

Abstract

Genes encoding reproductive proteins often diverge rapidly due to positive selection on nucleotide substitutions. While this general pattern is well established, the extent to which specific reproductive genes experience similar selection in different clades has been little explored, nor have possible targets of positive selection other than nucleotide substitutions, such as indels, received much attention. Here, we inspect for the signature of positive selection in the genes encoding five accessory gland proteins (Acp) (*Acp26Aa*, *Acp32CD*, *Acp53Ea*, *Acp62F*, and *Acp70A*) originally described from *Drosophila melanogaster* but with recognizable orthologs in the *D. pseudoobscura* subgroup. We compare patterns of selection within the *D. pseudoobscura* subgroup to those in the *D. melanogaster* subgroup. Similar patterns of positive selection were found in *Acp26Aa* and *Acp62F* in the two subgroups, while *Acp53Ea* and *Acp70A* experienced purifying selection in both subgroups. These proteins have thus remained targets for similar types of selection over long (>21 MY) periods of time. We also found several indel substitutions and polymorphisms in *Acp26Aa* and *Acp32CD*. These indels occur in the same regions as positively selected nucleotide substitutions for *Acp26Aa* in the *D. pseudoobscura* subgroup, but not in the *D. melanogaster* subgroup. Rates of indel substitution within *Acp26Aa* in the *D. pseudoobscura* subgroup were up to several times those in noncoding regions of the *Drosophila* genome. This suggests that indel substitutions may be under positive selection and may play a key role in the divergence of some Acps.