Feralization of horses

In a joint effort to understand the genetics of feralization, researchers and students from the Swedish University of Agricultural Sciences, Uppsala University and Linköping University have started a study on semi-feral horses.

Horses of Valley de Anciles

In the Valley de Anciles near Riaño in the mountains of northwestern Spain, a population of Pottoka horses, a native breed of Basque origin, has been kept under feral conditions since 2018. The group of horses currently encompasses 16 individuals, including three yearling foals. To avoid turmoil and injuries among the horses, only one stallion is present in the group.

The valley covers an area of around 600 hectares, and is bordered by fence, water and mountain slopes. Apart from horses, there are also a group of European bison (Bison bonasus) and a group of water buffalos (*Bubalus bubalis*). Wild animals, such as Iberian ibex (*Capra pyrenaica*), Pyrenean chamois (*Rupicapra pyrenaica*), red deer, (*Cervus elaphus*) wolves (*Canis lupus*) and brown bears (*Ursus arctos*) also frequent the valley.

The feralization process

Domestication has been an area of intense interest and study ever since Darwin, and is useful as a model for evolution and the effects of strong directional selection. Feralization, on the other hand, is a process that occurs when a domestic animal population is returned to the wild. It impacts species invasion biology, speciation, conservation, and hybridization and can be thought of as the reverse of domestication. Despite domestication being used to identify genes affecting many traits that change with selection, little is known about the genomic changes associated with feralization.

In addition to the genomic changes of an animal, feralization can lead to large changes in morphology, behavior, and microbiota, with the process of feralization involving the sudden return of both natural and sexual selection. Thus, feralization provides a unique opportunity to observe the genomic, phenotypic and microbiotic responses to selection from a known (domesticated) standpoint, and identify the genes underlying these selective targets.

Bringing back species

Feralization of domestic species for which the ancestral wildtype is extinct, such as horses, facilitates opportunities to bring back extinct breeds or species, or new equivalents of them, in order to restore ecosystem function in benefit of biological diversity. The measures taken in this project may thus be the first steps towards bringing back extinct fauna.

Pilot study

The first fieldwork effort during September 10-15, 2023, included the collection of samples from horses and European bison within the enclosure in Valley de Anciles and samples from reference horses outside the village of Riano. The samples will be used to extract

DNA for RAD sequencing of the horses (MSC project for Gaia Resmini) and for 16S rRNA metabarcoding of the gut microbiome of both the horses and the bison. Complementary samples from European bison in Sweden will be added for a BSc project at SLU and UU. The results will be published in referee-assessed scientific journals.

Finances

The horse genome project has financial support from grants to Dominic Wright at Linköping University and the microbiota project is funded by an internal research effort at the Department of Anatomy, Physiology and Biochemistry at SLU (to Carl-Gustaf Thulin).

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Project Partcipants

Gaia Resmini, MSc student, Linköping University gaire159@student.liu.se
Doortje Theunissen, PhD student, Linköping University doortje.theunissen@liu.se
Carl-Gustaf Thulin, researcher, SLU carl-gustaf.thulin@slu.se
Elin Videvall, researcher, Uppsala University elin.videvall@ebc.uu.se
Dominic Wright, professor, Linköping University dominic.wright@liu.se



The research group in Valley de Anciles, Riaño, Spain (from left Elin Videvall, Dominic Wright, Doortje Theunissen, Gaia Resmini & Carl-Gustaf Thulin).



Fieldwork among pottokas in Valley de Anciles, Riaño, Spain (from left Gaia Resmini, Doortje Theunissen, Dominic Wright & Elin Videvall.



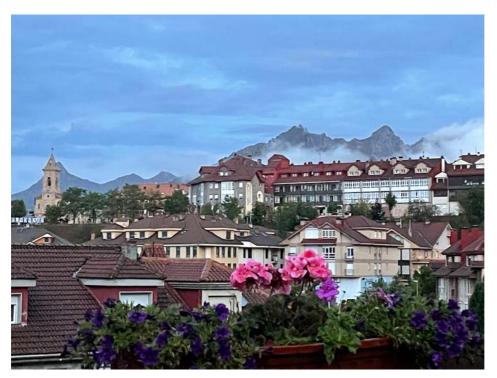
The pottokas horses of Valley de Anciles, Riaño.



European Bison of Valley de Anciles, Riaño.



Sampling horse droppings.



The city of Riaño.