**Glossary** – Table or Supplementary Information?

Associative overdominance – A type of overdominance generated by linkage wherein heterozygotes at a locus with neutral alleles (lacking fitness effects) appear to have superior fitness to both homozygotes at that locus. It arises because these neutral alleles are associated with alleles at nearby selected locus (via linkage disequilibrium). This concept was first described by Frydenberg (1963). Pseudo-overdominance generated by two or more deleterious recessive mutations linked in repulsion could also generate associative overdominance with neutral markers.

Background selection –selection on alleles at linked loci that results when strong selection occurs against highly deleterious alleles. Such selection can eliminate (midlly) favorable alleles linked in coupling and fix less deleterious alleles linked in repulsion.

Coupling – a situation where two or more alleles at linked loci are located on the same chromosome in a “cis” relationship.

Drift load – the fixed genetic load that accumulates in a population as a result of genetic drift. This term was introduced by Whitlock et al. (2000). It is equivalent to what Crow and Kimura (1970) called the “finite population load.”

Identity disequilibrium – the correlation in homozygosity (or heterozygosity) that exists across loci within inbred populations.

Linkage disequilibrium - non-random associations among alleles at different loci. Also known more exactly as gametic phase disequilibrium.

Overdominance – a type of balancing selection wherein the heterozygote at a particular locus is more fit than both segregating homozygotes.

POD – an abbreviation coined here to refer to blocks of two or more deleterious mutations linked in repulsion generating appreciable pseudo-overdomianance.

Pseudo-overdominance – The apparent overdominance emerging from the segregation of two or more recessive deleterious mutations that occur at closely linked loci. Although each individual mutation shows strict dominance, when these occur in repulsion to each other, heterozygotes segregate homozygotes for one or more of these mutations that show reduced fitness, mimicking true overdominance at a single locus. First defined and explored by Ohta (1971). Like associative overdominance, this form of overdominance emerges as a side effect of associations among alleles at nearby linked loci.

QTL - quantitative trait loci, often identified using mapped markers to identify locations of loci affecting a quantitative trait in crosses between recombinant inbred lines (RILs)

Repulsion - a situation where two or more alleles at linked loci occur on opposite chromosomes in a “trans” relationship.

Segregational load – the reduction in fitness expressed upon inbreeding. Also known as the inbreeding load. Estimated as the slope of the log fitness (or viability) regression on F, the individual inbreeding coefficient.

Viability loci – loci at which deleterious mutations can or do occur.