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the neuropeptide hormones tachykinin and myosuppressin are two neuropeptides involved in aggression and social behaviour [63 and 64]. tachykinin has also been shown to be important for brood parasitism, and to be under strong selection in brood-parasitic bees [37]. in the ant species *temnothorax ambiguus*, brood parasites, the slavemakers are shown to have higher amounts of myosuppressin in their hypopharyngeal glands [65]. furthermore, in the slavemaker species *t. americanus*, the amounts of myosuppressin in the hypopharyngeal glands and the brain are much higher than in the host species *t. albipennis* [66]. the slavemaking ant *t. americanus*, was described to not be able to feed themselves, and they completely rely on the care of their enslaved host workers [30]. in contrast, in the host species *t. albipennis*, the worker caste is highly polymorphic and shows great diversity in the antennal morphology [40]. this great variation in the morphology and physiology of the worker caste could be correlated with the behavioural differences of the species. however, the slavemaker also has some morphological differences in the antennae, mandibles and thorax compared to its host. these morphological differences are small, but show the trend of the reduced body size of slavemakers [44, 47]. therefore, the species specific differences between slavemakers and hosts might also be caused by body size differences, which would provide an alternative explanation for the evolution of social parasitism. however, no study has yet analysed the functional implications of the size difference between the host and the slavemaker.

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in the future, it will be interesting to see whether the identified slavemaker-specific genes are involved in the slavemaking behaviour, and in particular if caste-specific functions are involved. as social parasites have to overcome a variety of defence mechanisms of their host species, caste-specific genes might be involved in this process. the identification of these genes might allow for the development of new approaches to control social parasitism, for example by the genetic modification of social parasites. the phylogenetic tree was built by aligning the orthologous genes of the four host and the three slavemaker species via muscle (version 3.8.31) with default settings, followed by removal of the poorly aligned sequence. codeml was then run with default settings, except for the foreground branch model (model=0, nssites=0) and branch model (model=2, nssites=2).codeml was run twice for each foreground branch, once with and once without the foreground branch as foreground. the output of the foreground branch analysis was used to identify positively selected genes. in case of significance, the output was used to find orthologous genes with positive selection in each of the three slavemaker species, and then subjected to a gene enrichment analysis with david 6.7 [66]. we focused on biological processes only. each of the gene sets was annotated with gene ontology terms using the david 6.7 [66] and cluego 2.2.3 [77]. the resulting go terms were visualised with r 2.14.1. we used r to create heatmaps of genes annotated with go terms for each of the three slavemakers and the three hosts. 5ec8ef588b

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