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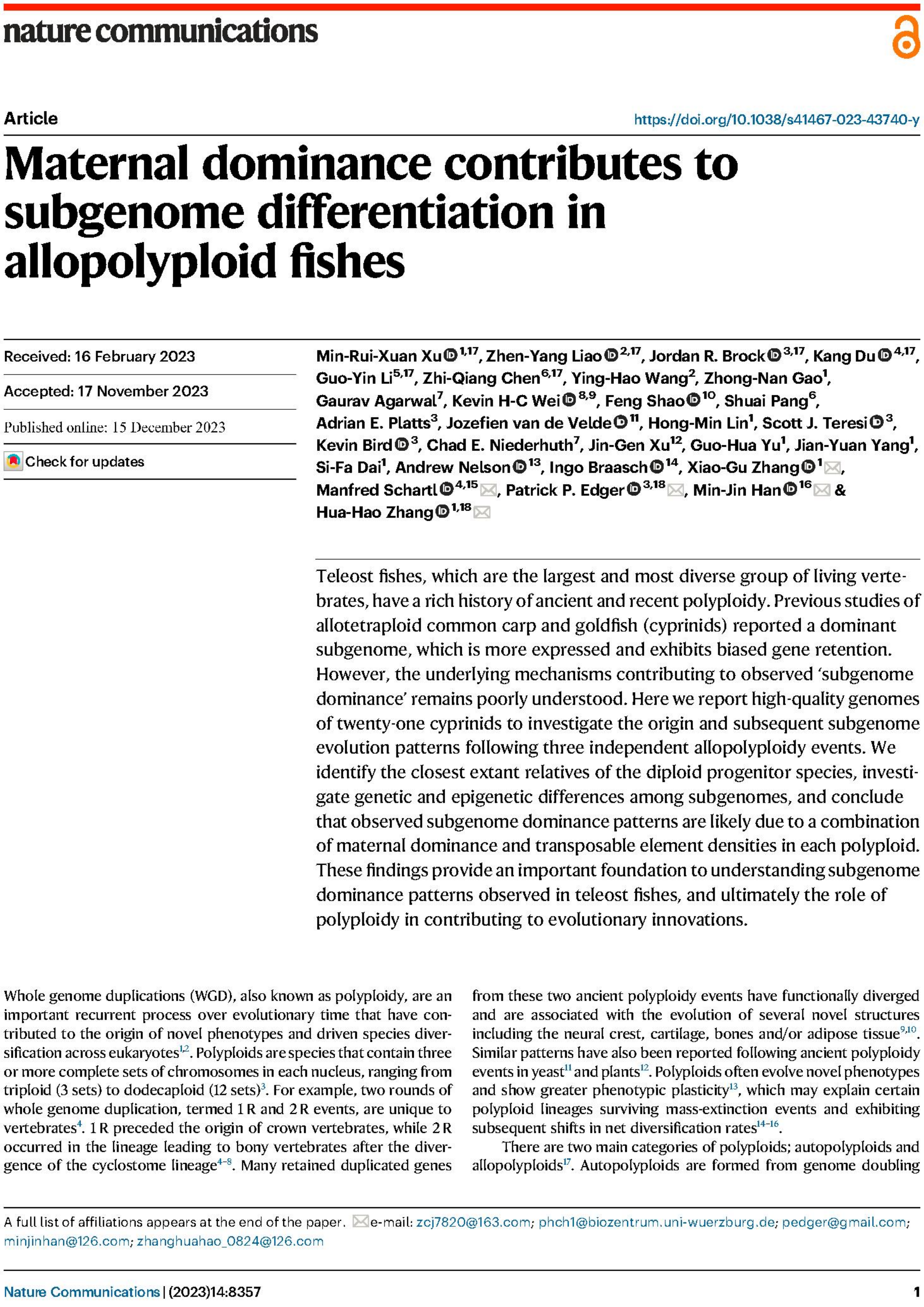

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Maternal dominance contributes to subgenome differentiation in allopolyploid fishes

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Min-Rui-Xuan Xu[1,17], Zhen-Yang Liao[2,17], Jordan R. Brock[3,17], Kang Du[4,17], Guo-Yin Li[5,17], Zhi-Qiang Chen[6,17], Ying-Hao Wang[2], Zhong-Nan Gao[1], Gaurav Agarwal[7], Kevin H-C Wei[8,9], Feng Shao[10], Shuai Pang[6], Adrian E. Platts[3], Jozefien van de Velde[11], Hong-Min Lin[1], Scott J. Teresi[3], Kevin Bird[3], Chad E. Niederhuth[7], Jin-Gen Xu[12], Guo-Hua Yu[1], Jian-Yuan Yang[1], Si-Fa Dai[1], Andrew Nelson[13], Ingo Braasch[14], Xiao-Gu Zhang[1] ✉, Manfred Schartl[4,15] ✉, Patrick P. Edger[3,18] ✉, Min-Jin Han[16] ✉ & Hua-Hao Zhang[1,18] ✉

