Evidence for reduced immune gene diversity and activity during the evolution of termites

18 cockroach and termite species, including 9 lower termites, 6 higher termites, 2 subsocial wood roaches and 2 solitary roaches were studied via *de novo* assembled transcriptomes. Each immune gene family presented in all species, except antifungal dorsomycin, which was lost in termites and wood roaches. Phylogenetic signal analysis revealed a loss of total immune gene diversity during termite evolution.

Antifungal peptide drosomycin was lost in ancestor of wood roach *Cryptocercus* and termites. C-type lectin (CTL) underwent two contractions in most recent common ancestor (MRCA) of (1) wood roach *Cryptocercus* and termites; and (2) Rhinotermitidae and Termitidae, but together with lysozymes, re-expanded in late branch of higher termites, *i.e.* MRCA of *Promirotermes* and *Dicuspiditermes*. Serine protease CLIP contracted in MRCA of Rhinotermitidae and Termitidae. Thiroredoxin peroxidase (TPX) and autophagy-related gene (ATG) contracted in Termitidae, while defensin expanded.

In bees, immune gene depletion seems to have preceded evolution of eusociality (Barribeau *et al.*, 2015), indicating immune gene depletion is unrelated with transition to sociality. Although there was contraction of immune genes in termite evolution, it can be interpreted as an expansion of immune genes in solitary cockroaches (Harrison *et al.*, 2018) followed by returning to a representative level.