

# SIGNALS OF SELECTION DURING DOMESTICATION IN OLD WORLD CAMELIDS

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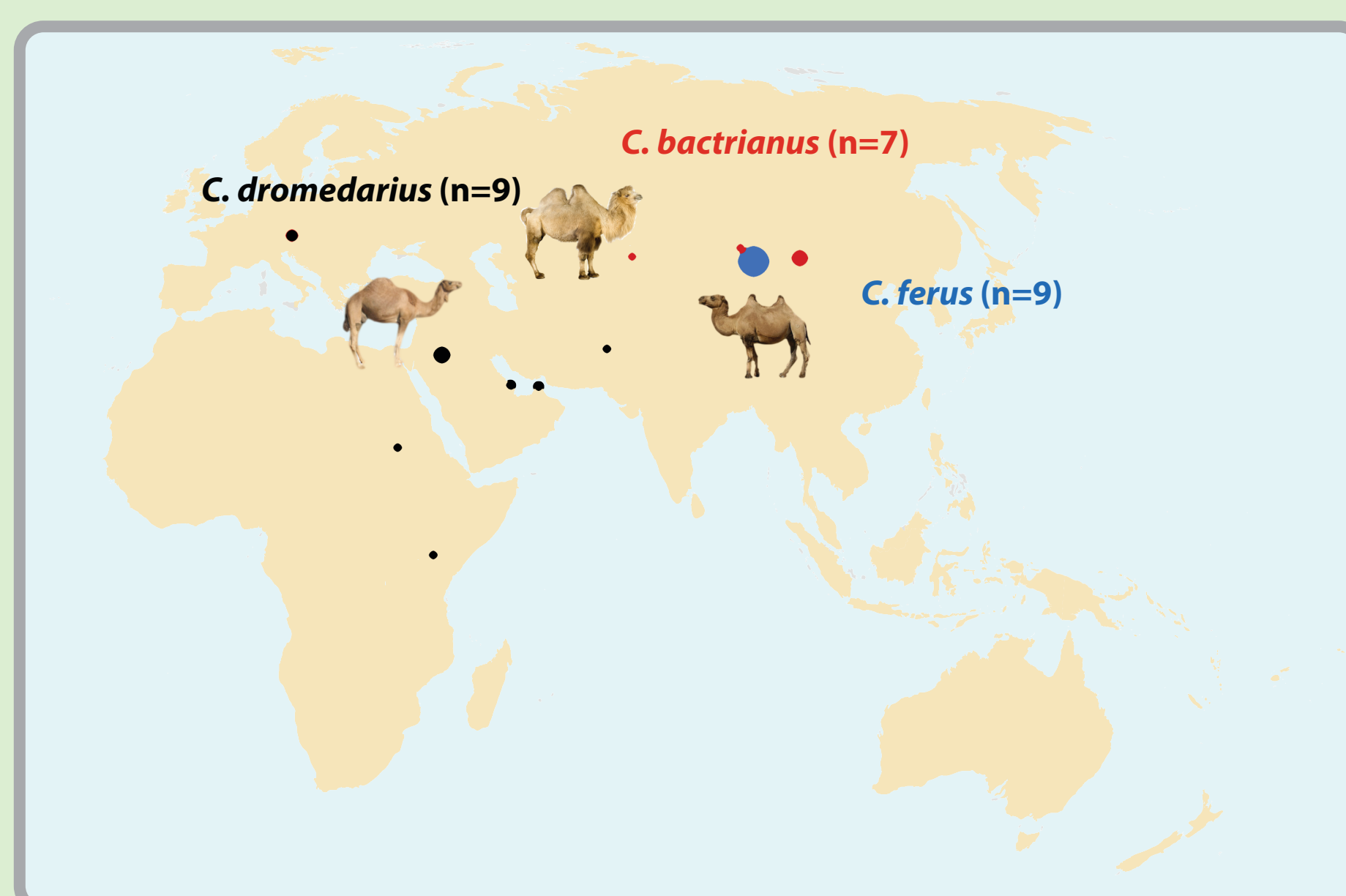
## ABSTRACT

