



Sociality Impact on Genome Evolution

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Background: Eusociality, one of the major evolutionary transitions, has arisen independently in many animal clades especially in insects. While many efforts have been applied into the quest to find the genomic basis leading to such a transition, little attention has been put on the consequences of eusociality on genome evolution.

Adapting to eusociality has a drastic impact on the population structure, notably a reduction of the sensus effective population size (N_e) (decreased number of individual reproducing within a population), which has consequences for evolutionary processes. Indeed, the reduction of N_e is known to reduce selection strength leading to a higher polymorphism and increased evolutionary rates.

Objectives: The present project is set to compare several genomic features (such as evolutionary & mutation rates, gene GC content, codon usage bias, and recombination rates) among Blattodea species being either solitary (cockroaches) or eusocial (termites).

Requirements:

- Interest in population genomics and genome evolution
- Basic knowledge of molecular evolution
- Basic knowledge of command line and scripting
- Ability to work independently

Methods: Estimation of dN/dS, codon usage bias, GC content will be calculated using available genomes from termites and cockroaches. Comparison will be carried out using several packages in R.

Supervision: Dr. Bertrand Fouks, b.fouks@uni-muenster.de, Molecular Evolution and Bioinformatics Group (<http://bornberglab.org/>).