

Replaying the tape of hybrid speciation in the laboratory reveals major consequences for whole-genome duplication



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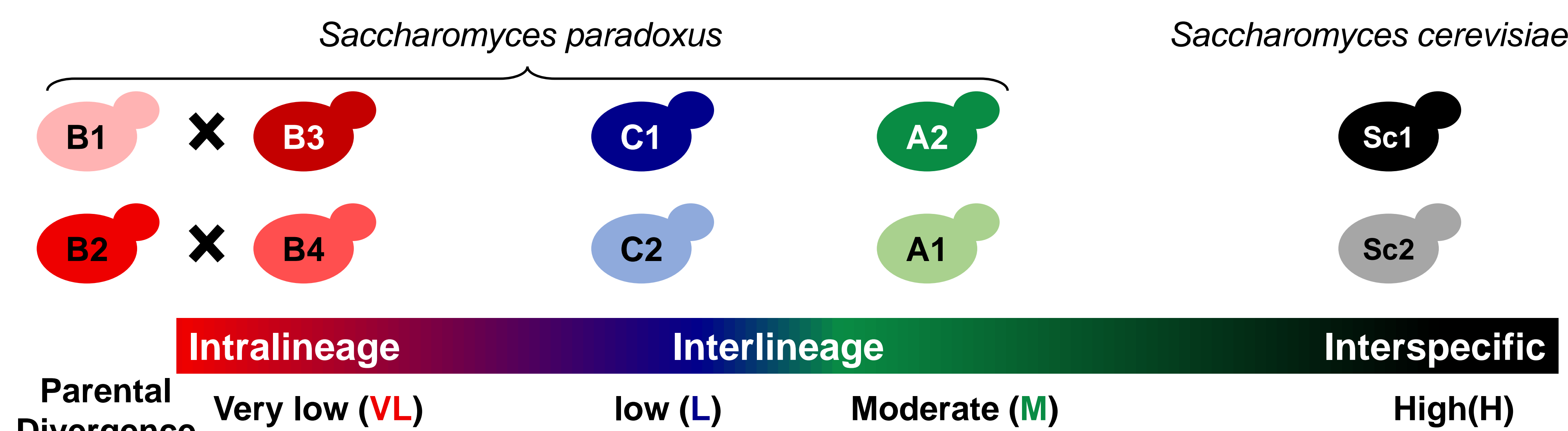


Introduction

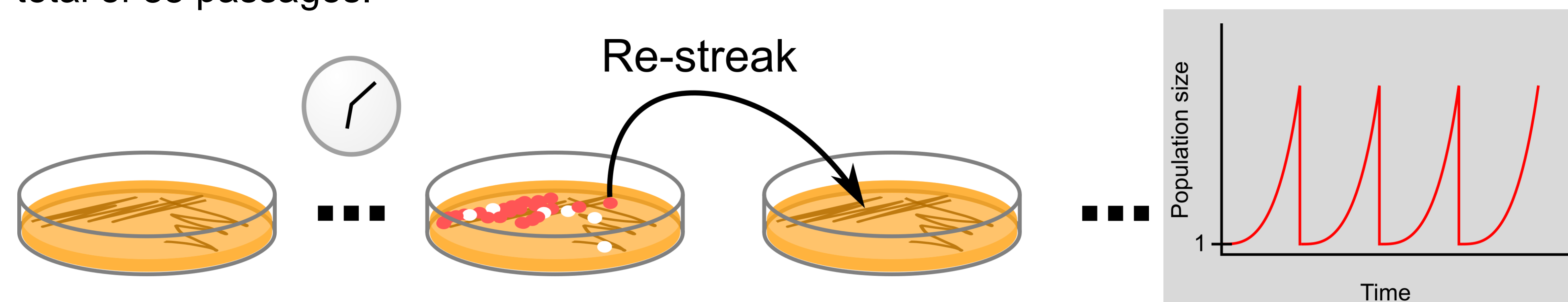
Many organisms bear traces of ancient hybridization events in their genomes under the form of introgressions and we now know that hybridization is a rather common event in nature [1]. However, hybrid lineages often show poor fertility resulting from incompatibilities between their parental species. This poor fertility can hinder their maintenance as independent populations and thus their speciation potential. One way for the hybrids to restore fertility is through repeated backcrosses with either parental species, promoting the formation of introgressed species rather than hybrid species [2]. Mitotic division could provide an alternative way to recover fertility that would also promote hybrid speciation. In order to test this, we evolved more than 600 yeast hybrid lines that span from 100,000 to 15M years of parental divergence for more than 700 generations. We show that, while hybrid fertility does not show clear pattern of systematic recovery, some evolved lines did recover to high fertility through whole-genome duplication.

