



Gene expression differences underlying aging in the termite *Cryptotermes secundus*: a long-run time series study

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In most animal species a trade-off between self-maintenance and reproduction exists but in eusocial insects this trade-off seems absent: reproductives live long and have plenty of offspring throughout their lives. To better understand the lack of the longevity-fecundity trade-off and aging in the termite *Cryptotermes secundus* (Kalotermitidae), whole body transcriptomes of old and young individuals were compared, and a time-series analysis was done using transcriptomes of queens ranging in reproductive age from one to 14 years. Significantly differentially expressed transcripts between old and young individuals were contrasted between queens, kings and workers. Our results revealed unique expression patterns for each caste, with some similarities between the reproductives. Both the kings and queens showed evidence of aging, while workers did not age. This is in line with life history theory, as workers are totipotent immatures in this species which develop with a high probability into reproductives. The long-run time-series analyses allowed us to identify reliable aging markers. These results were compared with similar aging studies of the fruit fly *Drosophila melanogaster*, another termite species with a high social complexity, and one ant species. We found few age-associated differentially expressed genes in common between the different species. We provided evidence for aging in *C. secundus* reproductives but not in the workers, which is in accordance with life history theory predictions. Our study contributes to a better understanding of the absence of the longevity-fecundity trade-off in eusocial insects and the evolution of aging.