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Dr. Jürgen Gadau Universität Wuerzburg- Biozentrum Institut für Verhaltensphysiologie und Soziobiologie Am Hubland 97074 Wuerzburg Germany

Dear Dr. Gadau (and Dr. Werren, PI),

I was very glad to hear of your group's efforts to generate a draft genomic sequence for the parasitoid wasp, *Nasonia vitripennis*. As a honey bee researcher, I can say that the draft sequence and assembly for honey bee has greatly accelerated our own projects and those of other applied and basic-research labs. I think that a similar resource for a *Nasonia* would do the same for your community. The parasitoid wasps rival the honey bee as a group providing worldwide benefits to agriculture. While not the most commonly used parasitoid species in agriculture, *Nasonia vitripennis* has been the primary model species for the group for several decades. This species provides an extraordinary base in terms of understanding development, genetics, species boundaries, and (recently) genomics.

Selfishly, a genomic resource for a parasitoid wasp would also be a boon for research on honey bees and other social Hymenoptera. The highly social species (social wasps, bees, and ants) are all derived from branches of the diverse parasitoid wasps. We would likely use this sequence both for improving gene predictions in honey bees and understand syntenic issues, and for a better understanding of how social insects differ from their non-social relatives. One specific area for which having a *Nasonia* species would is in identifying pathway members and effectors in the honey bee immune response. We have had some success using putative fly orthologs, but having a species closer by half (120 m.y. divergence) should greatly increase the power to find and confirm functional immune genes. This would help both for applied questions in bees and wasps and in effecting one of the goals of both genome projects; to develop these species as new models for understanding innate immunity and disease in humans.



Bee Research Laboratory Building 476, Beltsville, MD 20705 Looking toward the future, having annotated genomes for one or more parasitoid wasps will be a wonderful anchor for genomic projects in each of the three primary eusocial branches for the Hymenoptera (an argument you have made well in your early work on genomics in this important insect order).

In short, this is a well conceived and important project, and I wish you and Dr. Werren every success in getting it funded and carried out.

Best wishes, Ap 50000

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