Methods

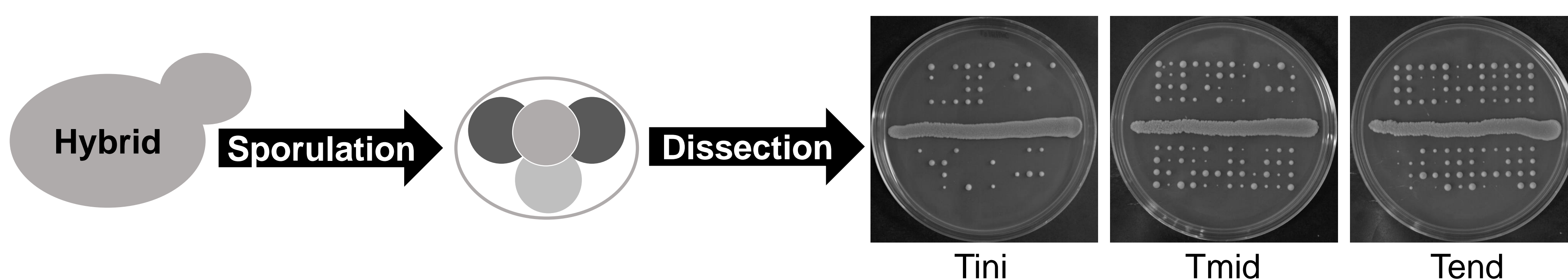
Experimental crosses: 2 independent sets of 4 crosses, 96 independent evolution lines per cross, except for the interspecific crosses (48 lines per cross), for a total of 672 evolution lines.



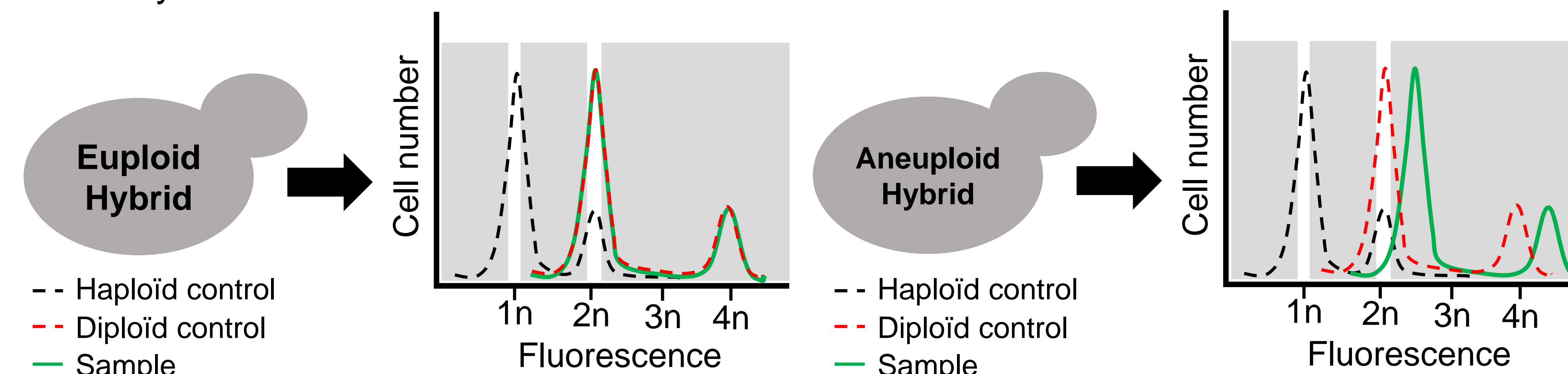
Experimental evolution: Single cell bottlenecks to reduce selection efficiency. Streaking to fresh media every 3 days (~22 mitotic generations per passage). Experiment lasted for a total of 35 passages.



Fertility measurements: Tetrad dissection for randomly chosen evolved lines (at least 24 per line) at three different time points; Initial (after hybridization, Tini), midpoint (Tmid, ~350 generations) and endpoint (Tend, ~770 generations)



Ploidy measurements: Total DNA fluorescent staining read with flow cytometer on the same randomly selected strains.



