

**Appendices to J Poll Ecol 37(19), Zenga et al.**

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Table S1. A Zero inflated with Gaussian distribution GLM was used to examine the relationship between the copy number of pathogens infecting *A. hesperia*, the type of pathogens, and the sex of the individuals. The model provided estimates, standard errors (SE), and p-values for each parameter. The Akaike Information Criterion (AIC) value for this model was 694.60. In comparison, a simple Gaussian model with link “identity”, had a higher AIC value of 1722.28.

Model was constructed as follow:

*number of copies(log10) SEX+TYPE +Pathogen, Ziformula = ~1+SEX +TYPE + Pathogen, family = gaussian (link = "identity")*

The results of the zero-inflation model show that the DWV and Nosema ceranae factors decrease the probability of obtaining zero pathogen copies, while in newly emerged individuals, the probability of obtaining zero pathogen copies is higher.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Conditional model |  |  |  |  |
| Coefficients: | Estimate | SE | *t value* | *p value* |
| Intercept (Female,Free ranging, ABPV) | 4.03  | 0.51  | 7.93 | 0.00 |
| SEX: Male | 0.24  | 0.19  | 1.25  | 0.21 |
| TYPE: Newly-emerged | -2.12  | 0.24  | -8.91  | 0.00 |
| AmFV | -0.72  | 0.77 | -0.94  | 0.35 |
| BQCV | 0.18  | 0.67  | 0.27  | 0.79 |
| *C.bombi* | -0.26  | 0.66  | -0.39  | 0.69 |
| CBPV | 0.46  | 0.55  | 0.84  | 0.40 |
| DWV | 0.23  | 0.53  | 0.44  | 0.66 |
| *N.ceranae* | 1.11  | 0.54  | 2.05  | 0.04 |
| SBV | -0.08  | 0.67  | -0.12  | 0.90  |
|  |  |  |  |  |
| Zero-inflation model: |  |  |  |  |
| Intercept (Female,Free ranging, ABPV) | 1.88  | 0.54  | 3.47 | 0.00 |
| SEX: Male | 0.35  | 0.28  | 1.25 | 0.21 |
| TYPE: Newly-emerged | 1.85  | 0.32  | 5.66 | 0.00 |
| AmFV | 0.29  | 0.80  | 0.37 | 0.71 |
| BQCV | -0.25  | 0.71  | -0.35 | 0.73  |
| *C.bombi* | -0.47  | 0.69  | -0.68 | 0.50 |
| CBPV | -1.97  | 0.61  | -3.2 | 0.00 |
| DWV | -4.44  | 0.66  | -6.74 | 0.00 |
| *N.ceranae* | -2.93  | 0.61  | -4.78 | 0.00 |
| SBV | -0.25  | 0.71  | -0.36 | 0.72 |

Table S2. Model estimate, standard error (SE), and *p value* of Poisson GLM. The AIC value of model was 153.69.

|  |  |  |  |
| --- | --- | --- | --- |
| Coefficients: | Estimate | SE | *p value* |
| Intercept (Female, *Bacillus licheliniformis*) | 0.640 | 0.511 | 0.211 |
| Male | 0.103 | 0.203 | 0.612 |
| *Bacillus thuringiensis* | -0.640 | 1.123 | 0.569 |
| *Enteococcus durans* | -0.743 | 1.122 | 0.508 |
| *Enterobacter aerogenes* | -0.693 | 0.866 | 0.424 |
| *Enterococcus faecalis* | -0.288 | 0.764 | 0.706 |
| *Fructobacillus fructosus* | 0.811 | 0.601 | 0.177 |
| *Gilliamella apicola* | 0.560 | 0.627 | 0.372 |
| *Gilliamella bombi* | 0.916 | 0.592 | 0.121 |
| *Gilliamella intestini* | 0.355 | 0.770 | 0.645 |
| *Gilliamella mensalis* | -0.693 | 0.866 | 0.424 |
| *Lactobacillus acetotolerans* | -0.288 | 0.764 | 0.706 |
| *Lactobacillus Firm-4* | 1.253 | 0.567 | 0.027 |
| *Lactobacillus Firm-5* | 1.179 | 0.572 | 0.039 |
| *Lactobacillus fructivorans* | 0.693 | 0.612 | 0.258 |
| *Lactobacillus kunkeei* | -0.288 | 0.764 | 0.706 |
| *Lactobacillus lindneri* | -0.640 | 1.123 | 0.569 |
| *Pseudomonas aeruginosa* | -0.640 | 1.123 | 0.569 |
| *Snodgrassella alvi* | 1.253 | 0.567 | 0.027 |
| *Streptococcus thermophilus* | 0.223 | 0.671 | 0.739 |
| *Staphylococcus epidermidis* | -0.640 | 1.123 | 0.569 |
| *Streptococcus epidermidis* | 0.053 | 0.873 | 0.952 |
| *Streptococcus saprophiticus* | -0.050 | 0.871 | 0.954 |

Table S3. Percentage of pollen grains composition for each analyzed specimen.

|  |  |  |  |
| --- | --- | --- | --- |
| ID sample | Compositae T form 1 | Compositae T form 2 | Others |
| Piedmont 1 | 96,0 | 4,0 | 0,0 |
| Emilia-Romagna 1 | 100,0 | 0,0 | 0,0 |
| Piedmont 2 | 59,3 | 28,4 | 12,3 |
| Campania 1 | 99,2 | 0,0 | 0,8 |
| Piedmont 3 | 91,8 | 7,9 | 0,2 |
| Piedmont 4 | 50,9 | 49,1 | 0,0 |
| Piedmont 5 | 100,0 | 0,0 | 0,0 |
| CREA 1 | 99,9 | 0,0 | 0,1 |
| CREA 2 | 97,3 | 2,7 | 0,0 |
| CREA 3 | 100,0 | 0,0 | 0,0 |
| CREA 4 | 99,8 | 0,0 | 0,2 |
| CREA 5 | 82,9 | 17,0 | 0,1 |
| CREA 6 | 99,8 | 0,2 | 0,0 |
| CREA 7 | 99,9 | 0,1 | 0,0 |
| CREA 8 | 100,0 | 0,0 | 0,0 |
| CREA 9 | 91,0 | 9,0 | 0,0 |
| CREA 10 | 99,9 | 0,1 | 0,0 |
| CREA 11 | 100,0 | 0,0 | 0,0 |