Teleost fishes, which are the largest and most diverse group of living vertebrates, have a rich history of ancient and recent polyploidy. Previous studies of allotetraploid common carp and goldfish (cyprinids) reported a dominant subgenome, which is more expressed and exhibits biased gene retention. However, the underlying mechanisms contributing to observed 'subgenome dominance' remains poorly understood. Here we report high-quality genomes of twenty-one cyprinids to investigate the origin and subsequent subgenome evolution patterns following three independent allopolyploidy events. We identify the closest extant relatives of the diploid progenitor species, investigate genetic and epigenetic differences among subgenomes, and conclude that observed subgenome dominance patterns are likely due to a combination of maternal dominance and transposable element densities in each polyploid. These findings provide an important foundation to understanding subgenome dominance patterns observed in teleost fishes, and ultimately the role of polyploidy in contributing to evolutionary innovations.

Whole genome duplications (WGD), also known as polyploidy, are an important recurrent process over evolutionary time that have contributed to the origin of novel phenotypes and driven species diversification across eukaryotes[1,2]. Polyploids are species that contain three or more complete sets of chromosomes in each nucleus, ranging from triploid (3 sets) to dodecaploid (12 sets)[3]. For example, two rounds of whole genome duplication, termed 1 R and 2 R events, are unique to vertebrates[4]. 1 R preceded the origin of crown vertebrates, while 2 R occurred in the lineage leading to bony vertebrates after the divergence of the cyclostome lineage[4–8]. Many retained duplicated genes from these two ancient polyploidy events have functionally diverged and are associated with the evolution of several novel structures including the neural crest, cartilage, bones and/or adipose tissue[9,10]. Similar patterns have also been reported following ancient polyploidy events in yeast[11] and plants[12]. Polyploids often evolve novel phenotypes and show greater phenotypic plasticity[13], which may explain certain polyploid lineages surviving mass-extinction events and exhibiting subsequent shifts in net diversification rates[14–16].

There are two main categories of polyploids; autopolyploids and allopolyploids[17]. Autopolyploids are formed from genome doubling

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A full list of affiliations appears at the end of the paper. ✉e-mail: zcj7820@163.com; phch1@biozentrum.uni-wuerzburg.de; pedger@gmail.com; minjinhan@126.com; zhanghuahao_0824@126.com

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Horizontal transfer and evolution of transposable elements in vertebrates

Hua-Hao Zhang[1,4], Jean Peccoud[2,4], Min-Rui-Xuan Xu[1], Xiao-Gu Zhang[1]✉ & Clément Gilbert[3]✉

Horizontal transfer of transposable elements (HTT) is an important process shaping eukaryote genomes, yet very few studies have quantified this phenomenon on a large scale or have evaluated the selective constraints acting on transposable elements (TEs) during vertical and horizontal transmission. Here we screen 307 vertebrate genomes and infer a minimum of 975 independent HTT events between lineages that diverged more than 120 million years ago. HTT distribution greatly differs from null expectations, with 93.7% of these transfers involving ray-finned fishes and less than 3% involving mammals and birds. HTT incurs purifying selection (conserved protein evolution) on all TEs, confirming that producing functional transposition proteins is required for a TE to invade new genomes. In the absence of HTT, DNA transposons appear to evolve neutrally within genomes, unlike most retrotransposons, which evolve under purifying selection. This selection regime indicates that proteins of most retrotransposon families tend to process their own encoding RNA (*cis*-preference), which helps retrotransposons to persist within host lineages over long time periods.

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[1] College of Pharmacy and Life Science, Jiujiang University, 332000 Jiujiang, China. [2] UMR CNRS 7267 Ecologie et Biologie des Interactions, Equipe Ecologie Evolution Symbiose, Université de Poitiers, 86073 Poitiers, France. [3] Laboratoire Evolution, Génomes, Comportement, Écologie, UMR 9191 CNRS, UMR 247 IRD, Université Paris-Saclay, 91198 Gif-sur-Yvette, France. [4] These authors contributed equally: Hua-Hao Zhang, Jean Peccoud. ✉email: zcj7820@163.com; clement.gilbert@egce.cnrs-gif.fr

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