In many parts of the Old World, domesticated camels (genus *Camelus*) are an essential resource, providing food, labor, commodities, and sport to millions of people. Of the three extant species, two have been domesticated (single-humped dromedaries, *Camelus dromedarius*, and two-humped Bactrian camels *Camelus bactrianus*) and one remains wild (two-humped wild Bactrian camels *Camelus ferus*). All three species possess a variety of adaptations to harsh desert conditions, including mechanisms to tolerate extreme temperatures, dehydration, and sandy terrain. Recent genomic studies of camels have identified patterns of selection consistent with the aforementioned adaptations in addition to quantifying genetic variation and examining demographic history. However, these studies are limited to analyses based upon a single genome from each species, thus biasing many inferences of selection and adaptation. Furthermore, draft genomes are susceptible to errors in gene annotation, thereby distorting conclusions of adaptation based upon orthologous genes between species. In this study, we take a **population genomics approach to inferring both positive selection and demographic history of Old World camelids**. By re-sequencing multiple genomes from all three species, our objectives were to **i) identify genes or regions under selection within and between species related to domestication or adaptation, ii) examine the recent demographic history and genome ancestry, and iii) provide an extensive set of genomic resources for future studies of camels.**

## MATERIAL AND METHODS

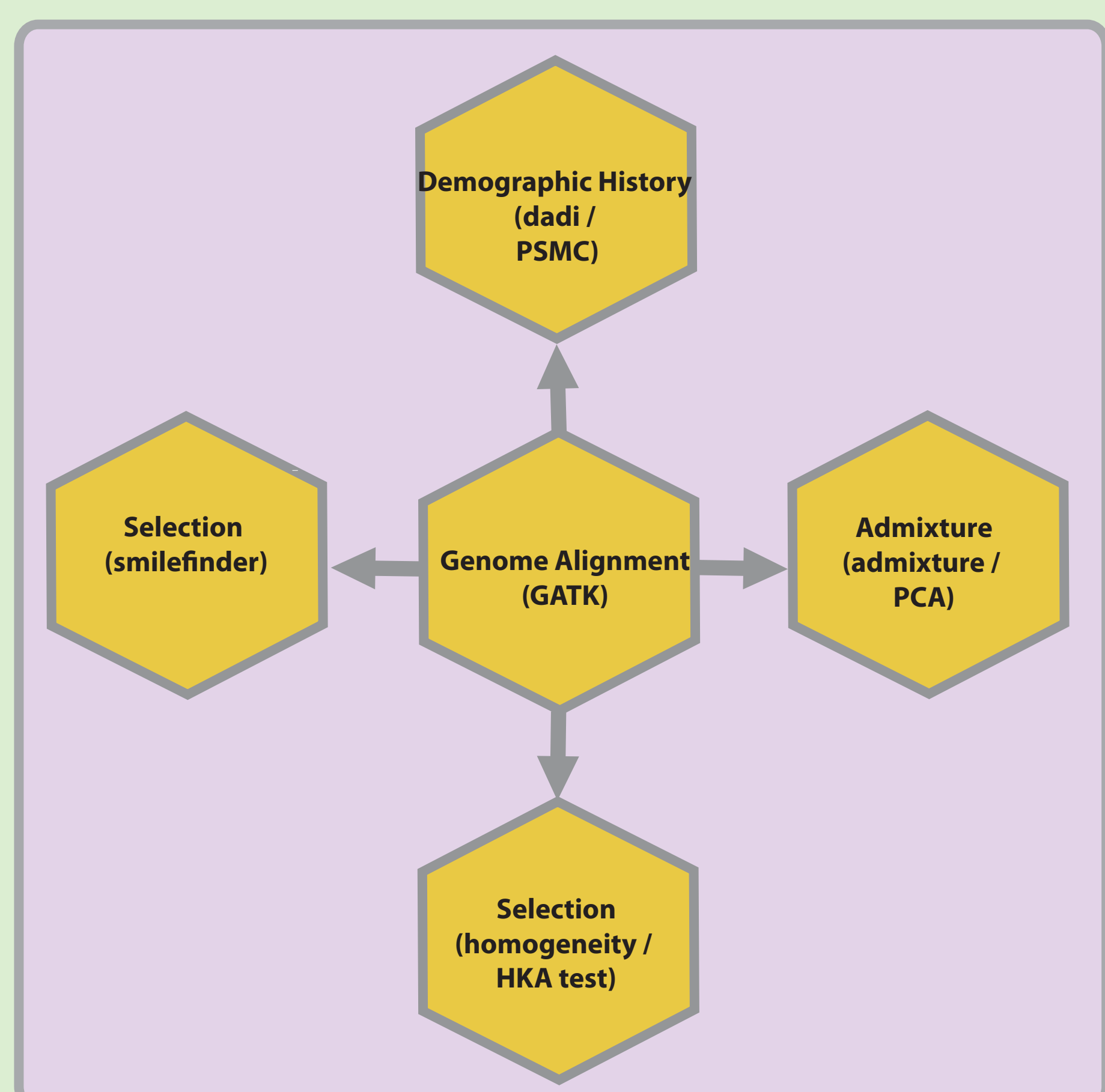
**Fig 1. Map of sample collection locations.** The size of each circle is proportional to the sample size for that location. Colors correspond to the three Old World camel species.

