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### Meeting Information

**When:** January 08 - 13, 2016

**Where:** San Diego, CA

## W122

### Genomic Footprints of Selection under Domestication in Old World Camelids

*Date:* Saturday, January 9, 2016

*Time:* 8:05 AM

*Room:* Royal Palm Salon 1-2

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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 extremely susceptible to errors in the estimated number of genes, 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 and/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.

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