Sorting duplicated loci disentangles complexities of polyploid genomes masked by genotyping by sequencing

Many plants and animals of polyploid origin are currently enjoying a genomics explosion enabled by modern sequencing and genotyping technologies. However, routine filtering of duplicated loci in most studies using genotyping by sequencing introduces an unacceptable, but often overlooked, bias when detecting selection. Retained duplicates from ancient whole-genome duplications (WGDs) may be found throughout genomes, whereas retained duplicates from recent WGDs are concentrated at distal ends of some chromosome arms. Additionally, segmental duplicates can be found at distal ends or nearly anywhere in a genome. Evidence shows that these duplications facilitate adaptation through one of two pathways: neo-functionalization or increased gene expression. Filtering duplicates removes distal ends of some chromosomes, and distal ends are especially known to harbour adaptively important genes. Thus, filtering of duplicated loci impoverishes the interpretation of genomic data as signals from contiguous duplicated genes are ignored. We review existing strategies to genotype and map duplicated loci; we focus in detail on an overlooked strategy of using gynogenetic haploids (1N) as a part of new genotyping by sequencing studies. We provide guidelines on how to use this haploid strategy for studies on polyploid-origin vertebrates including how it can be used to screen duplicated loci in natural populations. We conclude by discussing areas of research that will benefit from better inclusion of polyploid loci; we particularly stress the sometimes overlooked fact that basing genomic studies on dense maps provides value added in the form of locating and annotating outlier loci or colocating outliers into islands of divergence.

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