Results

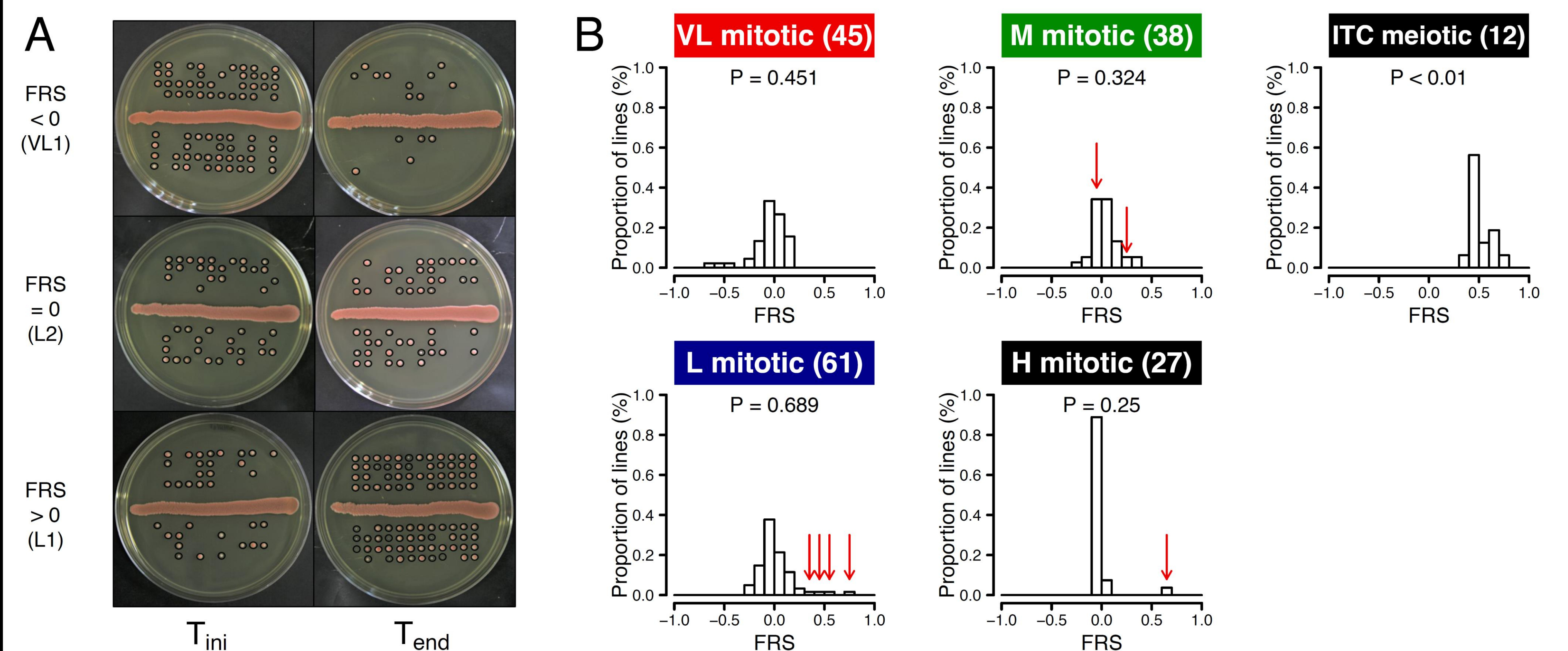


Figure 1: Fertility is behaving like a neutrally evolving trait. Evolved lines were assigned a Fertility Recovery Score (FRS) calculated as the difference in fertility between Tini and Tend (A). Fertility changes as indicated by FRS show no particular direction in the mitotically evolved lines. FRS for lines obtained by mating spores of the same tetrad (ITC) show large and systematic increases in fertility. Some evolved hybrids recovered fertility greatly (red arrows)

