.936 and 0.972), moderately with those of hsst₂ receptors (r = 0.800 and 0.502), and very little with those of hsst₃ receptors (r = 0.250 and 0.190). The PLC stimulation profile of fsst₃ and hsst₅ receptors correlated with r = 0.489, and of fsst₃ and hsst₃ very low (r = 0.167); hsst₂ receptors induced PLC activity only weakly, and therefore no profile could be established (Siehler and Hoyer, submitted (d)).

presenting $[^{3}H]$ -IP_x data.

Table 7: Fish sst₃ receptors: comparison of ligand potencies (pEC_{50} 's) to activate total [³H]-IP_x accumulation (table 6) (a) with affinities (pK_d 's) of the receptors labelled with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 or [¹²⁵I][Tyr³]octreotide, (b) with potencies (pEC_{50} 's) to stimulate [³⁵S]GTPγS specific binding (table 3), and (c) potencies to inhibit forskolin-stimulated adenylate cyclase (FSAC) activity (table 4)

	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	[¹²⁵ I]	[³⁵ S]	GTPγS	FS	SAC	tc	otal
	LTT-	[Tyr ¹⁰]	CGP	[Tyr ³]			act	ivity	[³ H	[]IP _x
	SRIF ₂₈	CST_{14}	23996	octreo						
				tide						
	pK _d	pK _d	pK _d	pK _d	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	8.93	8.87	9.53	9.99	100	8.19	100	7.71	100	7.21
SRIF ₂₈	8.84	8.61	9.64	10.21	103	7.55	105	8.24	100	6.59
LTT-SRIF ₂₈	8.94	8.71	9.56	9.55	80	7.55	102	7.75	52	6.16
	± 0.08	± 0.06	± 0.06	± 0.16						
SRIF ₂₅	9.00	8.85	9.93	10.32	81	7.25	93	8.29	72	6.88
[Tyr ¹⁰]CST ₁₄	8.54	8.32	9.37	9.98	78	7.64	96	7.59	132	6.17
seglitide	9.15	8.55	9.83	10.53	77	8.29	108	8.83	62	7.26
CGP 23996	7.16	6.78	8.24	8.94	72	6.68	107	6.58	40	5.73
octreotide	7.45	7.28	8.72	9.29	105	7.12	113	7.37	24	6.82
[Tyr ³]	6.91	6.31	8.36	8.42	74	6.64	115	6.85	17	7.43
octreotide	± 0.02	± 0.10	± 0.17	± 0.03						
L362,855	7.54	7.09	8.77	8.91	63	6.29	112	6.56	19	6.46
BIM 23056	6.32	5.88	6.97	9.83	-17	(-)	41	6.51	26	6.02
BIM 23052	7.92	7.68	9.15	7.90	79	6.77	113	7.24	23	7.03

The data are expressed as pK_d 's or pEC_{50} 's (-log M), or E_{max} -values [% stimulation or inhibition, respectively] of 3 different experiments; E_{max} -values were normalised to the stimulation/inhibition reached by SRIF₁₄ (= 100 %).

Table 8: Fish sst₃ receptors expressed in CCL39 cells: correlation coefficients (r) of linear regression analyses between (a) the affinity profiles of $[^{125}I]LTT-SRIF_{28}$, $[^{125}I][Tyr^{10}]CST_{14}$, $[^{125}I]CGP$ 23996 and $[^{125}I][Tyr^3]$ octreotide, (b) the pharmacological profile of stimulation of $[^{35}S]GTP\gamma S$ binding, (c) the pharmacological profile of inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity, and (d) the pharmacological profile of stimulation of total $[^{3}H]$ -IP_x accumulation

	[³⁵ S]GTPγS		inhibition of		[³ H]-IP _x	
	r P		r P		r	P
[¹²⁵ I]LTT-SRIF ₂₈	0.829	0.0016	0.888	0.0001	0.281	0.3763
[¹²⁵ I][Tyr ¹⁰]CST ₁₄	0.805	0.0028	0.853	0.0004	0.243	0.4470
[¹²⁵ I]CGP 23996	0.749	0.0079	0.842	0.0006	0.403	0.1935
[¹²⁵ I][Tyr ³]octreotide	0.789	0.0039	0.681	0.0148	0.056	0.8625
inhibition of FSAC activity	0.594	0.0417		-		-
[³ H]-IP _x accumulation	0.410	0.1857	0.424	0.1692	-	-

Data used for correlation analyses are presented in table 8.

