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der Universität Würzburg**  
Lehrstuhl für Verhaltensphysiologie und Soziobiologie (Zoologie II)

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Würzburg, den 13.3.2004

**To whom it may concern:**

This letter is in strong support of sequencing of the *Nasonia vitripennis* genome. *Nasonia* would be the second Hymenopteran species and the first solitary species for which we would than have a genome sequence. *Nasonia* belongs to the so called parasitic wasps which are extremely species rich and ecologically very important.

For the last six years I (Jürgen Gadau) used *Nasonia* as a model organism for the study of speciation and the evolution of adaptive traits. During this time multiple collaborators and I developed genetic tools (e.g. linkage maps, chromosomal microdissection, chromosomal anchored microsatellites, etc.) to study the genetic basis and architecture of adaptive traits using a QTL approach. For the next steps like positional cloning and identification of genes underlying our QTL and a detailed analysis of the interaction within the genome we would profit greatly by the availability of a complete genome sequence. Additionally, since we are also interested in a population genomics approach to identify regions with signs of a recent selective sweep we would gain a lot by an annotated genome sequence where we could pick candidate genes or regions including coding and non-coding sequences.

We are currently planning to concentrate on chromosome 1 and 4 and will develop partial BAC-contigs of these chromosomes around our QTL regions. Additionally, we are

also mapping identified genes into our linkage map in an effort to create scaffolds for our contigs.

In collaboration with the **Department for Bioinformatics at the University of Würzburg (Thomas Dandekar)** we would be interested to join the common effort to annotate genome of *Nasonia*. Our department has a long standing interest in comparative metabolic modeling. A number of such bioinformatics projects building both on our own and on other genome annotation efforts has been carried out in the department. We would use our expertise both in getting a complete annotation of all metabolic enzymes as well as for the overall metabolic network structure of *Nasonia*. A further interest is the identification and analysis of *Nasonia* specific protein families, in particular kinases or receptor families. For both points we are willing to give our expertise as well as to join into fruitful collaborations with other partners interested in the same areas.

Dr. Jürgen Gadau

Prof. Dr. Thomas Dandekar