**Dromedary:** Saudi Arabia, Qatar, UAE, Kenya, Sudan, Pakistan  
**Bactrian camel:** Kazakhstan, Mongolia  
**Wild camel:** Mongolia

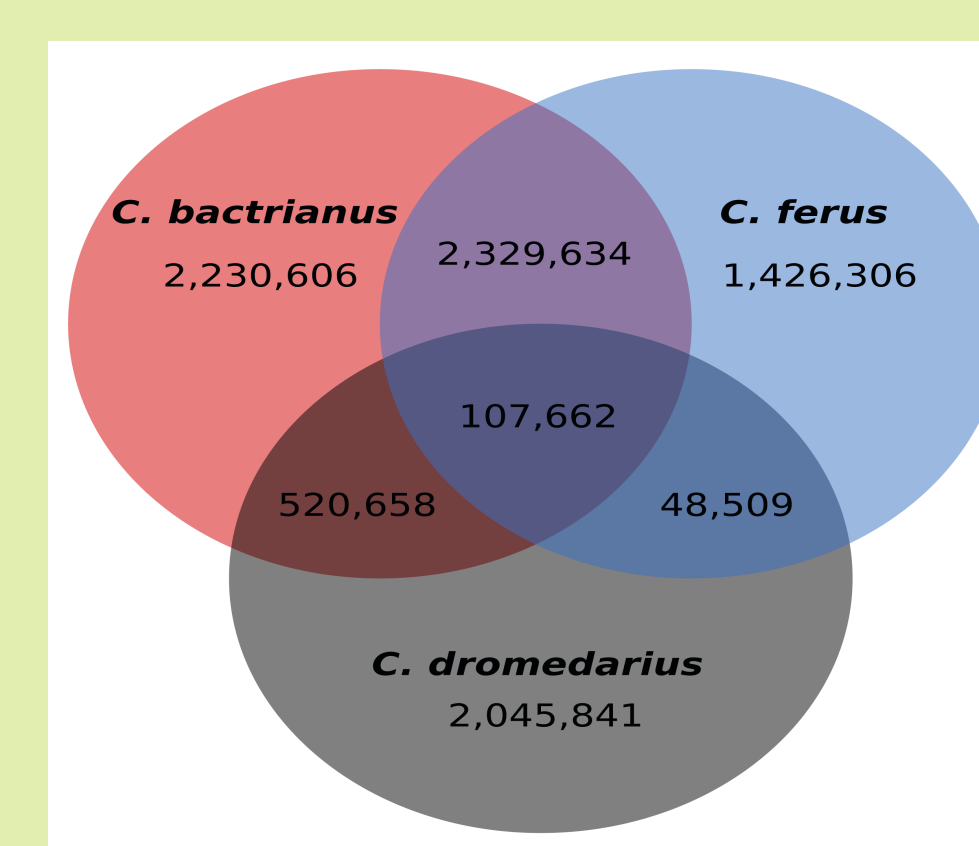


