Modelling the Impact of Non-Native Honey Bee Importation on Native *Apis mellifera mellifera* Populations

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Introduction

A. m. carnica

A. m. ligustica

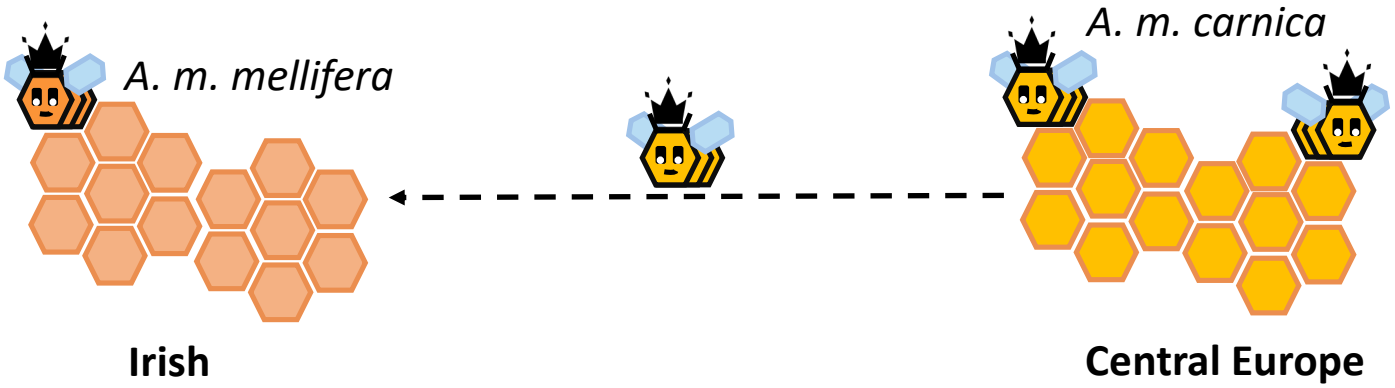
A. m. mellifera

The aims of this study

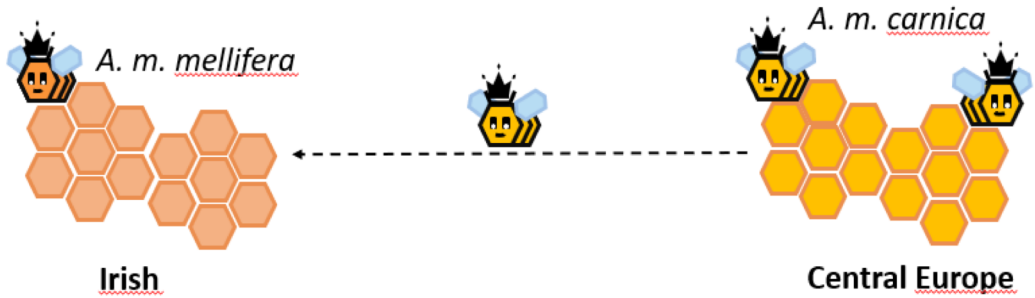
- Model that simulates different importation scenarios between native and non-native populations.
- Quantify the magnitude of introgression and its impact.
- Set a framework for future research.

Materials and Methods

- SIMplyBee: honey bee population simulator.
- Two honey bee populations: Irish and Central European.
  - Irish: *A. m. mellifera*.
  - Central European: *A. m. carnica*.
- Yearly cycle
- Imports of queens from the Central European to Irish population.

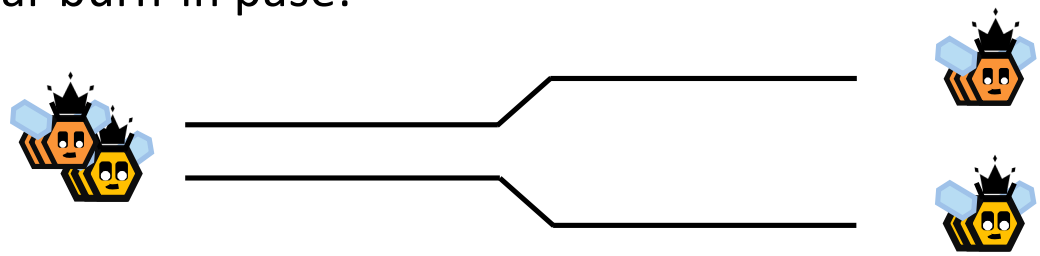


Materials and Methods



- 4 traits (100 QTLs per chromosome):
  - Fitness in Ireland and fitness in Central Europe.
  - Honey yield in Ireland and honey yield in Central Europe.

