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Dear Sir/Madam,

We give our strongest possible support for the *Nasonia* genome initiative.

We are using *Nasonia vitripennis* as a model organism for studying adaptation and the evolutionary process. Specifically, we are using the way in which individuals control the sex of their offspring in response to environmental conditions, as a model trait for examining the precision with which adaptation can produce 'perfect' organisms.

If the *Nasonia* genome initiative goes ahead, then this will offer us exceptional opportunities for studying the genetic basis of this behaviour. Specifically, we will use developing gene expression technologies to assay and identify the genes expressed during sex allocation under different environmental conditions. This work is of particular significance because this is one of the best understood animal behaviours in the world – from the point of view of how it influences Darwinian fitness, but also mechanistically with the cues and sensory processes involved.

In addition, the two sister species to *N. vitripennis*, *N. giraulti* and *N. longicornis*, differ in their ecology and sex allocation patterns. This means we can also consider the comparative genomics of adaptation by extending our work to these species. Consequently, this gives us an almost unique opportunity to study the genetic basis of an incredibly well understood trait. This represents a major step forward in the growing field of ecological genomics.

Yours sincerely

Stuart West & David Shuker