**Fig 2. Bioinformatic pipeline.**

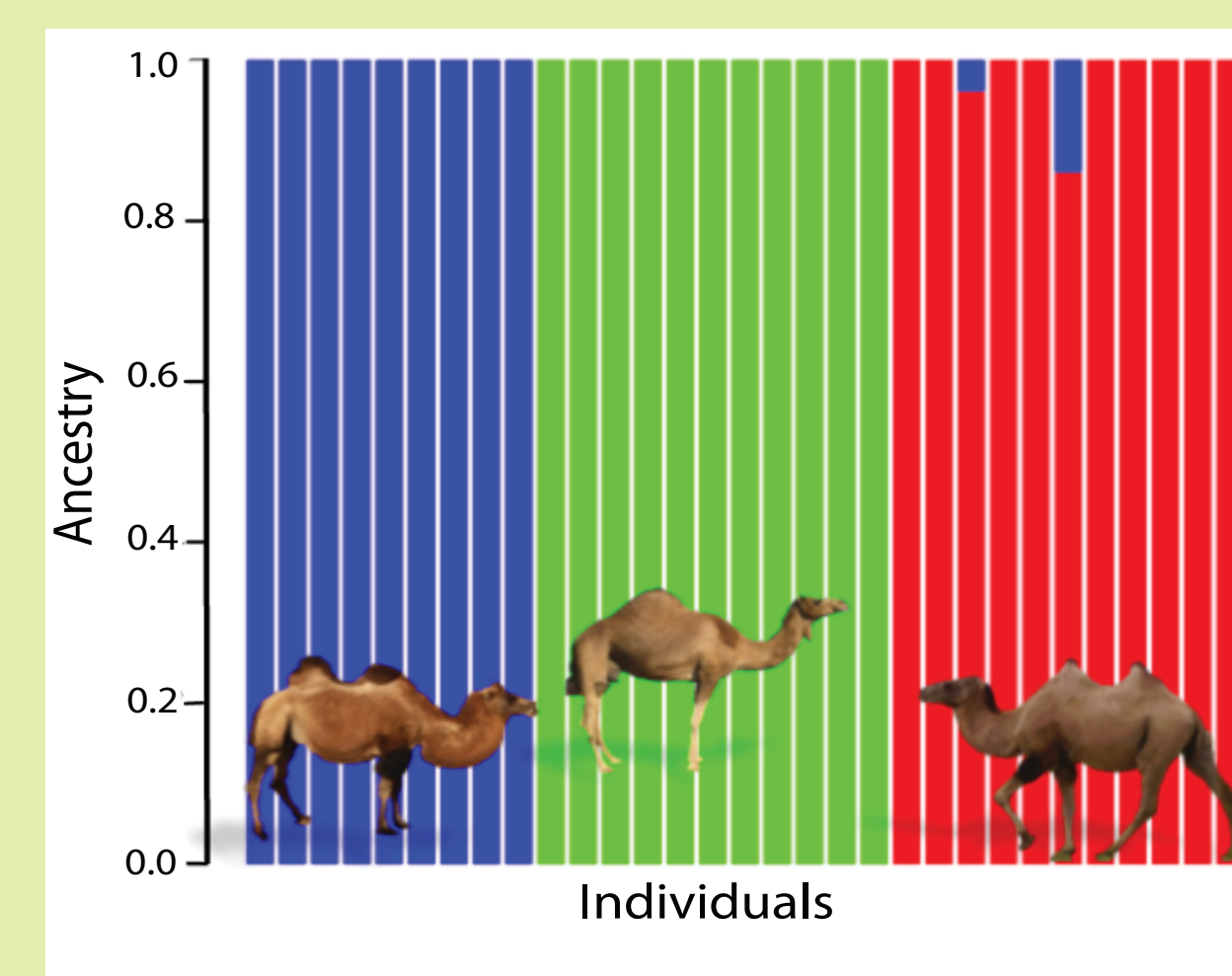
Genome alignment, SNP calling, demographic history inference, admixture, selection tests