- 10 year burn-in pase:



- After 10 year burn-in, balancing selection on fitness, imports and different scenarios.

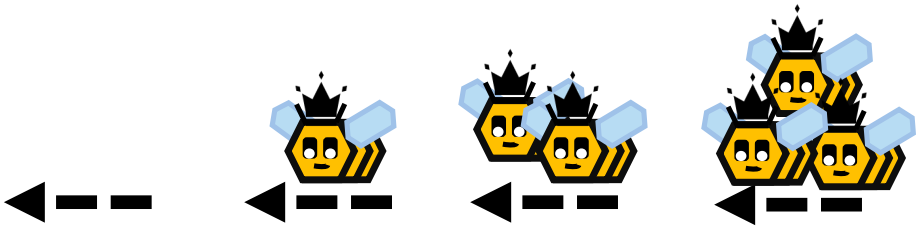
- Meassure introgression, mean traits and the spread of introgression.

Materials and Methods

Scenarios:

Change of the percentage of imports:

- 0%, 1.5%, 4% and 10%.



Change in genetic correlations between fitness in both environments:

- From 0.75 to 0.25, -0.25 and -0.75 genetic correlations.

G x E

Point of entry:

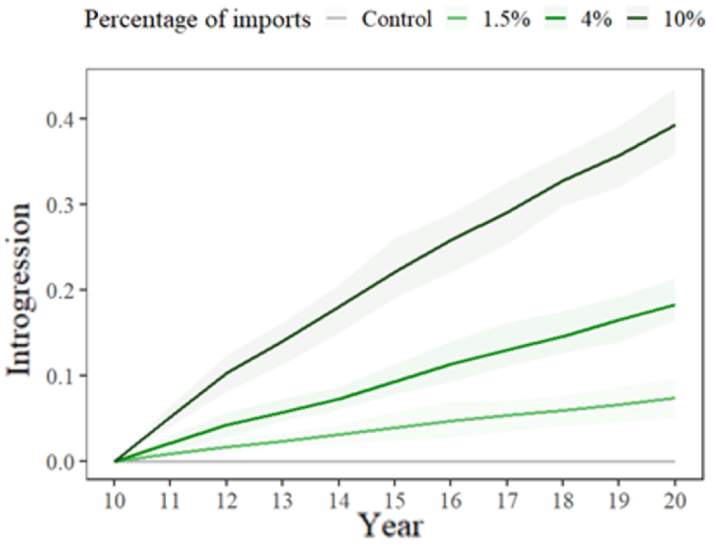
- A single point of entry of the imports.

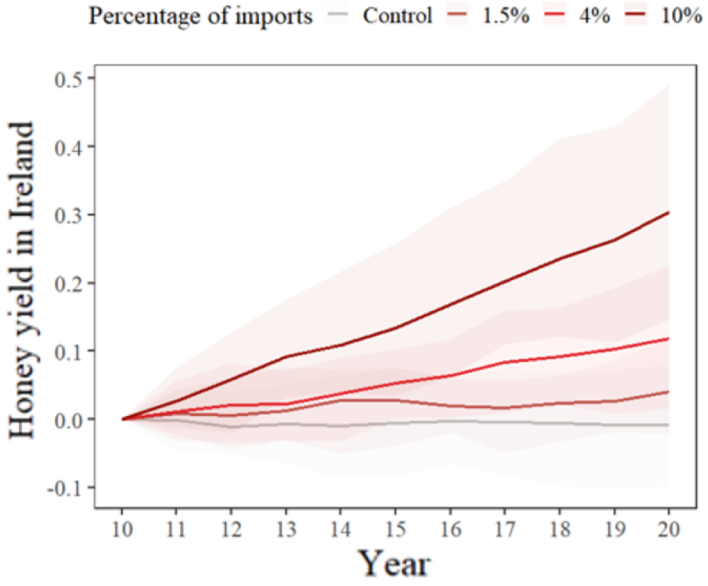
Importation halt:

