

SIGNATURES OF SELECTION IN THE IBERIAN HONEY BEE: A GENOME WIDE APPROACH USING SINGLE NUCLEOTIDE POLYMORPHISMS (SNPs)

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BACKGROUND

Detection of signatures of selection across genomes and identification of their role in adaptive population divergence is a central issue in evolutionary biology.

The Iberian Peninsula harbours the greatest honey bee genetic diversity and complexity in Europe. The challenge of deciphering the mechanisms underlying such complexity has led to numerous surveys of the Iberian honey bee (IHB). Yet, the evolutionary processes underlying patterns of IHB genetic diversity remain poorly understood.

With the sequencing of the honey bee genome and development of high density SNPs, the IHB genome can now be scrutinized for adaptive divergence. Herein, we show a preliminary exploration of a genome scan to detect signatures of selection on the Iberian honey bee genome.

GENOTYPING

All individuals were genotyped for a panel of 1536 SNP's with Illumina BeadStation 500G using a custom Oligo Pool Assay

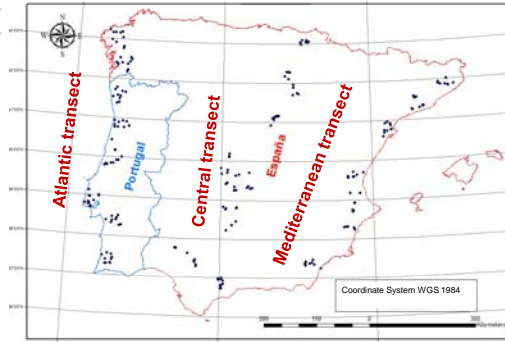


SAMPLING

A total number of 665 georeferenced drone samples was collected across 3 transects in the Iberian Peninsula. Thirty colonies were sampled in each location. A reference collection of the African *A. m. intermissa* (N=28) and the western European *A. m. mellifera* (N=33) was also made.



SAMPLING TRANSECTS



SNPS SUMMARY

Of the 1536 SNPs, 99 were unscored for every individual. For the remaining 1437 SNPs, 63 were invariable. The minimum allele frequencies (MAF) are shown in the table.

| MAF | 0 | ≥0.005 | ≥0.01 | ≤0.02 | ≥0.05 | ≥0.1 |
|------------|----|--------|-------|-------|-------|------|
| Nº of SNPs | 63 | 1292 | 1214 | 1120 | 629 | 352 |