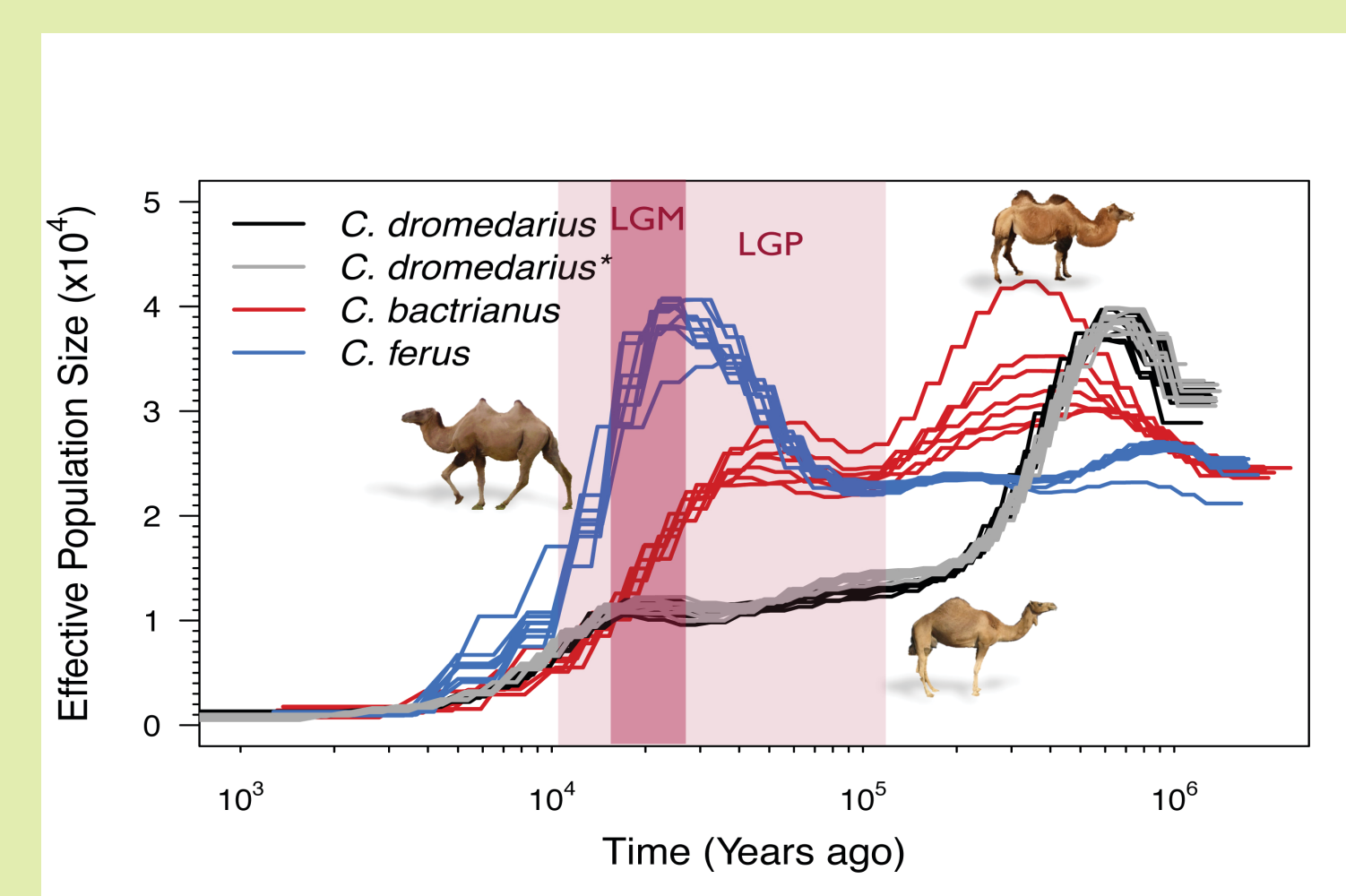
## RESULTS



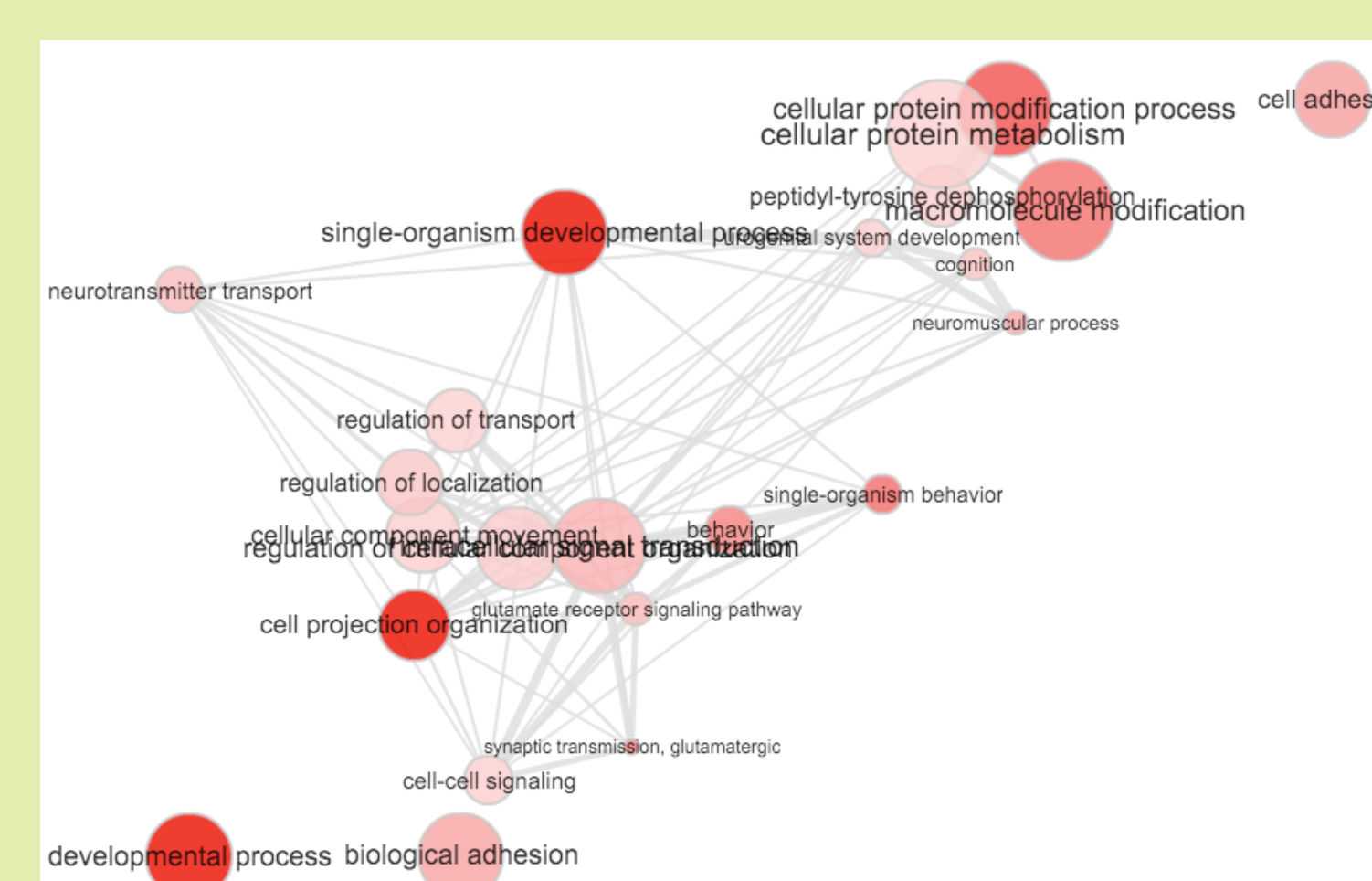
**A) The number of single nucleotide polymorphisms (SNPs)** segregating among all three species of Old World camels. An additional 2.1 million SNPs fixed between species are not shown.



**B) Admixture analysis** using whole genome SNP data of dromedary (green) Bactrian (blue) and wild (red) camels. Each bar represents the genomic ancestry of a single individual, mixed colors indicate a mixed ancestry between two species.



**C) Demographic History of Old World Camelids.** Historical effective population size inferred in PSMC. The result is scaled using a generation time (g) of five years and a per-base mutation rate (μ) of 2.5x10<sup>-8</sup>. The light-purple and pink shaded regions indicate the last glacial period (LGP) and last glacial maximum (LGM), respectively. \*C. dromedarius reads were mapped to the C. dromedarius reference genome.



**D) Network of enriched gene ontology (GO) terms** among genes located in regions determined to be under selection in *C. dromedarius*. Colors (increasing red tint) correspond with decreasing FDR adjusted p-values.

## CONCLUSION

1. Introgression of *C. bactrianus* into the wild *C. ferus* may be relatively common, thus threatening the genomic integrity of the endangered wild camel.
2. Wild camels may have experienced a rapid population expansion prior to the last glacial maxima, followed thereafter by a massive bottleneck.
3. Selection during the domestication of camelids appeared to have substantial effects on genes associated with neurological functions including signaling and behavior, consistent with the "domestication syndrome" hypothesis.

## ACKNOWLEDGEMENTS

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