11.3. Discussion

GppNHp-inhibited binding of radiolabelled ligands

In saturation binding experiments, the presence of the GTP-analogue GppNHp reduced the apparent receptor density determined with [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide by 4-fold and 8-fold, but did not affect [¹²⁵I]LTT-SRIF₂₈ or [¹²⁵I][Tyr¹⁰]CST₁₄ binding, although the affinities of all 4 iodinated ligands were not significantly altered by GppNHp.



Figure 8: Fish sst₃ receptors expressed in CCL39 cells: correlation analyses.

Data of $[^{35}S]$ GTP γ S binding experiments were correlated to (a) the affinity profiles of $[^{125}I]$ LTT-SRIF₂₈, $[^{125}I]$ [Tyr¹⁰]CST₁₄, $[^{125}I]$ CGP 23996 or $[^{125}I]$ [Tyr³]octreotide, (b) the FSAC inhibition profile, as well as (c) the $[^{3}H]$ -IP_x accumulation profile. Data are from tables 7 and 8. Correlation coefficients (r) are indicated in all plots.

This might explain the different receptor densities determined when using various radioligands at the same receptor subtype: e.g. $[^{125}I]LTT-SRIF_{28}$ labelled about 3-times more receptor sites than $[^{125}I][Tyr^3]$ octreotide (4470 and 1520 fmol/ mg, respectively) (Siehler et al., 1999).



Figure 9: Fsst₃ receptors: correlation of pharmacological profiles.

 pEC_{50} (adenylate cyclase)

However, binding of $[^{125}I][Tyr^{11}]SRIF_{14}$ to rat sst₂ receptors was also found to not be fully sensitive to a GTP-analogue (Gu et al., 1995). Differential GppNHp-sensitivity was observed for the two endogenous ligands – pancreatic polypeptide and peptide YY – of rat Y₄ receptors (Walker et al., 1997). We already reported radioligand-dependent receptor densities observed at human sst₅ receptors; similarly, binding of radioligands to this receptor subtype was differently GppNHp-sensitive (Siehler et al., 1998b).



Figure 10: Fsst₃ receptors: correlation of affinity profiles with the PLC activation profile.

Affinity profiles obtained with the 4 different radioligands were correlated to the total $[^{3}H]$ -IP_x accumulation profile. Data are from tables 7 and 8; correlation coefficients (r) are shown all 4 graphs.

Saturation data were confirmed by using increasing concentrations of GppNHp: the binding of [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide was drastically inhibited, but not that of the other two radioligands studied. GTP-analogue induced ligand dissociation from the receptor indicates that the receptor is coupled to G-proteins (Brown and [¹²⁵I]CGP 23996 Schonbrunn. 1993). Thereby, our data suggest and ¹²⁵I][Tyr³]octreotide to preferentially bind to G-protein-coupled fsst, receptors, whereas [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ seem to label fsst₃ receptors in both states, but surprisingly for an agonist, with a high proportion in an uncoupled state.

Table 9: Fish sst₃ receptors and human SRIF₁ receptor subtypes expressed in CCL39 cells: comparison of ligand potencies obtained by measurement of stimulation of $[^{35}S]GTP\gamma S$ binding, inhibition of FSAC activity, and stimulation of $[^{3}H]$ -IP_x accumulation

	fsst ₃		hsst ₅		hsst ₂		hsst ₃	
	E _{max}	pEC ₅₀						
SRIF ₁₄	100	8.19	100	8.39	100	6.95	100	7.32
SRIF ₂₈	103	7.55	101	7.65	116	6.14	104	6.96
LTT-SRIF ₂₈	80	7.55	107	7.63	110	6.78	119	7.44
[Tyr ¹⁰]CST ₁₄	78	7.64	69	7.43	39	6.28	43	6.83
seglitide	77	8.29	84	7.89	137	7.39	49	5.78
CGP 23996	72	6.68	67	7.12	95	6.06	81	7.14
octreotide	105	7.12	107	6.89	94	6.52	42	6.70
[Tyr ³]octreotide	74	6.64	72	6.56	131	6.57	47	5.76
L362,855	63	6.29	79	6.29	52	5.65	23	6.27
BIM 23056	-17	(-)	0	(-)	-35	(-)	-10	(-)
BIM 23052	79	6.77	100	6.80	53	5.91	93	6.29

