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Title:	Behaviour, Chemical Ecology And Genetic History Of Nasonia
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Abstract:	<p>The Pteromalid parasitoid wasp, <i>Nasonia</i> (Hymenoptera: Chalcidoidea: Pteromalidae), is a popular genetic model system due to its haplodiploidy, ease of laboratory rearing and unique biology. The genus comprises of four species, <i>N. vitripennis</i>, <i>N. longicornis</i>, <i>N. giraulti</i>, and <i>N. oneida</i>. The hosts that <i>Nasonia</i> females parasitize are available as a patchy resource and each female often parasitizes multiple hosts. Despite a female-biased offspring sex ratio, male wasps experience intense competition to access emerging females as mating is usually restricted to the natal host patch. Therefore, males are expected to develop additional reproductive strategies to maximize individual fitness. This dissertation uncovers a previously unknown reproductive strategy in the males of <i>Nasonia</i>, especially the capability to identify which fly hosts contain adult females inside. Behavioural assays revealed that only one out of the four species, <i>N. vitripennis</i>, can distinguish which hosts specifically have adult female wasps, indicating a species-specific reproductive strategy. Results of gas chromatography-mass spectrometry analyses and behavioural data suggest that female-signature cuticular hydrocarbons (CHCs) are used as chemical cues, possibly emanating from within the host. <i>N. vitripennis</i> has a cosmopolitan distribution whereas the other species (<i>N. longicornis</i>, <i>N. giraulti</i> and <i>N. oneida</i>) have only been found in the western North America and eastern North America, respectively. However, the geographic origin of <i>Nasonia</i> remains unknown. In theory, the world-wide distribution of <i>N. vitripennis</i> is thought to be anthropogenic because it is a generalist that parasitizes many fly species that have undergone range expansions primarily driven by anthropogenic causes, which has further confounded the origin of the <i>Nasonia</i> clade. The emergence of the <i>Nasonia</i> genus has been placed in the early Pleistocene era around 1 million years ago (MYA), with <i>N. vitripennis</i> diverging first and the other three species diverging around 0.4 million years ago. This dissertation also tries to resolve the divergence and colonization of <i>Nasonia</i>. The patterns of molecular evolution were analysed for the mitochondrial and nuclear genome sequence data obtained from multiple strains of <i>Nasonia</i> populations sampled across the world (divided into three major continents, Europe, North America and India). The results suggest that the oldest lineage is that of Europe (from Italy) as it shows the oldest divergence time of 0.28 MYA. The divergence time estimates and phylogeographic pattern indicate a relatively recent <i>N. vitripennis</i> spread in North America through the Pacific, from Eurasia.</p>
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