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10 March, 2004

Dear Jack

Thank you for telling me about the initiative to sequence the genome of the parasitoid wasp *Nasonia vitripennis*. I think it is a very important and timely project, and one for which there will be great support in the UK.

Thanks to the work of many laboratories, yours prominently amongst them, *Nasonia* has become a model system for investigating a whole range of questions in evolutionary genetics and evolutionary ecology, in particular the genetics of speciation and the interaction between nuclear genes and those that are inherited in a non-Mendelian manner because they reside on such elements as mitochondria, B chromosomes, or maternally-inherited symbionts and pathogens. The availability of the full-genome sequence would revolutionise what could be done, and pave the way for a much more mechanistic approach to these and many other problems.

Sequencing a second haplodiploid hymenopteran (in addition to the honey bee) also raises a host of exciting questions in comparative genomics. One that immediately comes to mind is the study of sex determination in the two species; how the recently discovered molecular mechanism in the bee has been modified in the inbreeding *Nasonia*. Finally, and a little less directly, the first "Parasitica" genome would be an immensely valuable resource for the whole parasitoid-research community; it would help my group immensely in studying related parasitoids attacking aphids. And this would not only have implications for pure science; chalcidoid wasps are used widely in biological control, where they can be of huge economic value (for example, the programme that released a chalcidoid to control a cassava pest is estimated to have cost \$47M and to have saved \$9-20B).

I very much hope this initiative is successfully.

With best wishes

Yours sincerely



HCJ Godfray