

# Hill-Robertson Interference Causes Reduced Genetic Diversity on a Young Plant Y-chromosome Following Recent Recombination Suppression

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## ABSTRACT

X and Y chromosomes differ in effective population size ( $N_e$ ), rates of recombination, and exposure to natural selection, all of which can affect patterns of genetic diversity. On Y chromosomes with suppressed recombination, selection is expected to eliminate neutral variation and reduce the  $N_e$  of Y compared to X chromosomes or autosomes. However, non-selective factors including female biased sex ratios and high variance in male reproductive success can also reduce Y-linked  $N_e$ , making it difficult to infer the causes of low Y-diversity from natural populations. Here, we investigate the factors affecting levels of polymorphism during sex chromosome evolution in *Rumex hastatulus* (Polygonaceae), a dioecious plant with young sex chromosomes. Strikingly, we find that neutral diversity for genes on the Y is on average 2.1% of the value for their homologues on the X, corresponding to a chromosome-wide reduction of 93% compared to the neutral expectation. We demonstrate that the magnitude of this diversity loss is inconsistent with a reduced male  $N_e$  caused by neutral processes including female-biased sex ratios and high variance in male reproductive success. Instead, using forward simulations and estimates of the distribution of fitness effects of deleterious mutations, we show that diversity loss on the Y can be explained by purifying selection acting over a large number ( $\geq 800$  Kb) of genetically-linked sites. Our results are in agreement with theory on "interference selection", and provide empirical evidence that this effect can substantially reduce neutral diversity on a non-recombining chromosome. Given the recent origin of *R. hastatulus* sex chromosomes (15MYA), our results imply that Y-chromosome degeneration in the early stages may be largely driven by such interference effects rather than by positive selection for gene silencing followed by neutral genetic drift.