

OR102*Population-level differentiation between Yellow Crazy Ant supercolonies in South-East Asia***Jochen Drescher**, Heike Feldhaar, Nico Bluthgen, Thomas Schmitt, Damayanti Buchori, Stefan Scheu

The Yellow Crazy Ant (YCA) *Anoplolepis gracilipes* ranks among the most destructive social insect invaders in South-East Asia and the Indopacific. It is believed that their ability to form vast polydomous, polygynous supercolonies is the key to their ecological success. This is particularly true in Arnhem Land, NE-Australia, where a single supercolony spans up to 80km across, covering more than 15.000km² in total (Gruber et al. 2011). In Sabah, North-East Borneo, however, YCA population structure is very different. Here, YCA supercolonies are no larger than 300m across and many supercolonies of varying sizes compete for resources within the same population. Using data from two independent populations of supercolonies, we will demonstrate that YCA supercolonies in NE-Borneo are genetically and chemically (Cuticular Hydrocarbons) differentiated to such an extent that it suggests lack of gene flow between them. We argue that positive feedback between behavioral, genetic and chemical differentiation will further intensify intercolonial segregation, possibly leading to reproductive isolation between different YCA supercolonies and thus, speciation. Preliminary experiments using a limited set of laboratory colonies suggest a reproductive barrier between distantly related YCA supercolonies. It is currently unclear whether this is due to worker-policing or the inability of queens mated with males from foreign supercolonies to produce vital offspring. We aim at further studying the potential reproductive barrier between YCA supercolonies along a gradient of genetic similarity by cross-breeding males and queens from variably related supercolonies. To identify suitable supercolonies, we performed a population genetic analysis of YCA populations in Jambi, Central Sumatra, sampling from over 30 supercolonies that are as far as 100km apart. We thus present first genetic data on that population and discuss the experimental design with which we intend to identify the degree of genetic distance at which males and queens from different YCA supercolonies are reproductively isolated.