



Is there a genetic component to chalkbrood susceptibility?

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Abstract Text

In Denmark a spike in the occurrence of chalkbrood has been noted in the past two years, especially along the west coast towards the North Sea. In 2022 we received samples from a number of beekeepers, from pairs of colonies with and without problem situated in the same apiary.

In the lab we took note of the occurrence of infected brood cells, by opening and removing 50+ sealed cells to confirm the health status of each colony. Each colony was later categorised as uninfected, light infected with 1 to 3 cells or heavily infect, with more than 4 cells infected. In the most extreme cases more than half the cells were infected.

Given that most samples were received by mail, the stage of the brood was not very uniform, ranging from newly infected larvae with only a light growth of *Ascosphaera apis* on parts of the larvae to mummies with the typical dark spores.

We attempted to get SNP data from sick and healthy bees, using the SmartBees chip provided by Eurofins. Unfortunately, the diseased brood contained too little or too poor DNA to give valid results. Hence, we had to base the comparison of healthy and infected colonies only on comparing healthy bee larvae or pupae from each colony type. It would have yielded more power to the analysis if we were able to compare healthy and sick larvae from the same colony.

In spite of the reservations above, our data indicate that two SNPs on chromosome 11 are having a skewed distribution when comparing bees from healthy colonies to bees from sick colonies. Previous work on susceptibility to chalkbrood has similarly found linkage to chromosome 11 (Liu *et al.* 2016, Aronstein *et al.* 2015). We are inviting colleagues to cooperate by sending samples of pupae and mummies for genetic screening from infected apiaries. We have started to develop primers that can target the found SNP regions, so that we hopefully can get data also from samples of sick larvae, when still in an early stage. Likewise, we are interested in determining if diversity of the chalkbrood pathogen, (Jensen *et al.* 2012) could be involved, provided we can find funding.

Liu, Y., Yan, L., Li, Z., Huang, W.F., Pokhrel, S., Liu, X. and Su, S., 2016. Larva-mediated chalkbrood resistance-associated single nucleotide polymorphism markers in the honey bee *A. mellifera*. *Insect Molecular Biology*, 25(3), pp.239-250.

Aronstein, K., Colby, D. and Holloway, B.E.T.H., 2015. Validation of genetic markers associated with chalkbrood resistance. *Trends Entomol*, 11, pp.47-53.

Jensen, A.B., Welker, D.L., Kryger, P. and James, R.R., 2012. Polymorphic DNA sequences of the fungal honey bee pathogen *Ascosphaera apis*. *FEMS Microbiology Letters*, 330(1), pp.17-22.