Table 9(A) Stimulation of [³⁵S]GTPγS binding

These data are not explained by the "ternary complex model", which predicts agonists to bind only G-protein-coupled receptors with high affinity and to uncoupled receptors with low affinity (De Lean et al., 1980; Lefkowitz et al., 1993; Samama et al., 1993); the radioligands used behaved at fsst₃ receptors as full agonists in [35 S]GTP γ S binding and AC activity inhibition experiments.

	fsst ₃		$hsst_5$		hsst ₂		hsst ₃	
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀
SRIF ₁₄	100	7.71	100	8.13	100	8.15	100	7.76
SRIF_{28}	105	8.24	109	8.38	111	8.72	94	8.19
LTT-SRIF ₂₈	102	7.75	106	7.84	111	8.33	97	8.40
[Tyr ¹⁰]CST ₁₄	96	7.59	109	7.69	107	6.80	84	6.80
seglitide	108	8.83	119	9.33	107	10.03	89	6.68
CGP 23996	107	6.58	112	7.07	100	7.79	89	7.84
octreotide	113	7.37	123	7.68	104	8.44	97	7.01
[Tyr ³]octreotide	115	6.85	118	7.30	115	9.70	81	6.31
L362,855	112	6.56	143	6.81	137	6.87	58	6.70
BIM 23056	41	6.51	47	6.60	22	(-)	26	(-)
BIM 23052	113	7.24	125	7.40	122	6.74	104	7.43

Table 9(B) Inhibition of FSAC activity

Table 9(C) Stimulation of $[^{3}H]IP_{x}$ accumulation

	fsst ₃		hs	st ₅	hsst ₃		
	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	E _{max}	pEC ₅₀	
SRIF ₁₄	100	7.21	100	7.22	100	7.71	
SRIF ₂₈	100	6.59	66	6.90	98	7.36	
LTT-SRIF ₂₈	52	6.16	21	6.45	87	7.90	
$[Tyr^{10}]CST_{14}$	132	6.17	46	6.31	78	7.05	
seglitide	62	7.26	73	7.27	77	6.01	
CGP 23996	40	5.73	16	5.53	87	7.05	
octreotide	24	6.82	18	6.00	71	6.27	
[Tyr ³]octreotide	17	7.43	11	5.76	47	5.79	
L362,855	19	6.46	3	6.78	31	6.61	
BIM 23056	26	6.02	2	5.81	21	5.62	
BIM 23052	23	7.03	9	6.80	81	7.44	

The data are expressed as means of pEC₅₀-values (-log M) or of E_{max} -values [% stimulation or inhibition, respectively] of 3 independent experiments; E_{max} -values were normalised to the stimulation/ inhibition reached by SRIF₁₄ (= 100 %).

Table 10: Comparison of fish sst₃ receptors with human sst₂, sst₃, and sst₅ receptors expressed in CCL39 cells: correlation coefficients (r) of correlation analyses between pharmacological profiles obtained by measuring stimulation of [35 S]GTP γ S binding, inhibition of FSAC activity, and stimulation of total [3 H]-IP_x accumulation

	h	sst ₅	hsst ₂		hsst ₃	
	r	Р	r	Р	r	Р
[³⁵ S]GTPγS binding	0.936	< 0.0001	0.800	0.0055	0.250	0.0623
inhibition of FSAC activity	0.972	< 0.0001	0.502	0.1392	0.190	0.5987
[³ H]-IP _x accumulation	0.489	0.1273	-	-	0.167	0.6227

Data used for linear regression analyses are presented in tables 10(A)-(C).

