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A very recent whole genome duplication in Potamopyrgus antipodarum predates multiple origins of asexuality & associated polyploidy

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Abstract: *Potamopyrgus antipodarum*, a New Zealand freshwater snail, is a powerful system to study the maintenance of sexual reproduction. Obligate asexual *P. antipodarum* lineages include both triploids and tetraploids that are products of multiple separate transitions from diploid sexual ancestors. Distinct diploid sexual and polyploid asexual lineages coexist and compete; these separate lineages can be considered replicated natural experiments. We have shown that harmful mutations are accumulating at a higher rate in asexual than in sexual *P. antipodarum*, demonstrating the utility of this system as a model for investigating the evolution of sex at the genomic level. In order to better understand the causes and consequences of transitions to asexuality, we have sequenced multiple genomes and transcriptomes of *P. antipodarum* and a close relative, *P. estuarinus,* a diploid sexual species. The diploid genome size of *P. estuarinus* is ~0.6X of the genome size of diploid *P. antipodarum*, inspiring us to investigate whether the most recent common ancestor of *P. antipodarum* had experienced a whole-genome duplication (WGD) event prior to the diversification of its many sexual and asexual lineages. In addition to its clear relevance to understanding the evolutionary history of this species, by being so recent, this apparent WGD will also be especially powerful in understanding events immediately following WGD. Our initial genome assembly of a model sexual *P. antipodarum* lineage was consistent with this possibility, indicating high fractions (~35%) of scaffolds containing extended, nearly identical, duplicated regions. This result also partly explains our general difficulty with assembling the genome, despite generating >100X genome coverage using multiple methodologies. Even considering the limitations of our current genome assembly, we used the assembly to test a series of predictions under the hypothesis of recent whole-genome duplication, all of which are consistent with WGD. These include: 1) a marked excess of duplicated copies of genes in *P. antipodarum* which are maintained in single copy in other animals, 2) implausibly high "heterozygosity" estimates in our model *P. antipodarum* sexual genome, presumably resulting from non-allelic comparisons, 3) higher sequence identity between thousands of *P. antipodarum*-specific paralogous genes, when compared to their *P. estuarinus* orthologs. These and additional lines of evidence will be presented and evaluated. Together, our results hint that this initial genome-wide duplication event might have played a key role in the subsequent evolutionary trajectory of this species, potentially facilitating its repeated diversification into multiple asexual lineages. We are now generating additional long-range genome scaffolds for *P. antipodarum* using multiple methods, as well as improving the coverage and quality of the *P. estuarinus* genome. We will use these new data to conduct definitive phylogenomic tests of this especially remarkable whole genome duplication.

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