Abstract

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A unique example of a recombination-absent asexually reproducing vertebrate species, the Amazon molly has persisted as a lineage for a much longer time period than predicted by mutational accumulation and corresponding genomic decay. A significant body of work has identified a leaky mechanism of asexual reproduction by gynogenesis as a potential source of fragmented but novel genetic variation from sympatric sperm donor species into an otherwise stagnant system. However, what remains unclear is the frequency at which these events occur, and the time frame over which micro-chromosomes resulting from this paternal introgression accumulate. Additionally, the lack of a chromosome – scale genome complicates the identification of micro-chromosomes from resequencing data. Here, we assemble a de novo genome for the Amazon molly using high fidelity long read sequencing and Omni-C contact mapping. We take advantage of next generation sequencing data from several recently (less than 20 generations) isolated laboratory lines of the Amazon molly and realign these long reads to the de novo genome. We identify regions of elevated copy number and allele depth skew in eight different mollies, which we classify as putative micro-chromosomes. Documented micro-chromosomes include examples which are shared within and across lineages. Our next steps are to expand on sequencing efforts to facilitate sampling of lineages in multiple labs on a population level to investigate patterns of micro-chromosome acquisition over time.

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use aligned mitogenomes and approximate dates for the most recent common ancestor of individuals within lineages to build a time-calibrated phylogeny including eight different individuals from four different lineages. Using this phylogeny, we simulate the potential histories of introgression events to arrive at an approximate frequency of these events in terms of generations. We find that paternal introgression events in Amazon mollies occur at more rapid rates than have been documented in the past, and confirm that the micro-chromosomes resulting from these events remain stably inherited within short time scales (<10 generations).