Functional studies: GTPyS binding, FSAC inhibition, and PLC stimulation

In [35 S]GTP γ S binding and PLC stimulation, the potency of SRIF₁₄ was higher compared to that of SRIF₂₈ (pEC₅₀ = 8.19 and 7.55; 7.21 and 6.59, respectively), whereas it was the opposite when studying inhibition of AC activity (pEC₅₀ = 7.71 and 8.24). In contrast, affinities of both SRIF peptides were similar as determined in radioligand binding studies (Siehler et al., 1999). Rank orders of potency were different from one assay to the other. Seglitide was very potent in all 3 functional assays: GTP γ S binding (8.29), FSAC inhibition (8.83), PLC stimulation (7.26). In AC activity determinations, all tested compounds revealed full agonism, with the exception of BIM 23056, which showed weak agonist activity also in the other assays. Only SRIF₁₄, SRIF₂₈ and octreotide were full agonists to stimulate [35 S]GTP γ S binding at fsst₃ receptors; other ligands reached 63- 81 % efficacy compared to SRIF₁₄. Most ligands revealed even lower partial agonism in total [3 H]-IP_x accumulation measurements: full agonism could be seen with SRIF₁₄, SRIF₂₈ and [Tyr¹⁰]CST₁₄, but the efficacies of other ligands were in the range of 17- 72 % of the E_{max}-value of SRIF₁₄.



Figure 11: Fsst₃ receptors: correlation of GTP γ S binding, AC inhibition, and PLC stimulation data with those of human SRIF₁ receptors expressed in CCL39 cells.

Pharmacological profiles of $[{}^{35}S]$ GTP γS binding, FSAC activity inhibition, and total $[{}^{3}H]$ -IP_x accumulation of fsst3 receptors were correlated to those of human sst3 and sst5 receptors. pEC₅₀-values are from table 10. Correlation coefficients (r) are indicated in all graphs.

BIM 23056, which displayed weak agonism at $fsst_3$ receptors in all 3 functional assays, antagonised SRIF₁₄-induced phosphoinositide turnover with an pK_B of 6.83, but neither SRIF₁₄-induced [³⁵S]GTP_YS binding nor FSAC inhibition.

In contrast, at human sst₃ receptors, BIM 23056 antagonised SRIF₁₄-induced GTP γ S binding, AC inhibition, and PLC activation with pK_B-values of 6.33, 6.33, and 5.85, respectively (Siehler and Hoyer, submitted (b), (c), (d)).

The pharmacological profiles of GTP γ S binding, FSAC inhibition, and PLC stimulation correlated rather poorly with each other: r = 0.410- 0.594. More significant, although varying correlations were seen comparing the GTP γ S binding and FSAC inhibition profiles with the 4 radioligand binding profiles: r = 0.749- 0.829 and r = 0.681- 0.888; the [¹²⁵I][Tyr³]octreotide affinity profile (r = 0.681) was markedly less significantly correlated with FSAC inhibition compared to the other radioligands. Total [³H]-IP_x accumulation correlated little with the four binding profiles, suggesting other pathways to be more important than the PLC/IP₃ pathway in fsst₃ mediated signalling.

The expression of AC and PLC_{β} isoenzymes has not been established in CCL39 cells. The inhibition of FSAC activity by fsst₃ receptors in this cell line was shown to involve the PTX-sensitive G_i/G_o proteins (Siehler et al., 1999). G_i/G_o proteins inhibit AC type I, V and VI. In CCL39 lung fibroblast cells only type V and VI might be expressed and inhibited by recombinantly expressed fsst₃ receptors, since AC type I expression is neuron-specific (for review, Birnbaumer and Birnbaumer, 1995; Taussig et al., 1993; 1994). Stimulation of PLC activity by SRIF₁₄ at fsst₃ receptors was only partially affected by PTX (21 %); thus, other G-protein isoforms are suggested to be responsible for mediating this effect; possibly $G_q\alpha$ and $G_{11}\alpha$, which activate PLC_{β1-4}, whereas $G_{i/o}$ couple to PLC_{β2+3} activation (Berridge, 1993; for review: Exton, 1996). In fish, AC and PLC isoenzymes are not characterised yet, but different isotypes may also exist as known in mammals.

Fish sst₃ receptor: comparison with human sst_2 , sst_3 , and sst_5 receptors expressed in CCL39 cells

Mammalian SRIF receptor-modulated signalling cascades such as the cAMP/protein kinase A- and the PLC/IP₃ pathways (for review: Meyerhof, 1998) seem to be highly conserved among the vertebrate class, since the fsst₃ receptor is able to interact with these different second messengers when expressed in a mammalian cell line.

