

ADAM HULL, SHER HENDRICKSON-LAMBERT and DAVID B. WING, Dept. of Biology, Shepherd University, Shepherdstown, WV, 25443. Analysis of three alleles of the vestigial gene in *Drosophila melanogaster*.

The vestigial wing gene in *D. melanogaster* is a popular locus used to illustrate classical Mendelian inheritance patterns because the short, crinkled-wing phenotype directed by the vg^1 allele is easy to identify. Carolina Biological notes that its stock of vestigial wing flies also has flies with more developed, but still under-developed wings, the more common phenotype being a narrow plank-shaped transparent wing. A line of flies was bred that only displayed the “plank-wing” phenotype. Genetic analysis of the mutant allele, vg^{pl} , showed that it was recessive to the wild-type allele vg^+ , and mutants displayed variable expressivity. PCR products were generated from all three alleles: the products from wild-type DNA covered the whole gene while products from the mutant DNAs covered about 75% of the gene. The presence of retrotransposon 412 was confirmed in vg^1 and also found in vg^{pl} ; a reported second large insert in the vg^1 remains to be amplified. Sanger DNA sequencing of the first 4,812 bp, beginning 428 bp upstream of the transcription start site revealed allele specific point mutations and small insertions, some specific for each of the vg^1 and vg^{pl} alleles. The DNA sequence analysis so far confirmed the partial genetic reversion of the vg^1 to a new vg^{pl} allele. When complete, a full DNA sequence analysis should suggest nucleotide changes that cause the new “plank wing” phenotype.

This work was funded in part by the Research Challenge Fund through a Summer Undergraduate Research Experience Grant from the West Virginia Higher Education Policy Commission Division of Science and Research.