Quantifying the Drivers of Individual Variation in Mule Deer Migration

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Migration, defined as seasonal movement between home ranges [1], is fundamental to the life history of many ungulate species. Although the importance of migration is widely recognized, many ungulate species have experienced declines in migration behaviour, due primarily to climate change and habitat loss [2]. Migration behaviour is not uniform between species, populations, or even individuals, and while it is largely driven by the environment, additional causes of individual variation in migration behaviour, particularly genetic or physiological factors, have not been tested. Our objectives were to 1) quantify individual variation in timing and directionality in mule deer (Odocoileus hemionus) during seasonal migrations; 2) assess the repeatability and consistency of behaviours within and among individuals across years; and 3) identify target genes that explain population level differences in timing and directionality of migration. We used high-resolution GPS data and genetic data collected from 240 mule deer in Colorado from 2008-2015. The mule deer population exhibits near-complete migration to two different summer ranges with high variance in migration timing [3]. We quantified migration behaviours (i.e., timing and direction) using GPS data and assessed genetic differences in these behaviours using a high throughput Restriction site Associated DNA Sequencing (RAD-Seq) approach.

References