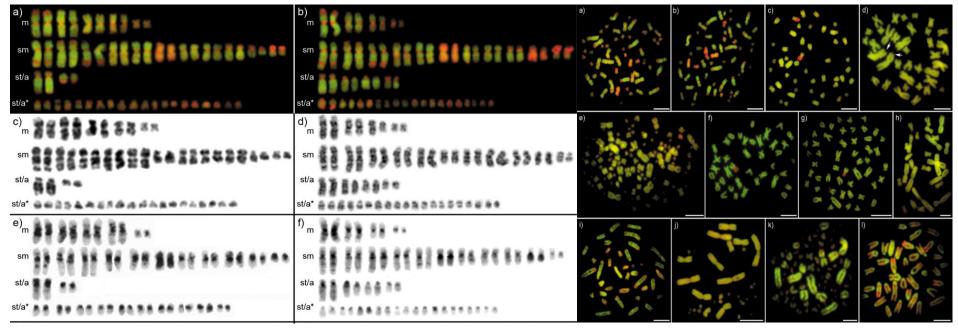
This project has received funding from the European Union's Molecular Cytogenomics in Vertebrates Horizon 2020 research and innovation programme under the

Marie Skłodowska-Curie grant agreement No 754462

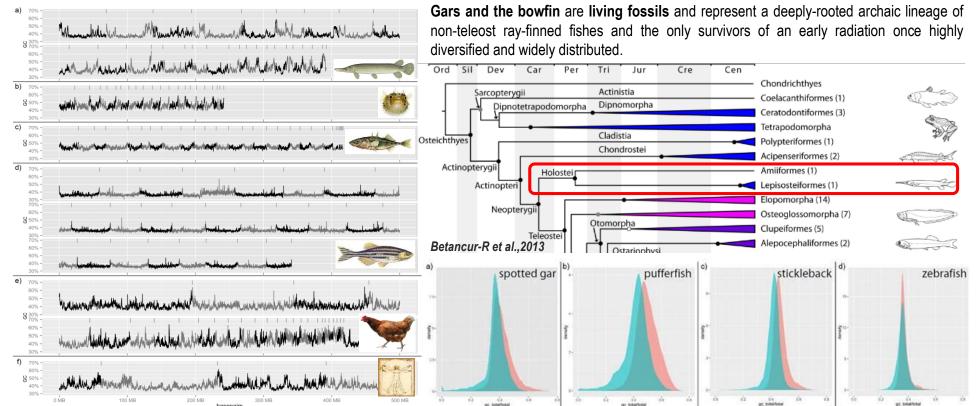
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Cytogenomic analyses in both of two gar genera have uncovered a pattern uncharacteristic for fish and generally for cold-blooded and anamniote vertebrates. The bioinformatic analysis has confirmed a remarkable level of genome AT/GC heterogeneity in spotted gar and revealed a gene richness in the GC-rich regions. This indicates a rather mammalian way of compositional organization of gar genomes. Bioinformatic comparisons exposed that the genome organization of the gar is in fact closer to the mouse and human than to the zebrafish.



Chromosomes stained with GC-specific CMA3 and AT-specific DAPI: a) tropical gar + b) spotted gar both pannels; right pannel: c) bowfin; d) bichir; e) sturgeon; f) eel; g) roach; h) frog; i) rapid racerunner; j) green anole; k) chicken and l) mouse; left pannel: G-banding pattern c)-d) and C-banding e)-f) in both gar genera



GC profiles along linkage groups, only partial profile shown for human, the panel f). (Symonová et al., 2017)

GC content in genes and intergenic regions. Density plots showing GC content in genes (pink) and intergenic regions (green), Symonová et al., 2017

