

# Can the erosion of allelic richness explain population bottlenecks in Hymenoptera reared for experiments?

Logan LEHMANN  
Module AF-23, SS 2021

## Abstract

In biological control experiments involving hymenopteran parasitoids, it is necessary to maintain a sufficiently large and genetically healthy population, so that genetic depression does not become the limiting factor. However, laboratory conditions exacerbate certain particularities of these species' reproduction cycle. First, since parasitism is a necessary part of this cycle, only successful offspring is kept as the experiment moves forward. This introduces a selection pressure, similar to that found in nature. Second, in these species, females store the sperm and use it on a case-by-case basis, deciding for each egg whether it should contain a male or a female embryo. Females generally have enough sperm after their first mating and so carry the genetic information of only one individual. This can be seen as a sort of gateway: in the laboratory, the population is isolated and its prospects in terms of genetic health are restricted to what is carried by the mated females. As the generations move forward, allelic richness, which is the number of alleles of one gene existing in a population, is drastically reduced.

During the parasitoid specificity experiments conducted at CABI in 2020, important fluctuations were seen in the sex-ratio across multiple populations. The parasitoid wasp *Chelonus insularis* (Braconidae) was tested on two Noctuid hosts (moths), *Spodoptera frugiperda* (the fall armyworm) and *Spodoptera exigua* (beet armyworm). In the most striking case, the sex-ratio fluctuated from 0.5 to 37! This was cause for concern, as the absence of females was believed to have caused the extinction of a previous wasp colony. Possible factors in the laboratory setting were investigated (climate stability, diet quality) but no definite explanation was found. Therefore, the cause must be looked for elsewhere.

In many Hymenopterans, sex is determined at a single locus in the genome. This mechanism is named sl-CSD. Quite simply, embryos that are hemizygous at that locus develop into males. Ones that are heterozygous develop into females. Unfertilized eggs laid by female *C. insularis* only have one set of chromosomes. Therefore, they develop into males. However, there is the possibility to have diploid males, because embryos that are homozygous at the sex-determining locus also develop into males. Diploid males are considered to be rare and have null fitness, because they are infertile. In honeybees, they are killed by workers upon hatching. However, there is an argument that in some species, diploid males could survive and remain undetected in the population. A 2007 study found that in the parasitoid wasp *Cotesia vestalis*, diploid males could father (infertile) triploid daughters. Overall, diploid males are a waste of resources at the scale of the population. In nature, the dispersion of individuals is believed to defuse the potential burden of sl-CSD.

In order to see whether diploid males could be cause of the observed sex-ratio fluctuations, a computer simulation was designed. The simulation takes as input the genotypes of males and females in a population at generation 0, and outputs the number of different genotypes, or allelic combinations, available after  $n$  generations. The simulation was run four times with the same base population, but each time adding respectively males, females or both, from an external population with entirely different alleles.

With this simple method, we can show that even though the number of available diploid male genotypes compared to the number of all male genotypes remains the same, it does represent a smaller proportion of all available genotypes when new alleles are brought from the outside. This proportion is 33% without, and 20% with outbreeding.

The actual effects of this finding remain to be determined, and might vary between species. The sex-allocation decision rests on the females, who follow precise strategies involving environmental parameters, population structure, and the cost of each egg laid.

## References

1. Wilgenburg, Ellen van, Gerard Driessen, and Leo W Beukeboom. "Single Locus Complementary Sex Determination in Hymenoptera: An 'Unintelligent' Design?" *Frontiers in Zoology* 3 (January 5, 2006): 1. <https://doi.org/10.1186/1742-9994-3-1>
2. Gross, Louis J. "Population Bottlenecks: Heterozygosity vs. Allelic Diversity." *Alternative Routes to Quantitative Literacy for the Life Sciences*, July 31, 2000. <http://www.tiem.utk.edu/~gross/bioed/bealsmodules/bottlenecks.html>
3. Greenbaum, Gili, Alan R. Templeton, Yair Zarmi, and Shirli Bar-David. "Allelic Richness Following Population Founding Events – A Stochastic Modeling Framework Incorporating Gene Flow and Genetic Drift." *PLOS ONE* 9, no. 12 (December 19, 2014): e115203. <https://doi.org/10.1371/journal.pone.0115203>
4. Boer, J. G. de, P. J. Ode, L. E. M. Vet, J. B. Whitfield, and G. E. Heimpel. "Diploid Males Sire Triploid Daughters and Sons in the Parasitoid Wasp *Cotesia Vestalis*." *Heredity* 99, no. 3 (September 2007): 288–94. <https://doi.org/10.1038/sj.hdy.6800995>

## Figures



**Fig. 1:** When conducting specificity experiments, the **rearing system** (red) takes two inputs, one of which flows from its own single output through the experiment runs (left). **Allelic richness** (green) could be a factor in the presence of infertile diploid males in the population. Without fertile males to mate with, females can only produce male offspring.