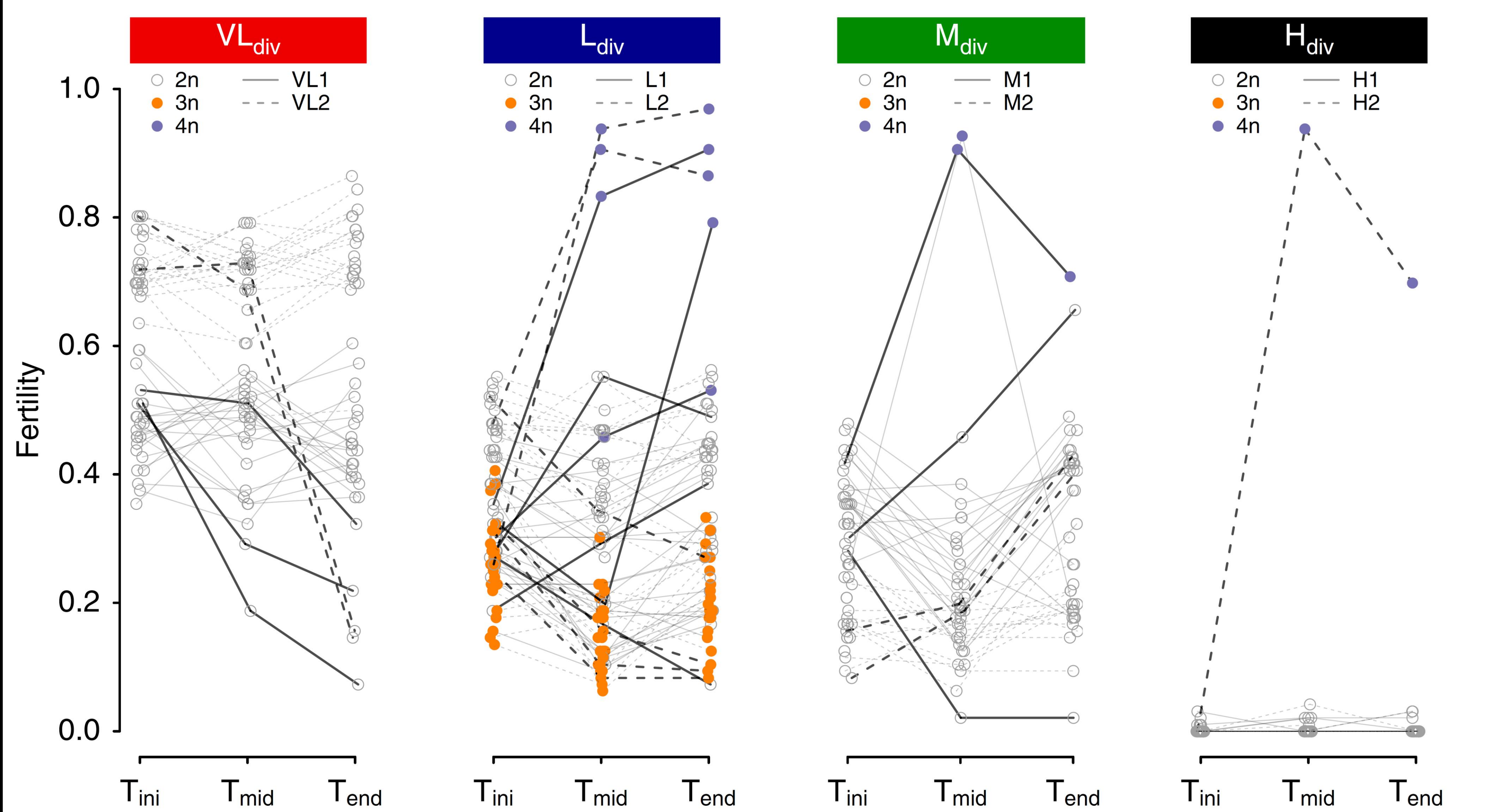


Figure 2: Tetraploidization leads to great fertility recovery. Each connected set of dots represents the fertility trajectories through the three measured timepoints for independent sets of evolution lines. Full and dotted lines are used to distinguish the two independent sets of crosses. Bolder lines represent strains with significantly different proportion of viable spores between Tini and Tend

Discussion

-There is no global directional fate to the changes in fertility in hybrid lineages when propagated mitotically while the efficiency of selection is diminished.

-One way for hybrids to restore their fertility is to duplicate their genome, which most likely restores correct chromosomal pairing during meiosis.

-While meiotic fertility may be restored by genome duplication, sporulation of the tetraploid leads to the formation of allodiploid spores that are not able to mate, generating another form of sterility which needs to be overcome.

-Other patterns of fertility changes would require a deeper study of the hybrid genomes in order to understand the underlying molecular causes.

References

- [1] Mallet J (2005) Hybridization as an invasion of the genome. *Trends in ecology & evolution* **20**, 229-237.
- [2] Marsden-Jones EM (1930) The genetics of Geum intermedium willd. Haud ehrh., And its back-crosses. *Journal of Genetics* **23**, 377-395.

Complete article

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