

## Genome size variation and novel sex determination in *B. treatae*

Within species variation in genome size has received little attention despite growing evidence of its prevalence in nature. Along with colleagues J. Spencer Johnson, (TAMU), S. E. Egan (Notre Dame) and NSF REU student, Carl Hjelman (Augustana College) we are investigating genome size variation in the haplodiploid and cyclically parthenogenic gall wasp, *B. treatae*. Within populations we are examining genome size among individuals and families produced by androphores and gynophores (all female or all male producing females) and between generations (sexual or asexual). Among populations we are examining genome size in relation to host plant affiliation (i.e., *Quercus fusiformis*, *Q. virginiana*, and *Q. geminata*) and geographic region. Our results demonstrate significant differences in genome size associated with ecology and lifecycle stage and suggest a novel sex determining system. We are further extending this research by using our results to construct testable models of genome size determination in this species and are currently conducting reciprocal crosses among gall-former populations to test model predictions.

