

The manuscript “Relaxation of purifying selection suggests low effective population size in eusocial Hymenoptera and pollinating bees“ by Weyna & Romiguier uploaded to bioarxiv and under review for PCI Evolutionary Biology deals with the evaluation of causes and consequences of the evolution of sociality in Hymenoptera, which occurred repeatedly. I will outline major pros and cons of the manuscript but due to the lack of line numbers I cannot address all minor issues and typing errors.

In the second paragraph of the results section you mention that only *B. rupestris* represents a parasitic species amongst the species with elevated dN/dS. This is not completely true as *Sphcodes* is a parasitic species of Halictidae and Colletidae.

In the section Antophila bees and high rates of protein evolution you claim to have 5 eusocial species represented while these are effectively only four species and one socially parasitic species (*B. rupestris*). This should be corrected as socially parasitic bumblebees show a range of different levels of gene evolution (e.g. Erler et al. 2014 Infect Genet Evol; Helbing & Lattorff 2016 Infect Genet Evol; Fouks & Lattorff 2016 Front Ecol Evol).

For differences in recombination rates you might also cite Jones et al 2019 Mol Biol Evol.

The argument of inbreeding as prerequisite for creating high relatedness and thus favouring the evolution of sociality needs a valid explanation in the light of the genetic load at the sex locus. Single locus sex determination (SLSD) has been shown to occur in a range of species with the exception of the few parasitoid species that might have a whole genome sex determination system. As also a range of very basal members of the Hymenoptera have the SLSD, it might be the ancestral state.

My major point here is, why you have not chosen more eusocial taxa to be sampled? Quite a range of sequenced genomes are available which could have been utilized (okay, the gene annotation is a bit more complicated, but for some of them also transcriptomes are available). Certainly there will be variation within the eusocial species as well and they might differ in important aspects as annual vs perennial colonies, colony size, at what age sexuals are produced (generation-time effect, some ants produce sexuals after years, bumblebees produce them after a few months). Thus, increased sampling within the eusocial lineages might cover more of these aspects.

Furthermore, I wondered that there is no link to the distribution of species. For Antophila you use the argument that pollen collection might constraint the N_e because of the limited availability of this resource. Agreed, but this might only be true for species of temperate regions, while in the tropics/subtropics pollen might be a less limited resource. Furthermore, the number of eusocial species (relative number) is higher in tropical/subtropical habitats compared to temperate regions (e.g. stingless bees only occur in such regions, the hotspot of honeybee evolution and diversification is in South-East Asia). There is also an effect for the occurrence of nest parasites of social bees, wasps, and ants, which are more frequent in temperate regions (Wcislo 1987 Biol Rev) probably to factors like seasonality and hence predictability of developmental stage of a colony to attack. Hence external environments might affect certain characteristics that in turn might have an influence of sociality but also pollen collection. I suggest to infer the distribution data for at least the species of interest or at least discuss this issue.