In all functional assays ($[^{35}S]$ GTP γ S binding, FSAC inhibition, and PLC activation) highest correlation coefficients were observed comparing pharmacological data of fsst₃ and hsst₅ receptors: $\mathbf{r} = 0.936$ and 0.972 comparing GTP γ S binding and AC inhibition. In contrast, the functional data obtained with fsst₃ and hsst₃ receptors did not correlate ($\mathbf{r} = 0.167$ - 0.250). This finding may not be surprising, since previous comparison of affinity profiles of human SRIF₁ receptors with the fsst₃ receptor revealed higher similarity with hsst₅ receptors than with hsst₃ receptors, although the fsst₃ protein sequence is more similar to the mammalian sst₃ receptor subtype (Zupanc et al., 1999).

In summary, the differential GppNHp sensitivity of the four agonists [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide binding suggests labelling of various agonist-specific fsst₃ receptor states, which are predominantly coupled to G-proteins in the case of [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide, but rather uncoupled in the case of the other two radioligands. Modulation of signalling pathways by somatostatin receptors (stimulation of GTP_γS binding, inhibition of AC activity, induction of PLC activity) are conserved, even when comparing such distantly related species as fish and man/ rodents.

The apparent differences in receptor profile observed in radioligand binding and the various second messenger cascades studied, suggest that agonist-specific receptor-trafficking is taking place. In other words, an agonist may favour a ligand-receptor complex, which then preferentially activates one pathway preferentially to another. This has already been suggested by previous work carried out with hsst₅ receptors and elegantly demonstrated for the human 5-HT_{2c} receptors (Berg et al., 1998a, 1998b, 1998c) in agreement with a three-state receptor model suggested by Scaramellini and collaborators (Leff et al, 1997, 1998; Scaramellini et al., 1998).

Conclusions

The aims of this thesis were multiple:

1) We wanted to compare the pharmacological and transductional features of the five cloned human SRIF receptors: to this end, all five receptor subtypes were recombinantly expressed in a cell line known to tolerate well G-protein-coupled receptors negatively linked to adenylate cyclase, a common feature that has been documented for all 5 cloned SRIF receptors, although not always in a consistent manner. Therefore, the CCL39 hamster lung fibroblast cell line was chosen.

2) A second aim was to define the binding features of a number of somatostatin analogues at the five human SRIF receptors, and subsequently to compare the pharmacological profiles defined at a same receptor subtype by several different radioligands: to this end, radioligand binding studies were performed with two analogues of the natural peptides, $[^{125}I]LTT$ -SRIF₂₈ and $[^{125}I][Tyr^{10}]CST_{14}$, and two synthetic analogues, i.e. $[^{125}I][Tyr^3]$ octreotide and $[^{125}I]CGP$ 23996.

3) A third goal was to use the five human SRIF receptors expressed in the same cellular environment to perform not only radioligand binding studies, but also to measure receptor-G-protein interactions (effects of GppNHp and agonist-stimulated GTP γ S binding), and to characterise transductional features of the receptors by studying cAMP, PLC and Ca²⁺ accumulation, i.e. the protein kinase A and PLC cascades.

4) A fourth aim was to characterise in a similar manner and in the same cellular environment the first cloned non-mammalian somatostatin receptor, namely the fish sst₃ receptor: thus we established in stably transfected CCL39 cells the binding features of the fsst₃ receptor using the four radioligands [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996 and [¹²⁵I][Tyr³]octreotide, studied the effects on receptor-G-protein interactions, and the transductional cascades, as previously done for the human SRIF receptors.

In addition, we compared the pharmacological profile of the fsst₃ receptor with that of human SRIF receptors to establish possible species differences, and finally, we also compared the profile of the recombinant fsst₃ receptor with that of endogenously expressed receptor binding sites present in various tissues, specially brain and liver.

5) The ultimate goal was to compare all the data in order to provide support or to reject the hypothesis, that some SRIF receptors may display different pharmacological profiles depending on the nature of the ligand-receptor interaction considered: radioligand binding, G-protein activation, second messenger studies. Indeed, a survey of the literature shows, that various groups working on the same recombinant receptor, report very different affinity and potency values for a number of compounds depending on the cell line, binding test or second messenger system studied. In addition, it becomes evident that at least for some receptors (e.g. 5-HT_{2a}, 5-HT_{2c}, PACAP receptors), the possibility of receptor trafficking may exist, although final proof has not yet been provided.