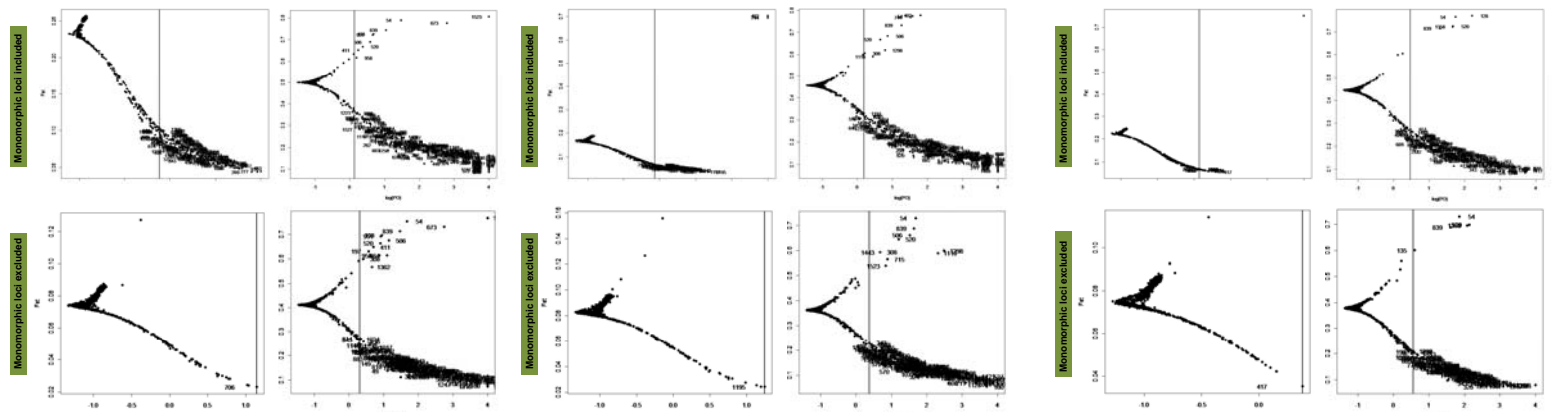
SCANS FOR IDENTIFICATION OF OUTLIER LOCI POTENTIALLY UNDER SELECTION

Candidate loci under selection were identified using a Bayesian likelihood method implemented with the software BayeScan. Simulations were run considering each Iberian transect separately and the total Iberian data set. Simulations were performed including reference populations (right) and monomorphic (0.98 cutoff) loci (top) and removing reference populations (left) and monomorphic loci (down).

ATLANTIC TRANSECT

CENTRAL TRANSECT

MEDITERRANEAN TRANSECT

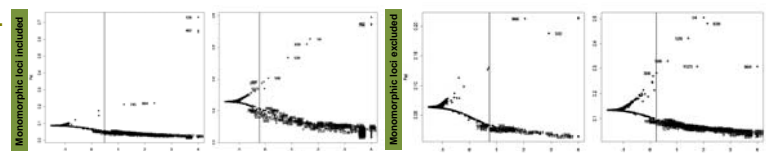


Exclusion of monomorphic loci reduces the number of potential loci under selection.

Inclusion of reference populations increases the number of potential loci under selection.

The greatest number of potential loci under selection is detected for the total data set (Iberia with reference populations)

IBERIAN PENINSULA



FUTURE DIRECTIONS

- > Refine simulations with BayeScan.
- > Employ other frequentist (e.g. DetSel, Fdist) and haplotype-based methods and landscape genetics tools to alleviate the problem of detecting false positives and excluding positives.
- > Identify and interpret the spatial structure generated by loci under selection
- > Reveal the molecular basis of the observed adaptive differentiation.