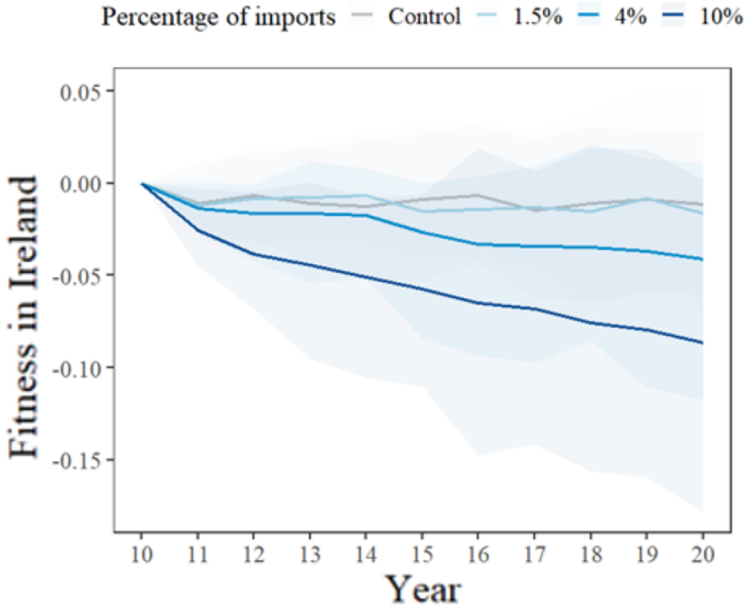
- Stopping importation after 10 years.