 $[^{125}I][Tyr^{10}]CST_{14}$, an iodinated analogue of the recently cloned cortistatin (CST) (De Lecea et al., 1996, 1997a; Fukusumi et al., 1997), bound with similar high affinity to $[^{125}I]LTT$ -SRIF₂₈ to all five human somatostatin receptors recombinantly expressed in CCL39 cells, as well as the non-iodinated analogues $[Tyr^{10}]CST_{14}$ and CST_{17} ; binding of CST to the SRIF receptors suggests CST to belong functionally to the somatostatin peptide family. In addition, the affinity profiles established with $[^{125}I][Tyr^{10}]CST_{14}$ and $[^{125}I]LTT$ -SRIF₂₈ were comparable. The CNS-specific expression of the CST-prepropeptide (De Lecea et al., 1996, 1997a; Fukusumi et al., 1997) suggests CST-specific functions solely in the brain compared to SRIF, which possesses multiple functions in the brain and periphery. It remains to be seen whether there exist receptors selective for SRIF or CST.

Octreotide has antiproliferative properties in vitro and in vivo in hormone-secreting tumours, and is used in the treatment of acromegaly, neuroendocrine and gastroenteropancreatic tumours, and AIDS-related diarrhoea. These effects are assumed to be mediated by SRIF₁ receptors, primarily the sst₂ type. In CCL39 cells, the analogue [125 IJ][Tyr³]octreotide labelled not only human sst₂ receptors as previously reported (Hoyer et al., 1994b; Piwko et al., 1997; Schoeffter et al., 1995), but also human sst₅ receptors. Therefore, results of autoradiographic/ binding studies using [125 IJ][Tyr³]octreotide possibly document the presence of sst₂ and sst₅ receptors, when both subtypes are expressed in the tissue studied; similarly, the antiproliferative effect of octreotide on tumour growth might be mediated by both, human sst₂ and sst₅ receptors. It should however be realised that sst₅ receptors show overall very low expression levels.

At human sst₅ receptors, apparent receptor densities (920- 6950 fmol/mg) and binding affinities (up to 1000-fold variation) were dependent on the radioligand used ([¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide = full agonists); e.g. [¹²⁵I][Tyr³]octreotide recognised the lowest receptor number, and affinities of competing peptides were higher compared to other radioligands. However, this radioligand-dependency of binding data was not observed to that extent at human sst₁₋₄ receptors (whereas at fsst₃ similar findings were made).

Binding of the four radioligands to human sst₅ receptors was, to a various extent, sensitive to the presence of the GTP-analogue GppNHp, explaining the different B_{max} -values: the binding of e.g. [¹²⁵I][Tyr³]octreotide was highly inhibited, which suggests [¹²⁵I][Tyr³]octreotide to label almost exclusively G-protein-coupled sst₅ receptors, and therefore only low receptor densities; in contrast, the binding of [¹²⁵I]LTT-SRIF₂₈ and [¹²⁵I][Tyr¹⁰]CST₁₄ was rather GppNHp-insensitive, which suggests labelling of predominantly G-protein- uncoupled sst₅ receptors, and hence of higher receptor density. Distinct GppNHp sensitivity was also found for the two endogenous peptides of NPY₄ receptors (Walker et al., 1997). Binding of the radioligands to human sst₂ or sst₃ receptors was highly guanine nucleotide sensitive, and rather insensitive at sst₁ or sst₄ receptors, although all ligands used display agonism all five SRIF receptor.

This suggests at least that all agonists do not favour an "active" receptor state, some may even favour the "inactive", assuming that the two species can be distinguished by GppNHp sensitivity or absence of it. One may even suggest more than two states for Gprotein-coupled receptors in the SRIF family. Indeed, the findings at human sst₅ receptors cannot be explained by the ternary complex model (De Lean et al., 1980; Lefkowitz et al., 1993; Samama et al., 1993), since the cold peptides of all radioligands used behave as full agonists in functional assays (De Lecea et al., 1996; Hoyer et al., 1994b), but rather by proposing multiple receptor conformations induced by different agonists, which has been already suggested by functional data for β_2 -adrenergic receptors (Krumins et al., 1997).