ACKNOWLEDGEMENTS

Numerous people have contributed for this work. We owe special thanks to Antonio Gómez Pajuelo, Ana, Anabela Mendes, Antonieta Susana Caeiro, Armada Nunes, Amílcar Fernandes, Beatriz, Blai Llambich Subirats, Bruno Martins, Eládio Torrente Rodríguez, Fernando Cabayrol, Francisco Iglesias, Gonzalo Calvo, Henrique Simão, Inmaculada Segura Guzmán, Ismael Liria, Isidro, Jaume Cambra, José Pires, Julia Gómez Zardoya, Laura García Peña, Lola Moreno, María José, María Rebelo, Manuel Jardim, Miguel Gil, Miguel Alaria, Nazario Ferrández, Paulo Varela, Pascual Domingo, Pau Bars, Ricardo Pereira, Rita, Simão Parreira, Tânia Marras, Vicente García Fernández, and Vesna Aksoy for providing beekeepers contacts and helping with sampling. We are deeply indebted to numerous beekeepers who gave permission for collecting. They are: Adolfo Sampa, Adolfo, Albano Barros, Alberto, Alberto Manuel Teixeira Aguiar, Alfredo Oliveira Gomes Silva, António Guerreiro Sousa, António Homenegildo, António Mateus Rosendo, António Nuno Fernandes Tavares, Artur Justino, Armindo Almeida, Aurora Gonçalves Azevedo, Abel Dias Mateus, Adelfo Gilaberto Ortega, Adolfo Gamo, Afonso Montes, Agostinho Romero Guerrero, Albert Tor, Algel Andres Redondo, Anastasio Antonio, Antonio Campoy, Antonio Domingo, Antonio Malval, Antonio Torres, Apícola Brul Casanova, Anastasio Moron Sabido, Blai Llambich Subirats, Bruno Monteiro, Calisto Gordo, Carmen Fusti, Cecilio Lopez, Celestino Arroyo, Constançio Barbauro, Carlos Batista, Carlos Manuel Cardozo Mendes, Carlos Teixeira, Centro de Formação Experimentación Agro-Forestal de Segovia, Claudio Tregheo, Claudio, Cristina Martins Peres, Custodio José Plasadas, David Godinho, David Pinheiro, Diego Alberto, Diego Jimenez, Domingo Gordo, Eládio Torrente Rodríguez, Escuela Forestal Santa Coloma de Farners, Esperanza Fernández, Ester, Esther Muñoz, Emilio Ramirez, Fernando da Silva Oliveira, Francisco Iglesias, Francisco Ribeiro, Fernando Cabayrol, Floran Jimenez, Francisco Jimenez, Francisco Marín Azorin, Francisco Mirra Yala, Francisco Soler Borlino, Gabriel Morguila, German, Guillermo Rosel Carbonel, Harizo Davila, Henrique Simão, Ignacio Rodríguez, Héctor José Soler, Isabela García, Isel Espino, Ismael Liria, Isidro dos Santos Manuel, João Esteves Manso, João Gandino Dias, Joaquim Gomes, Joaquim Marques, Joaquim Neves Alexandre, Joaquim Romão, Joaquim Romão, Jorge Novais, José Afonso, José António Sequeira, José Augusto Alves, José Carneiro, José Coelho, José da Costa Guerrero Silva, José Heleno Ferreira, José Janeiro Lamas, José Lourenço, José Luís Pinho, José Luis Rubiales Rei, José María Pais do Nascimento, José Manuel Duarte Silva, José Manuel Flores Serrano, José Ribeiro, Juan José Garrido, Julio Agro Blanco, Julio Jesus Jorge, Julio Pivas, Jaime Guzmán, Jordi Guaspé, Jordi Murat Balmer, Jordi Saco, Jorge Bela Mora, José, José Antonio, José Antonio Altamirano, José Francisco, José Gabriel González, José García, José Gil, José González, José Luis González, Jose Maria Oliva, Jose Macarellé Sanchez, José Masi, José Navarro, José Roberto, José Vicente, Josicarmen Martín, Juan, Juan Bustaba, Juan José, Juan José Liria, Juan José Martínez Martínez, Juan José Naudolter, Juan Pedro, Julia Gómez Zardoya, Julian, Luis Esperanza Ferreira Lourenço, Manuel Barbosa Rodrigues, Manuel Dovampo, Manuel Francisco Marca, Manuel Jardim, Manuel Marques, Manuel Tercero, Manuel Simon Vallejo, Marco Pereira, Marina Lopez Lourenço, Melchior Silva Ferreira, Miguel Mendes Lopes, Maria Carmen, Maria José Pinco Carballo, Manuel González Melo, Manuel Robledo, Marcin Rico, María Tereza Sierra, Mariano, Martín Colufio Cano, Martín Esteves, Miguel Serrano Martínez, Nicolás Espino, Nofriana Gomes da Mata, Nuno Lopes, Paulo Manuel Dionísio, Pedro Jorge Camêra Barreiro, Pascual Domingo, Pau Bars, Pedro, Rafael Anton Palacios, Rafael Ribas, Ramon Ferré, Raul Molino Rimeñez, Ricardo González, Rogelio Rodríguez Alvarez, Rogme Lena Varela, Rui Vasco Martins Castro, Rodolfo Montaña Palao, Ruan Garcia, Ruan Rubio Azeite, Sakiuni, Salvador Lopez, Salvador Malheiro, Severina Salgado, Sérgio Cavadas, Simões Alegria, Simão Parreira, Tiago Moreira, Vittorio Martin, Xavier, Xavier Colaba, Xavier Lopez Guay, Xosé Ramon Rodríguez. Numerous people provided samples for the reference populations collection: Andrew Abrahams, Björn Dahlé, Gabriele Soland, Gilles Fert, Jevrosima, Lionel Gannery, raffaele diallo, Romeo Van der Zee, Saïd Abdoullahi, Santiago Saenz, Whilde Louf. Special thanks to Pier Kogler, who provided samples and contacts. Pier's contribution was very precious. Andriela Brandão and Inês Moura assisted with sampling. Special thanks to Margarida Neto for her precious assistance in the Atlantic transect sampling. DNA extractors and SNP genotyping was performed by Colette. Abbey, who was deeply committed to this project. Special thanks to Colette. We owe apologize and thank the people whose names were unintentionally underacted. Julio Chávez Galarza is supported by Fundação para a Ciência e a Tecnologia through the scholarship SFRH/BD/68682/2010. Spanish Ministry of Education provided financial support to Irene Muñoz (FPU program). This research was funded by Fundação para a Ciência e a Tecnologia and COMPETE/EQUER/EU through the project PTDC/BIA-BEC/09840/2008.