

Improving the Biocontrol of the Argentine Stem Weevil; Using the Parasitic Wasp *Microctonus hyperodae*

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Abstract : The Argentine stem weevil (ASW; *L. bonariensis*) is an economically important pasture pest in New Zealand, which causes about \$200 million of damage per annum. *Microctonus hyperodae* (Mh), a parasite of the ASW in its natural range in South America, was introduced into New Zealand to curb the pasture damage caused by the ASW. Mh is an endoparasitic wasp that lays its eggs in the ASW halting its reproduction. Mh was initially successful at preventing ASW proliferation and reducing pasture damage. The effectiveness of Mh has since declined due to decreased parasitism rates and has resulted in increased pasture damage. Although the mechanism through which ASW has developed resistance to Mh has not been discovered, it has been proposed to be due to the different reproductive modes used by Mh and the ASW in New Zealand. The ASW reproduces sexually, whereas Mh reproduces asexually, which has been hypothesised to have allowed the ASW to 'out evolve' Mh. Other species within the *Microctonus* genus reproduce both sexually and asexually. Strains of *Microctonus aethiopoides* (Ma), a species closely related to Mh, reproduce either by sexual or asexual reproduction. Comparing the genomes of sexual and asexual *Microctonus* may allow for the identification of the mechanism of asexual reproduction and other characteristics that may improve Mh as a biocontrol agent. The genomes of Mh and three strains of Ma, two of which reproduce sexually and one reproduces asexually, have been sequenced and annotated. The French (MaFR) and Moroccan (MaMO) reproduce sexually, whereas the Irish strain (MaIR) reproduces asexually. Like Mh, The Ma strains are also used as biocontrol agents, but for different weevil species. The genomes of Mh and MaIR were subsequently upgraded using Hi-C, resulting in a set of high quality, highly contiguous genomes. A subset of the genes involved in mitosis and meiosis, which have been identified through the use of Hidden Markov Models generated from genes involved in these processes in other Hymenoptera, have been catalogued in Mh and the strains of Ma. Meiosis and mitosis genes were broadly conserved in both sexual and asexual *Microctonus* species. This implies that either the asexual species have retained a subset of the molecular components required for sexual reproduction or that the molecular mechanisms of mitosis and meiosis are different or differently regulated in *Microctonus* to other insect species in which these mechanisms are more broadly characterised. Bioinformatic analysis of the chemoreceptor complement in *Microctonus* has revealed some variation in the number of olfactory receptors, which may be related to host preference. Phylogenetic analysis of olfactory receptors highlights variation, which may be able to explain different host range preferences in the *Microctonus*. Hi-C clustering implies that Mh has 12 chromosomes, and MaIR has 8. Hence there may be variation in gene regulation between species. Genome alignment of Mh and MaIR implies that there may be large scale genome structural variation. Greater insight into the genetics of these agriculturally important group of parasitic wasps may be beneficial in restoring or maintaining their biocontrol efficacy.

Keywords : argentine stem weevil, asexual, genomics, *Microctonus hyperodae*

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