

Paper: “Low MHC DRB class II diversity in the mountain goat: past bottlenecks and possible role of pathogens and parasites”

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Summary: Population bottlenecks hinders evolution as the reduction in population size results in low genetic variability. The paper examines MHC DRB exon 2 variability in Caw Ridge mountain goats that had experience population bottlenecks in the past. The authors seek to understand the relationship between MHC DRB allelic diversity and the demographic growth of the population, along with their resistance to infectious diseases. The authors hypothesizes that the allelic diversity of MHC DRB exon 2 genes in the Caw Ridge mountain goats is attributed to their latitudinal distribution. Furthermore, the authors also hypothesized that the MHC diversity of the mountain goats will be low due to past population bottlenecks, isolated lifestyles, and low pathogenic diversity. The authors predicted that if MHC DRB allelic diversity in mountain goats varies based on latitudinal distribution, then at greater latitudes MHC diversity should be lower. The authors studied a population of Caw Ridge mountain goats at Alberta, Canada that have been closely monitored since 1990. Nearly every individual in the population has been marked and observed daily from May to September each year providing an accurate population count. Additionally, since 1994, samples of ear skin have been collected from every goat for genetic analyses. From these samples, 14 random samples are selected to sequence a 249-bp fragment of the MHC DRB exon 2. In addition, the tissue sampled were also obtained from two populations in British Columbia to further expand the investigation of allelic diversity at the species level. LA31-K and LA32-K primers, previously used to amplify thimhorn sheep, were used to amplify the MHC DRB exon 2 levels during the PCR process. The experiment was aimed in determining the relationship between the total number of MHC DRB exon 2 alleles and their latitudinal distribution. The authors found the results showed a significant relationship ($p < 0.05$) in supporting their prediction of MHC diversity decreasing with increasing latitude. While the data supported a decrease in MHC diversity at increasing latitudes, many factors still exist that could have resulted in the low genetic diversity, with one being past population bottlenecks as with Pleistocene glaciations. With the depleted gene pool, inbreeding and genetic drift could impact the population greatly in further decreasing MHC diversity. In conclusion, low MHC diversity is attributed to many factors such as population bottlenecks, latitude distribution, parasite-based balancing among many others. The effects of low MHC diversity are minimal with mountain goats as with their favorable location; however, they are vulnerable to many infectious diseases that ran rampant in today’s world.

Critique: My critique on this experiment would be to sample other animal species found at higher latitudes and compare their MHC diversity with the same species found at higher and lower latitudes. Many factors can affect MHC diversity and some animals at higher latitudes such the Reindeer population do have a high MHC diversity. The authors should have accounted for a wider animal range rather than focusing on a specific species. Additionally, further research

should have happened for pathogen analysis as such that some pathogens needs a host to thrive and the transfer between hosts at colder temperatures is more difficult than warmer temperatures.