

Conservation of the Nordic brown bee *Apis mellifera mellifera*

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- Joint Nordic institute under the Nordic Council of Ministers
- 3 sectors: Plants, Farm Animals and Forest
- Has an ex situ gene bank of plants in Alnarp, Sweden & administers Svalbard Global Seed Vault
- ‘NordGen Farm Animals’ is a service and knowledge center for sustainable management of farm animal genetic resources for the Nordic countries
- <http://www.nordgen.org>



Apis mellifera - Out of Africa

- two expansions from Africa into Europe
- geographically close, but genetically distant groups



Apis m. mellifera - Historic beekeeping

- before 19th century: forest beekeeping
 - 19th century: modern beekeeping with wooden hive boxes and movable frames; 'bee package'
- intense transport of bees and thus hybridization



Current status - Nordic brown bee

- 2011: NordGen initiated an inventory project
- aim: document current status & conservation activities of *A. m. mellifera* in the Nordic and Baltic region



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some excellent characteristics for beekeeping:

- high winter hardiness
- strong drive to collect pollen
- high longevity of the worker bees and queen
- flight strength even in cold weather



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BUT: negative characteristics

- runny on the comb
- high swarming tendency
- aggressive and defensive
- sensitivity to brood diseases
- difficult to identify queen



Current state – the Nordic region

- historically: Nordic Brown bee
- last 150 years: Improvement of Nordic brown bee by introgression and replacement -> endangered?
- for example: 1990 >95% of 40.000 Finnish bee colonies were mostly *A. m. ligustica*

Is this a problem?



Do we have a problem?

- on one hand:

MOLECULAR ECOLOGY

Molecular Ecology (2012) 21, 4414–4421

doi: 10.1111/j.1365-294X.2012.05614.x

FROM THE COVER

Management increases genetic diversity of honey bees via admixture

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old-world progenitor populations in Africa, East and West Europe. Managed bees had highly introgressed genomes representing admixture between East and West European progenitor populations. **We found that managed honey bees actually have higher levels of genetic diversity compared with their progenitors in East and West Europe, providing an unusual example whereby human management increases genetic diversity by promoting admixture.** The relationship between genetic diversity and honey bee declines is tenuous given that managed bees have more genetic diversity than their progenitors and many viable domesticated animals.

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tion owing to admixture. Our results demonstrate that honey bees do not suffer from reduced genetic diversity caused by management and, consequently, that reduced genetic diversity is probably not contributing to declines of managed *Apis mellifera* populations.

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Management increases genetic diversity of honey bees via admixture

BROC
Depart:

MOLECULAR ECOLOGY

Molecular Ecology (2013) 22, 3208–3210

- BUT:

NEWS AND VIEWS

COMMENT

Conserving genetic diversity in the honeybee: Comments on Harpur *et al.* (2012)

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F. A. MORITZ§¶ and F. BERNHARD KRAUS§
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selection over extended periods of time.

Deliberate crossing and the use of non-native honeybees in beekeeping promote the creation of admixed populations, which introgress into native populations. The resulting hybrid bees may indeed have a higher genetic diversity, but will also have lost the combination of traits, long-shaped by natural selection, that made them particularly well adapted to their local environment (Strange *et al.* 2007; Costa *et al.* 2012). It is therefore

that 'Management by beekeepers has allowed for honey bees to admix and produce 'mongrel' populations of



- signatures of positive selection detected:
 - SNP panel: genome-wide signature of positive selection acting on ~ 10% of genes (Zahed and Whitfield 2008)
 - 40 genomes: strong signatures of positive selection (Hapur et al. 2014)

Apidologie (2012) 43:634–642
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DOI: [10.1007/s13592-012-0138-9](https://doi.org/10.1007/s13592-012-0138-9)

Original article

Differences in colony phenotypes across different origins and locations: evidence for genotype by environment interactions in the Italian honeybee (*Apis mellifera ligustica*)?

Cecilia COSTA¹, Marco LODESANI¹, Kaspar BIENEFELD²



et al. 2008). However, the significant interactions between origin and test location, which we observed in our study of colony performance traits, points to the existence of locally adapted *A. mellifera ligustica* populations in Italy. In honeybees, a specific adaptation to environment had been observed 50 years earlier, in a field study by Louveaux (1966) on a French honeybee population (*A. mellifera ligustica*).

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Do we have a problem?

