

Bio E1a Laboratory – TF: Clark Magnan (Section Monday-F)
Lab 5 Writeup: Ant/Wolbachia PCR Analysis
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genus Tetramorium – pavement
genus Camponotus – carpenter

	Infected	% Infected	Uninfected	% Uninfected
Genus Tetramorium	42	43%	55	57%
Genus Camponotus	51	73%	19	27%

Table 1: Infection rates of Wolbachia in ants by genus. Two genera of ant, Tetramorium and Camponotus, were analyzed via PCR, using an insect-specific primer as a control and a Wolbachia-specific primer to identify infected samples.

Discussion

The X^2 was calculated to be 14.40, greater than the calculated critical value 3.841 (see Appendix for calculations.) As such, the null hypothesis H_0 must be rejected, and the alternate hypothesis H_1 that the populations from the two sampled genera are not homogeneous with respect to infection by Wolbachia must be conditionally accepted.

This experiment could be refined by including samples of ants from a broader physical sample area (as the majority of ants included in this study are from the greater Boston area.) It could also be refined by examining more than two genera of ant, or by grouping into populations by factors other than genus. For example, grouping ants into populations based on other observed phenotypes could yield statistical evidence toward the genotypic linking of traits, i.e. the distance between genes. You could also test hypotheses of antibiotic treatment by treating a subset of the ants with such a hypothesized treatment and measuring the distribution of infection of their offspring.

Appendix: X^2 calculations

The following data was used to calculate the X^2 value:

	Category 1 (Infected)	Category 2 (Uninfected)	Totals
Population T (Genus Tetramorium)	42	55	97
Population C (Genus Camponotus)	51	19	70
Totals	93	74	167

Number of populations $r = 2$. Populations are: $r \in \{T, C\}$.

Number of categories per population $c = 2$. Categories are: $c \in \{1, 2\}$.

$$\begin{aligned}\text{Degrees of Freedom } DF &= (r-1) * (c-1) \\ &= (2-1) * (2-1) \\ &= 1 * 1 \\ &= 1\end{aligned}$$

Total number of data points in sample data set $n = 167$

Expected Frequency count by row r , and category c : $E[r,c] = n_r * n_c / n$

$$\begin{aligned}E[T,1] &= n_1 * n_T / n \\ &= 93 * 97 / 167 \\ &= 54.02\end{aligned}$$

$$\begin{aligned}E[T,2] &= n_2 * n_T / n \\ &= 74 * 97 / 167 \\ &= 42.98\end{aligned}$$

$$\begin{aligned}E[C,1] &= n_1 * n_C / n \\ &= 93 * 70 / 167 \\ &= 38.98\end{aligned}$$

$$\begin{aligned}E[C,2] &= n_2 * n_C / n \\ &= 74 * 70 / 167 \\ &= 31.02\end{aligned}$$

Chi-squared value $X^2 = \text{SUM}((O[r,c] - E[r,c])^2 / E[r,c])$ for observed value $O[r,c]$ and expected value $E[r,c]$ summed over each population r and category c .

$$\begin{aligned} X^2 &= (O[T,1] - E[T,1])^2 / E[T,1] \\ &\quad + (O[T,2] - E[T,2])^2 / E[T,2] \\ &\quad + (O[C,1] - E[C,1])^2 / E[C,1] \\ &\quad + (O[C,2] - E[C,2])^2 / E[C,2] \\ &= (42-54.02)^2 / 54.02 \\ &\quad + (55-42.98)^2 / 42.98 \\ &\quad + (51-38.98)^2 / 38.98 \\ &\quad + (19-31.02)^2 / 31.02 \\ &= 2.67 + 3.36 + 3.71 + 4.66 \\ &= 14.40 \end{aligned}$$

For $DF=1$, significance value $S=0.05$, the X^2 critical value = 0.05 (as specified in Table 2 of lab assignment).

X^2 value $14.40 >$ critical value 0.05 .

Sources

Infection data was collated and provided by the teaching staff of the Fall 2008 section of Harvard Extension school course Biology E-1a.