

# Immune-related genes and pathways in disease-vector mosquitoes

**Immunity-related genes:** 285 *Drosophila melanogaster* (Dm), 338 *Anopheles gambiae* (Ag), and 353 *Aedes aegypti* (Aa) genes from 31 gene families and functional groups implicated in classical innate immunity or defense functions such as apoptosis and response to oxidative stress.

**Orthology groups (whole genome):** 4951 orthologous trios (1:1:1 orthologs in the three species) and 886 mosquito-specific orthologous pairs (absent from Dm).

**Orthology groups (immune-related):** 91 trios and 57 pairs, plus a combined total of 589 paralogous genes in the three species.

**Immune-related orthology trios are more divergent than that of whole genome:** Phylogenetic distances of genes in each trio is measured by amino acid substitutions. With Dm as reference, immune-related trios of Ag and Am are more divergent (on average) compared with trios of whole genome, and several Ag immunity genes are considerably more divergent than their Aa orthologs.

**Large variation exists in different immune families in their proportions of orthologous trios, mosquito-specific pairs and species-specific genes:** (1) Predominantly trio orthologs: apoptosis inhibitors (IAPs), oxidative defense enzymes [superoxide dismutases (SODs), glutathione peroxidases (GPXs), thioredoxin peroxidases (TPXs), heme-containing peroxidases (HPXs)], class A and B scavenger receptors (SCRs).

(2) Rarely trio orthologs: immune effectors, including three antimicrobial peptides.

(3) Intermediately: C-type lectins.

**Strong divergent evolution of immune recognition genes:** Fruit fly and mosquito recognition proteins mostly form distinct clades within each gene family.