Variation of *Nosema* levels among sub-families within colonies

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Variation in infection levels of *Nosema ceranae* is high among individual bees within a single colony. We explored why this occurs and if there is potential for using this variation for breeding for resistance to *Nosema*.

Approach

In order to test if genetic resistance to *Nosema ceranae* exists among honey bees, we compared pathogen levels among sub-families within ten honey bee colonies, five of the Russian lineage and five of the Italian lineage. We predicted that we would find variation in levels of *Nosema* within individual colonies and that those colonies with higher numbers of sub-families would have higher variation in resistance to *Nosema*.

Short-term goal: Determine stock differences in *Nosema* variation as it relates to sub-family level variation to resistance within single colonies.

Long term goal: Breed for improved resistance to *Nosema* using natural sub-family variation.

Polyandry

Polyandry: Multiple mating by a single queen results in multiple sub-families of worker bees within a single colony.

Extreme Polyandry: Single queen mates with more than 10 drones.

Benefit of Polyandry: Increased diversity within a colony may improve disease resistance.

Nosema ceranae

- Emerging pathogen of *Apis mellifera*
- Higher virulence than *N. apis*
- High levels of variability of infection levels both within and among colonies
- May contribute to colony losses

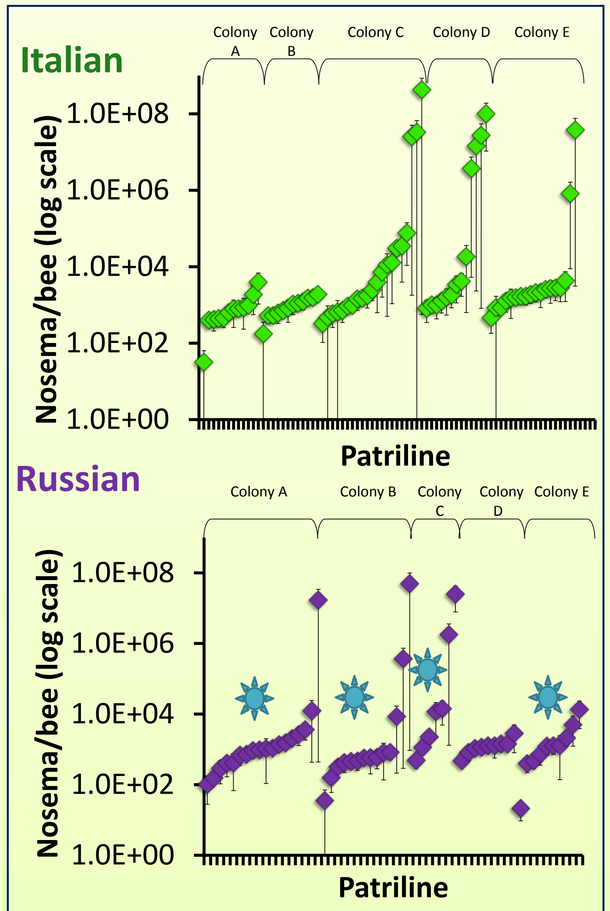
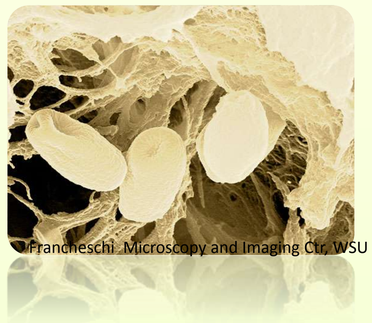


Figure 1. Patriline assignment and *Nosema* levels in 5 colonies of Italian and Russian honey bees. Each bar represents the mean and SEM of a single sub-family. A "✹"was placed over the colonies that showed significant differentiation among sub-families. Data are plotted on a logarithmic scale.

Results



- Significant differentiation of *Nosema* infection levels was found among:
  - Stocks ($P < 0.0001$)
  - Colonies of both stocks ($P < 0.0001$)
  - Russian sub-families ($P = 0.0235$)
- Positive relationship between abundance and prevalence of *Nosema* levels among Russian sub-families ($P = 0.007$) was found, meaning that as the infection level rises in a sub-family, so does the number of bees that are infected.

Conclusions

- This is the first report that variation in genetic resistance to *Nosema* occurs in honey bees, specifically Russian honey bees.
  - First documented discovery of variance in resistance to *Varroa* in honey bees was also in the parent population of the Russian stock.
- 150 generations of sympatry with *Apis cerana's* parasites is sufficient for *A. mellifera* to respond to natural selection and develop genetic variance in resistance to parasites.
- Future research will focus on using information on sub-family level resistance to *Nosema* to improve colony level resistance through breeding efforts.
- Genes/markers associated with resistance will be identified to aid breeding efforts through marker-assisted selection.

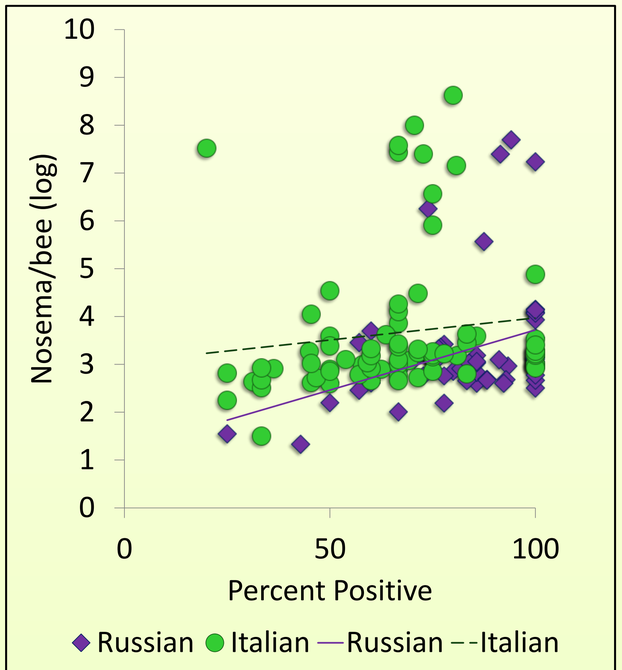


Figure 2. Scatterplot of incidence and abundance of *N. ceranae* in Russian and Italian patrilines.