- **Yes!**
- because we are losing populations of bees that have unique combinations of traits that are adapted to specific local environments
- Bee-specifics exacerbate the problem:
 - Sex-determination: haplodiploidy -> high degree of inbreeding leads to collapse of population quickly
 - mating system makes controlled breeding difficult

Back to the Nordic brown bees

Not clear:

- which of the negative characteristics are universal
- which of them are due to using the wrong ecotype
- which of them can be remedied by *A. m. mellifera*-specific management
- to what degree inbreeding is a problem in specific colonies
- which colonies are “pure”
(only small scale studies; Jensen et al 2005)



Genomic data can help to

- a) detect populations with declining effective population sizes in need of introduction of new genetic material
- b) identify pure *A. m. mellifera* colonies for breeding purposes
- c) detect differential gene expression between healthy and parasitised colonies, which may be useful to predict the 'health' of a population
- d) identify the genetic basis of important production traits
- e) identify selective sweeps and adaptation of different *A. m. mellifera* populations to various environments

members of the NordGen Brown bee working group:

- Bjørn Dahle, Senior Adviser, Norwegian Beekeepers' Association, Norway
- Per Ideström, Chairman of Association and Project NordBi, Sweden
- Armads Krauze, Chairman of Latvian Beekeepers Association, Latvia
- Per Kryger, Senior Researcher, Aarhus University, Denmark
- Lauri Ruottinen, Reseacher, MTT Agrifood Research Finland, Finland





Differences in colony phenotypes across different origins and locations: evidence for genotype by environment interactions in the Italian honeybee (*Apis mellifera ligustica*)?

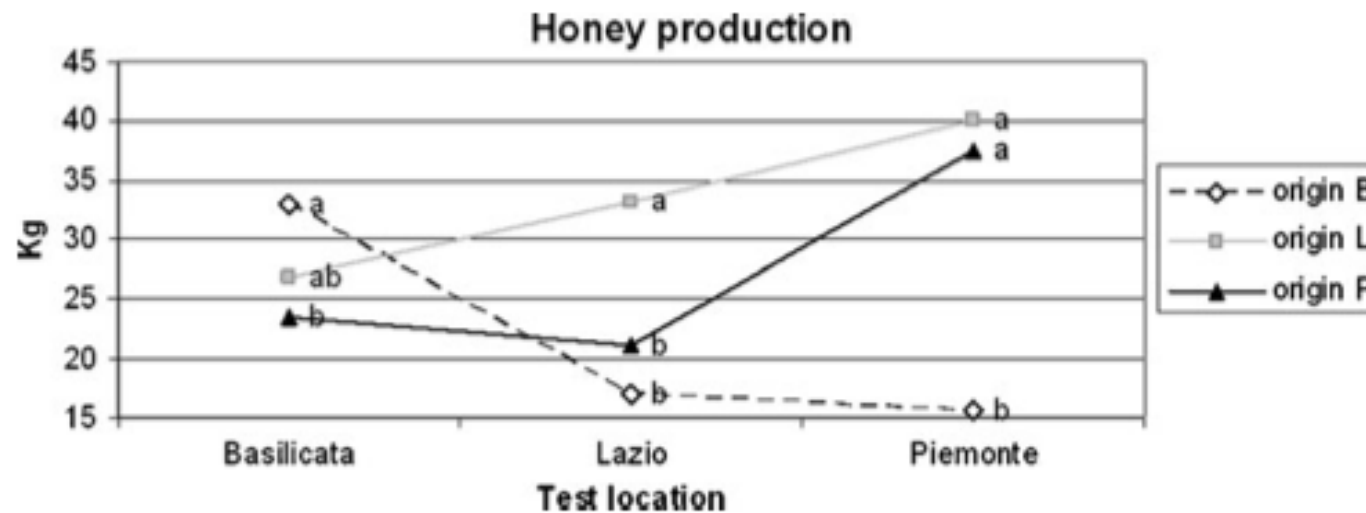


Figure 3. Effect of the location on the honey production (kilogram of harvested honey) of colonies belonging to the three *A. mellifera ligustica* subpopulations (originating from *B* Basilicata, *L* Lazio, *P* Piemonte). The *y*-axis reports the LS means of honey production. The existence of genotype–environment interactions is evident due to the crossing of the *Norms of Reaction*. Different letters next to the values indicate significant differences at $P < 0.05$, within each location.