Negative selection in *Drosophila melanogaster* missense alleles

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Effects of missense mutations which are present in natural populations on functions of the affected proteins vary widely, from negligible to drastic. In particular, a substantial proportion of missense mutations impair function but only slightly. How does negative selection operate in alleles of protein coding genes that carry such slightly deleterious missense mutations? If different deleterious mutations that affect a particular protein act sinergistically, we can expect negative selection in such alleles to be stronger than in wild-type alleles. Here, we investigate this question by comparing nucleotide diversities at synonymous and nonsynonymous sites of wild-type and missense-carrying alleles of genes in Zambian population of *Drosophila melanogaster*.