The African Catfish (Clarias Gariepinus) Reference Genome – A Near Telomere-To-Telomere (T2T) De Novo Chromosome-Level Assembly

Conference Poster

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The African catfish (*Clarias gariepinus*) reference genome – a near telomere-to-telomere (T2T) *de novo* chromosome-level assembly

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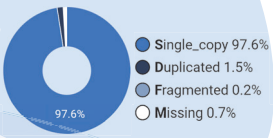
Sequencing technology

Data type	N50	Coverage
Oxford Nanopore	~32 kb	118 x
PacBio HiFi/CCS	~16 kb	82 x
illumina PE-150	2x150 bp	84 x
illumina PE-150 Hi-C	2x150 bp	24 x

Assembly method Hifiasm v. 0.16.1

BUSCO analysis (4.1.4)



Assembly metric

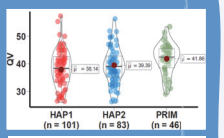
Genomic DNA sample	1 male
Genome size	969.7 Mb
Gapless length	100 %
Number of chromosomes	28
Number of organelles	1
Base accuracy	41.86
Number of scaffolds	47
Scaffold N50	33.7 Mb
Scaffold L50	12
Number of contigs	47
Contig N50	33.7 Mb
Contig L50	12
GC percent	39
Genome coverage	>100.0x
Assembly level	Chromosome
Genes and pseudogenes	40.491
Protein-coding genes	24.297
Non-coding genes	15.318
Transcript alignment rate	91,52 %
Repetitive content	49.49 %

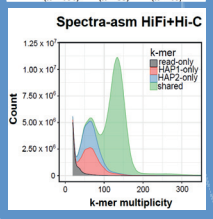
North African catfish, *Clarias gariepinus* (Burchell 1822)

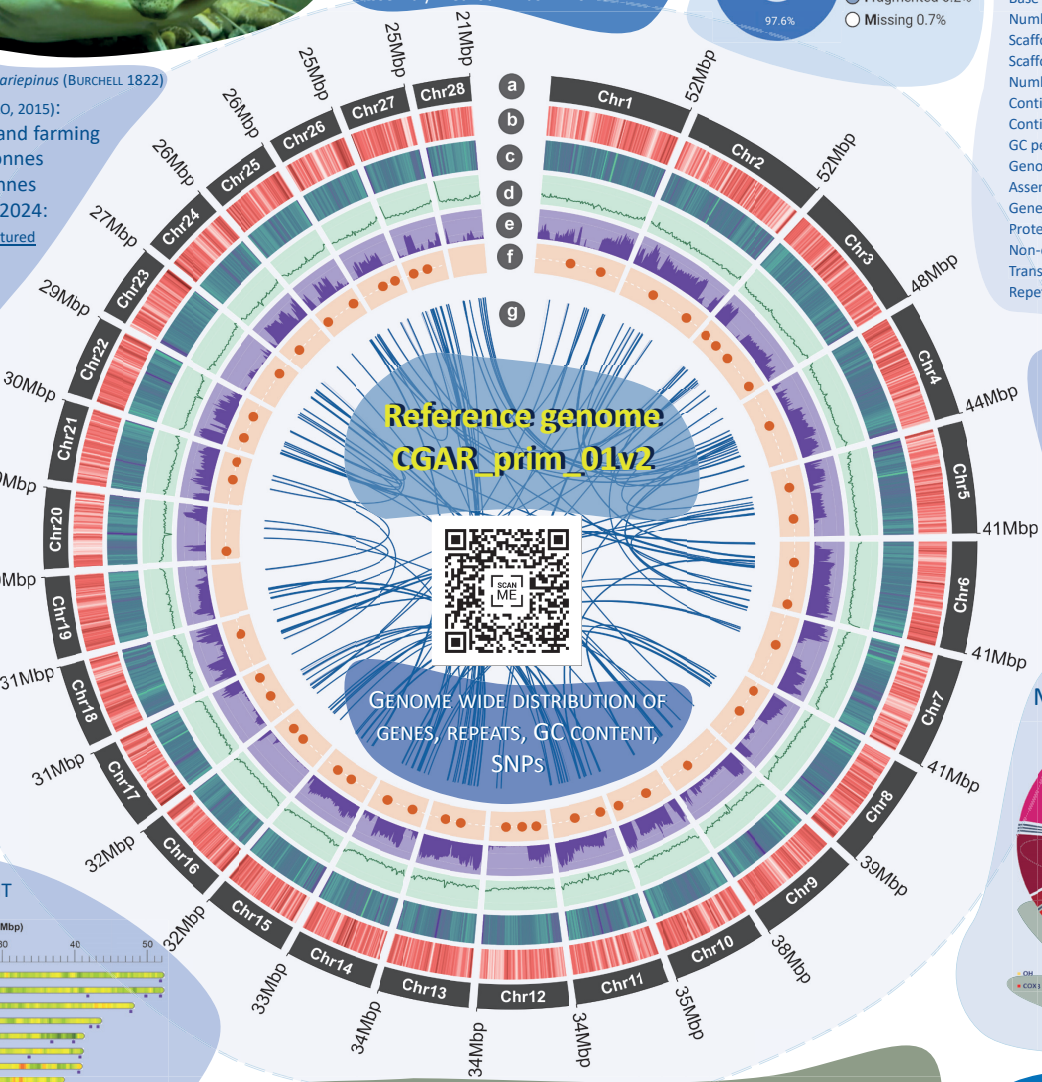
- Aquaculture production (FAO, 2015):
  - 2.5% of world finfish inland farming
  - Aquaculture: 182.000 tonnes
  - Wild catches: 50.000 tonnes
- More information on FAO, 2024:
  - www.fao.org/fishery/en/cultured species/clarias_gariepinus/en