Percentage of imports

0%, 1.5%, 4% and 10%



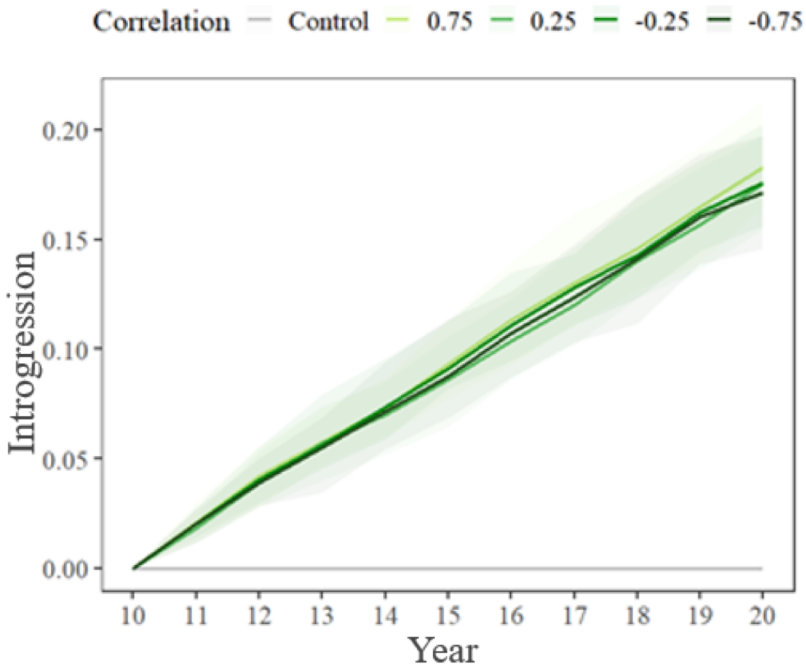


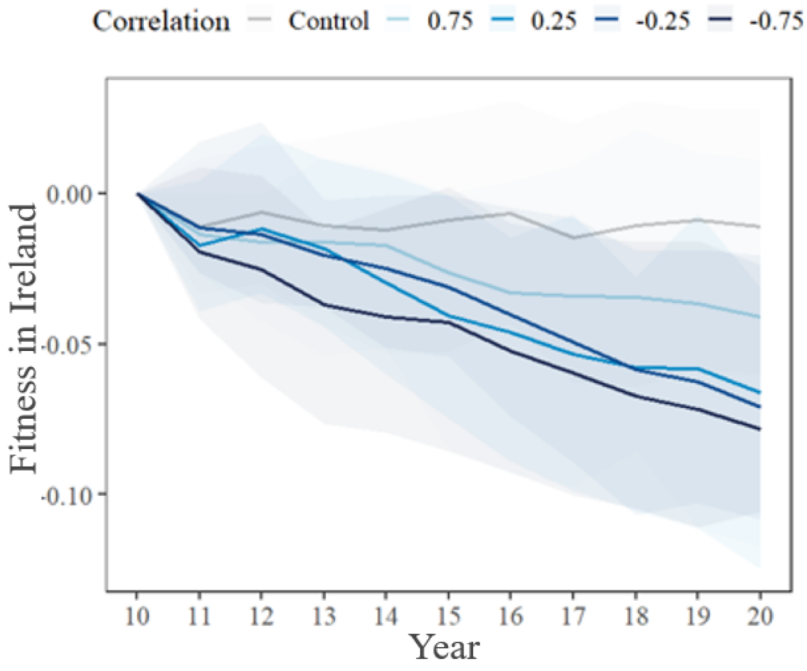


Changing genetic correlation

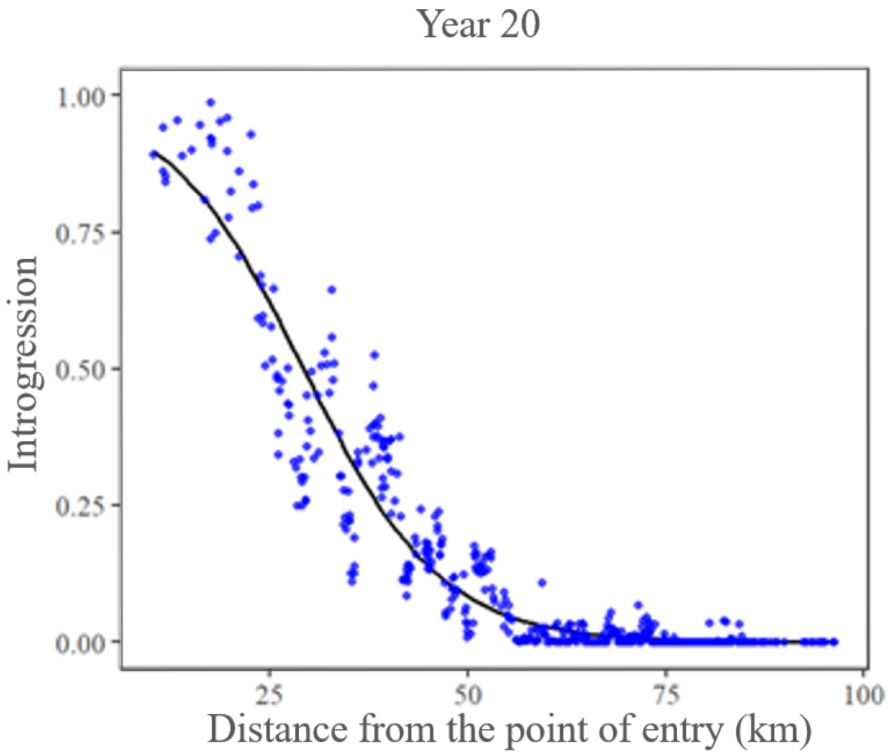
Between fitness in Ireland and fitness in central Europe:

from 0.75 to 0.25, -0.25 and -0.75 genetic correlations.

