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Dear Jack:

I am very enthusiastic about the prospects for full genome sequencing of Nasonia. I have conducted QTL mapping and gene discovery projects in many species of plants and insects over the last twenty years. The successful identification of major genes responsible for complex traits depends to some extent on the technology employed but the organism itself is usually the limiting factor. The powerful model systems of the plant community (maize and Arabidopsis) are difficult to match in animals but Nasonia comes close. Nasonia has a short generation time, is easily maintained under laboratory conditions and is amenable to controlled crosses. The males are haploid, making genetic mapping straightforward. Interspecific crosses are possible and the offspring of such crosses are viable. In addition, a moderately small genome size (~ 335 Mb) makes Nasonia an excellent choice for a positional cloning project.

I am also eager to participate in the microarray projects we have discussed. During the last two years I have worked on the statistical analysis of microarrays using Affymetrix and other technologies in *Arabidopsis thaliana*, *Drosophila melanogaster* and *Aedes aegypti*. The Nasonia project offers the opportunity to use this technology for focused gene discovery.

 As you know, I am the PI on an NSF grant that funded production of the Nasonia BAC library, and I have the library now in my lab. We can screen the Nasonia BAC library filters with radiolabeled amplicons from primers for clones selected from regions containing QTL determinants for wing cell size. We will then end sequence all the positive BAC clones, build contigs, and then design new DNA markers for testing in segregating populations. Assuming that the library has a low frequency of gaps, we have a good chance at identifying the BAC clones containing the genes of interest.

The statistical design of microarray projects depends on the technology and the hypothesis under investigation but I can bring considerable experience to the problem and would be delighted to work on such a promising insect system for this technology.

Sincerely,

Jeanne Romero-Severson
Associate Professor