

## EVOLUTIONARY GENETICS RESEARCH GROUP (EG)

### Brief description of research lines

#### 4) Evolutionary processes in domestic animal populations

We are engaged in understanding the possibility of local domestication events of some species in the Iberian Peninsula and in the study of the development of modern Iberian breeds. We are also investigating the genetic signatures of changes in phenotypic traits over time due to artificial selection and adaptation to specific environments, some of them pivotal for the long-term persistence of some endangered populations. Our laboratory facilities and expertise are available for outreach activities and services to the community, such as consultancy to breeders' associations and veterinary laboratories regarding paternity tests, individual identification and defining breeding strategies.

##### a. Genetic diversity and population structure of domestic animal species

We apply unconventional molecular markers (*e.g.* whole-genome SNPs and STRs) in order to provide a genome-wide assessment of the genetic diversity and population structure of extant domestic species, particularly horses, cattle and dogs. We intend to design a refined set of molecular markers (*e.g.* breed-specific SNPs) to investigate the evolutionary trajectories of genetically differentiated breeds from the Iberian Peninsula and Northwest Africa. Historical influences, adaptation to particular environments, genetic drift, artificial selection and management have contributed to the particular gene-pool of Iberian domesticates. We make use of a combination of theoretical and methodological approaches embracing phylogenetics, demographic inferences and conservation genetics to capture temporal and geographical changes in the genetic composition of Iberian native breeds, some of which are critically endangered.

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*National collaborators: J Matos (INIAV-Lumiar, Lisboa); LT Gama (Univ. Técnica de Lisboa); Breeders Associations; Direcção Geral de Alimentação e Veterinária (Governmental Agency); Fundação Alter Real; National Germplasm Bank; INIAV-Vale de Santarém; Portuguese Kennel Club.*

*International collaborators: A Martínez-Martínez (Univ. Cordoba, Spain); BP Chowdhary (Texas A&M University, USA); C Penedo (Univ. of California, USA); C Edwards (Oxford Univ., UK); EG Cothran (Texas A&M Univ., USA); E Hill (UC Dublin, Ireland); JA Lenstra (Utrecht Univ., NL); JL Vega-Pla (Laboratório de Investigación Aplicada, Córdoba, Spain); L Ouragh (Institut Agronomique et Vétérinaire Hassan II Rabat, Morocco (MA); BIOBOVIS Consortium (<http://biobovis.jimdo.com/>); Horse Genome Project (<http://www.uky.edu/Ag/Horsemap/>).*

##### b. The archaeogenetics of Iberian domesticates

Our major goal is to perform a phylochronological study of domestic animals using ancient DNA analysis. The scrutiny of genetic data across time and space allows for the direct investigation of changes within populations over time, and helps to disentangle the patterns of admixture between domestic animals and their wild ancestors. Wild ancestor species and their domestic counterparts coexisted in Iberia for millennia (and in some cases still persist) raising the question of whether local domestication and/or admixture events have contributed to the genetic makeup of local varieties. We conduct whole-genome sequence analyses in well-preserved specimens for a refined phylogenetic study, and identification of new polymorphisms which can be further screened at the population level. We use targeted high-throughput sequencing of nuclear regions to recover signatures of human-driven selection related with animal domestication and improvement.

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#### c. Genetic basis of phenotypic variation in modern animals

We aim to characterize the morphological variation of extant Iberian domesticates and investigate genetic signatures of changes in phenotypic traits, particularly those of economic interest or involved in the differentiation of breeds. More specifically, we are investigating the impacts of animal improvement on different phenotypic traits, in association with breeding practices, namely in horses and cattle. Our group is particularly engaged in the study of coat color and fertility traits using several methodologies such as molecular cytogenetics, whole-genome SNPs genotyping and genome-wide association analysis.

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*National collaborators: National Breeders Associations, Direcção Geral de Alimentação e Veterinária (Governmental Agency), Fundação Alter Real.*

*International collaborators: BP Chowdhary & T. Raudesepp (Texas A&M Univ., USA); C Penedo (Univ. of California, USA).*

#### d. Services to the community and outreach activities

It is consensual that comprehensive molecular data and pedigree analysis are essential to characterize, define and carry out proper conservation programs of domestic Animal Genetic Resources (AnGR). Accessing temporal changes in genetic variability and demographic structure of extant endangered native domestic breeds is important and can result in crucial and objective information to support breed-specific plans for management and conservation. We provide individual identification and paternity testing (particularly for horse and dog breeds), as well as genetic and demographic analyses based on pedigree data of endangered and commercial breeds to support breeding plans for long term conservation.

We are also engaged in reporting and disseminating our expertise and studies to the breeders and owners community, as the end-users of some of the results of our applied research.

*CBA researchers: MM Oom, J Kjällström, R Matoso Silva.*

*End-users: Breeders Associations, private breeders, Veterinary Clinics.*