

The Mechanisms of Speciation in Yeasts

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Hybrids between different species are usually inviable or sterile. One of the possible mechanisms causing postzygotic reproductive isolation is incompatibility between genes (speciation genes) from different species. These speciation genes are hypothesized to be some interacting components that cannot function properly when mixed with alleles from different species. Evolution of speciation genes is generally thought to be driven by adaptive evolution. Identifying these genes will provide more information how speciation occurs.

The effect of incompatible genes can be masked in the diploid F1 progeny if they work recessively. However, the incompatibility will become evident in the haploid F1 gametes or homozygous diploid F2 progeny. We have set up a screen to determine whether such genetic incompatibility exists between two yeast species, *Saccharomyces cerevisiae* (Sc) and *Saccharomyces bayanus* (Sb). Chromosome replacement lines were constructed in which one or a few chromosomes were derived from Sb and the rest were from Sc. Most of the replacement lines exhibited only mild defects in fitness and sporulation, suggesting that either these chromosomes don't carry the speciation genes with strong effects or the interacting components locate on the same chromosome. Nonetheless, complete hybrid sterility was observed in one hybrid line containing the 13th chromosome of Sb. Aep2, a mitochondrial protein encoded on the 13th chromosome was identified to cause this sporulation defect. We showed that in the hybrid diploid cells, Sc-mitochondria were preferentially transmitted to the progeny and the Sb-Aep2 protein could not function properly in Sc-mitochondria. This hybrid incompatibility will result in loss of the respiratory ability and cause the sporulation defect. These results represent the first Dobzhansky-Muller incompatible genes identified in yeast.

Some incompatibility may affect specific pathways that will not be easily detected in normal conditions. We try to address this issue using data from the whole genome gene expression pattern in different replacement lines. We will focus on the genes or pathways that are mis-regulated in those hybrid lines. Information from this experiment will provide us a more general idea how incompatibility evolves.

Finally, we will expand our studies to other *Saccharomyces sensu stricto* yeasts including *S. mikatae* and *S. paradoxus*. By comparing the incompatible genes between different species, we hope to extract the principles behind speciation.