On the other hand, the binding of analogues of the endogenous peptides $SRIF_{28}$ and CST to G-protein-uncoupled SRIF receptors may suggest coupling to G-proteinindependent signalling pathways, like that inhibiting Na^+/H^+ exchange activity and discovered for β_2 -adrenergic receptors (Hall et al., 1998); SRIF receptors are known to mediate PTX-insensitive inhibition of Na^+/H^+ exchange activity (Barber et al., 1989; Hou et al., 1994).

The [35 S]GTP γ S binding profile established at sst₂₋₅ correlated significantly, although to various degrees with the different radioligand binding profiles at human sst₄/ sst₅ receptors, and modestly at sst₂/ sst₃ receptors. Similarly, affinity profiles of sst₃₋₅ receptors correlated well, but differentially with inhibition of forskolin-stimulated adenylate cyclase (FSAC) activity, although modestly at sst₁/ sst₂ receptors. In CCL39 cells, human sst₃ and sst₅ receptors, but not the other SRIF receptors, couple significantly to stimulation of PLC activity (IP_x accumulation) and intracellular Ca²⁺ increase. PLC stimulation was partially PTX-sensitive suggesting other G-proteins in addition to G_{i/o}, to be primarily involved. IP_x accumulation correlated for both receptor subtypes well with the radioligand binding profiles, although to a various degree, but rather poorly with forskolin-stimulated adenylate cyclase activity.
The rank orders of affinities/ potencies was specific for each receptor subtype and for the second messenger system considered (radioligand binding, [35 S]GTP γ S binding, AC inhibition, PLC induction). The results of the two studied signalling pathways (AC/ protein kinase A, PLC/ IP₃) may suggest human sst₁/ sst₂ receptors to preferentially couple to the Ras/ Raf/ MAPK pathway, which has been reported to be modulated by SRIF receptors.

Recently, the first non-mammalian somatostatin receptor (fish sst₃) was cloned from the fish *Apteronotus albifrons* (Zupanc et al., 1999); weak expression in brain was shown by RT-PCR. The [125 I]LTT-SRIF₂₈ profile of fsst₃ receptors recombinantly expressed in CCL39 cells correlated highly with that of *Apteronotus* brain, but not of liver. In addition, biphasic competition curves obtained with brain tissue binding, as well the different profile observed in liver preparation suggests the existence of at least one further SRIF receptor subtype in fish.

Like the mammalian receptors, fish sst₃ receptors in CCL39 cells, couple negatively to adenylate cyclase via PTX-sensitive G-proteins (G_i/G_o), and to PLC stimulation in a partially PTX-sensitive manner. Similarly to human sst₅ receptor, affinities and receptor densities defined with [¹²⁵I]LTT-SRIF₂₈, [¹²⁵I][Tyr¹⁰]CST₁₄, [¹²⁵I]CGP 23996, [¹²⁵I][Tyr³]octreotide were radioligand-dependent, and radioligand binding was differentially inhibited by GppNHp. In contrast to PLC activation, [³⁵S]GTP_γS binding and AC correlated significantly, although to different extents with the affinity profiles. Thus, the comments made about multiple receptor states and receptor effector coupling made for some mammalian SRIF receptors also apply to the fish species. The binding and functional data of fish sst₃ receptors display highest similarity with those of human sst₅ receptor, although the amino acid sequence matches better with mammalian sst₃ receptors. The results indicate that the signal transduction cascades modulated by SRIF receptors were highly conserved during evolution of the vertebrate class.

Taken together, the results suggest (1) that multiple agonist-specific receptor conformations can be achieved at recombinant SRIF receptor subtypes, which are G-protein coupled and/ or G-protein uncoupled, (2) that the nature of agonist-modulated receptor/ G-protein/ effector interactions might be more complex than initially suggested by the ternary complex model, and (3) different rank orders of apparent potency can be observed at SRIF receptors depending on the nature of the ligand/ receptor interaction studied (radioligand binding, [³⁵S]GTP γ S binding, AC activity, PLC activity); this suggests that receptor-effector trafficking can take place, as proposed for the human 5-HT_{2c} receptor (Berg et al. 1998a, 1998b, 1998c; Leff et al., 1997, 1998; Scaramellini et al., 1998), i.e. that each agonist-specific receptor conformation triggers specifically the modulated signalling pathways.