Assembly consensus

Quality values

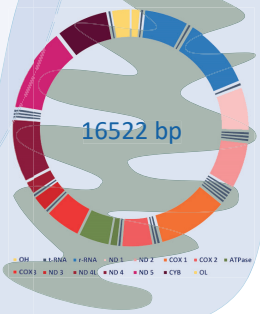




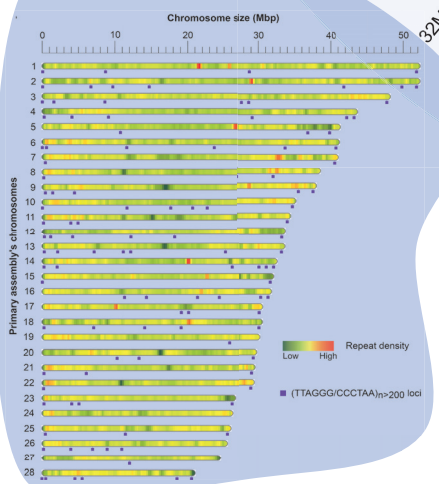


a Chr Chromosome
b Gene density
c Repeats density
d GC cotent (%)
e SNP density
f HR genes
g Syntenic genes
HR hypoxia-responsive

Mitochondrial genome

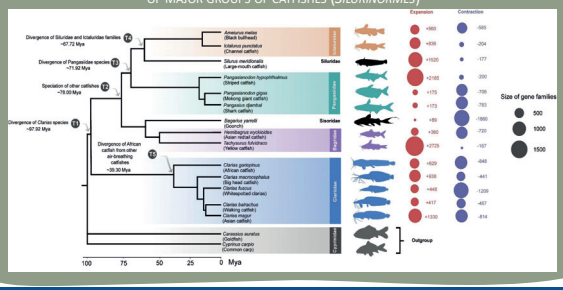


Telomere portrait

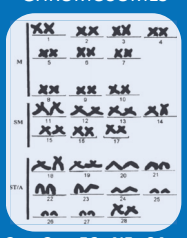


Phylogenomic relationships

of major groups of catfishes (*Siluriformes*)



Chromosomes



2n = 2x = 56; NF= 94
18 m + 20 sm + 18 st/a
Siraj et al. (2009) Malays Appl Biol 38(1)

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MV tut gut.
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