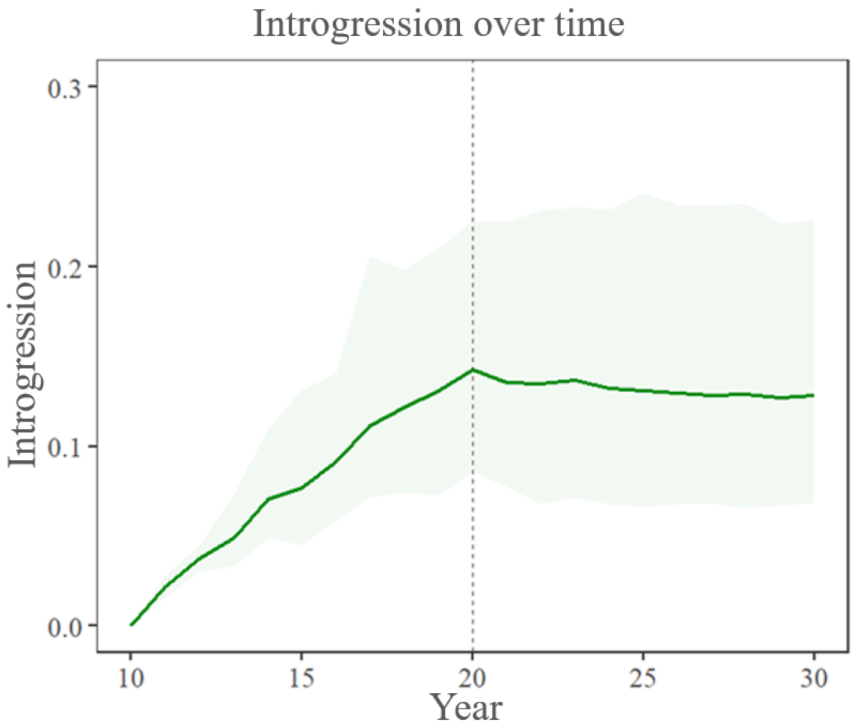




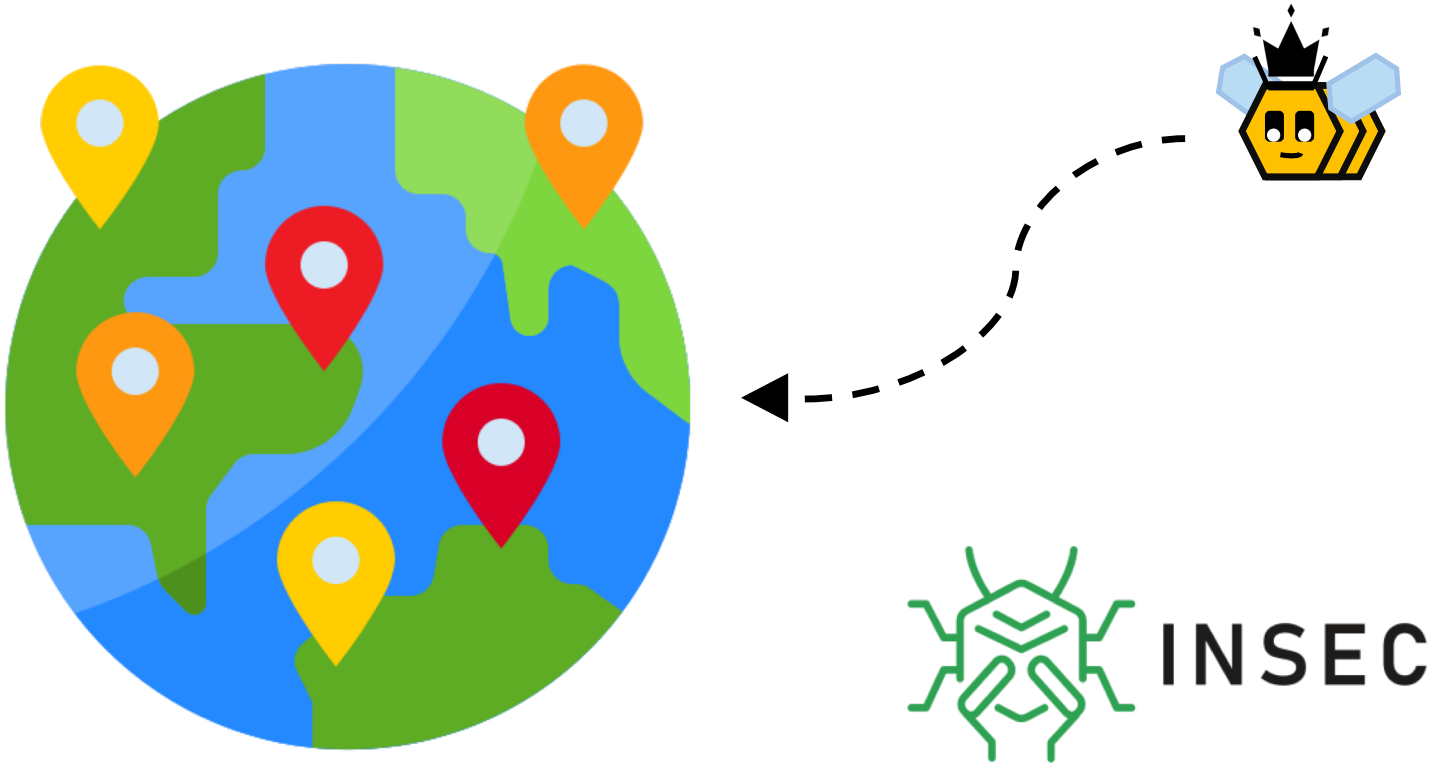
Point of entry



Importation halt



Practical value



We acknowledge the funding from the COST Action 22140 Insect-IMP: Improved Knowledge Transfer for Sustainable Insect Breeding.