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List of publications

- (1) Siehler S, Seuwen K, Hoyer D (1998) $[^{125}I][Tyr^3]$ octreotide labels human sst₂ and sst₅ receptors. European Journal of Pharmacology, 348: 311-320.
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- (6) Siehler S, Seuwen K, Hoyer D. Characterization of human recombinant somatostatin receptors: 1) radioligand binding studies. Naunyn-Schmiedeberg's Archives of Pharmacology, submitted.
- (7) Siehler S, Hoyer D. Characterization of human recombinant somatostatin receptors: 2) modulation of GTPγS binding. Naunyn-Schmiedeberg's Archives of Pharmacology, submitted.
- (8) Siehler S, Hoyer D. Characterization of human recombinant somatostatin receptors: 3) modulation of adenylate cyclase activity. Naunyn-Schmiedeberg's Archives of Pharmacology, submitted.
- (9) Siehler S, Hoyer D. Characterization of human recombinant somatostatin receptors: 4) modulation of phospholipase C activity. Naunyn-Schmiedeberg's Archives of Pharmacology, submitted.
- (10) Siehler S, Zupanc GKH, Hoyer D. Fish somatostatin sst₃ receptor: comparison of radioligand and GTPγS binding, adenylate cyclase and phospholipase C activities reveals agonist-dependent pharmacological differences. Neuropharmacology, submitted.

Meeting abstracts

- Siehler S, Seuwen K, Hoyer D (1998) [¹²⁵I]Tyr³ octreotide labels human sst₂ and sst₅ receptors expressed in CCL39 cells. Naunyn-Schmiedeberg's Archives of Pharmacology 357: R35 (Meeting Abstract of the 39th Spring Meeting, Mainz, Germany).
- (2) Siehler S, Zupanc, GKH, Seuwen K, Hoyer D (1998) Pharmacological characterization and expression of the cloned fish somatostatin sst₃ receptor, a member of the SRIF₁ family. Society of Neuroscience Abstract No. 234.15, Vol. 24, 591 (Meeting Abstract of the 28th Annual Meeting, Los Angeles, USA).
- (3) Siehler S, Zupanc, GKH, Seuwen K, Hoyer D (1999) Characterisation of the cloned fish somatostatin receptor sst₃, a member of the SRIF₁-receptor family: atypical pharmacological features. British Journal of Pharmacology 126: 25P (Meeting Abstract, Brighton, England).
- (4) Siehler S, Seuwen K, Hoyer D (1999) System- and agonist-dependent ligandreceptor interactions at human somatostatin hsst₅ receptors: radioligand and [³⁵S]GTPγS binding and adenylate cyclase inhibition studies. British Journal of Pharmacology 126: 26P (Meeting Abstract, Brighton, England).
- (5) Siehler S, Seuwen K, Hoyer D (1999) System- and agonist-dependent ligandreceptor interactions at human somatostatin hsst₅ receptors. Naunyn-Schmiedeberg's Archives of Pharmacology 359: R17 (Meeting Abstract of the 40th Spring Meeting, Mainz, Germany).
- (6) Zupanc GKH, Siehler S, Jones EMC, Seuwen K, Furuta H, Hoyer D, Yano H (1999) Molecular cloning and pharmacological characterization of a fish-specific somatostatin receptor subtype. Göttingen Neurobiology Report Vol II: 822 (Meeting Abstract of the 27th Neurobiology Conference, Göttingen, Germany).
- (7) Zupanc GKH, Siehler S, Jones EMC, Seuwen K, Furuta H, Hoyer D, Yano H (1999) Molecular cloning and pharmacological characterization of a somatostatin receptor subtype in a teleost fish. Biological Chemistry, submitted (Meeting Abstract of the Society of Biochemistry and Molecular Biology, Hamburg, Germany).
- (8) Zupanc GKH, Siehler S, Jones EMC, Seuwen K, Furuta H, Hoyer D, Yano H (1999) Molecular cloning and pharmacological characterization of a somatostatin receptor subtype in the gymnotiform fish *Apteronotus albifrons*. Society of Neuroscience Abstract, submitted (Meeting Abstract of the 29th Annual Meeting, Miami, USA).