Uncovering ancient UK male lineages

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It is possible to trace sire lines and horse movement through the male sex chromosome which is preserved as it is passed on from father to son. The domestic horse population today represents only a fraction of the male lineages that would have been present in the ancestral horse population that roamed the earth 5.5 million years ago. This is due to the selection and use of only a few stallions during domestication and during two later import waves; first the Spanish stallions during the Napoleonic movement (16th century) and then the Oriental stallions, responsible for the foundation of the Thoroughbred, during the 19th and 20th century. As a result, the majority of modern horse breeds descend paternally from only a few Oriental stallions. These Oriental stallions originated from a group of male horses that carried the same male sex chromosome around 700 years ago. This is known as the 'crown group'. Having said this, the geographically isolated Shetland pony has escaped both the Spanish and Oriental import waves representing the most ancient known male lineage in the UK. Previously, only a limited number of UK breeds had been researched however, this summer I investigated a wider range of UK breeds, including the Eriskay, to uncover how import waves have influenced UK breeds.

I read the genetic code of 81 male horses belonging to 15 different Northern European breeds. Several horse breeds including the: Clydesdale, Dale, Dartmoor, Fell, Irish Draught, New Forest, Sire and Suffolk Punch all cluster within the 700-year-old crown group at the Ad-b locus suggesting that these breeds have been impacted by the import waves. The male descendants of the pure-bred Eriskay pony stallion Eric however, cluster in a unique group outside of the 'crown group'. This confirms that the Eriskay's male lineage not only escaped the influence of the Spanish and Oriental import waves but also represents one of the most ancient known male lineages in the UK along with the Shetland pony.

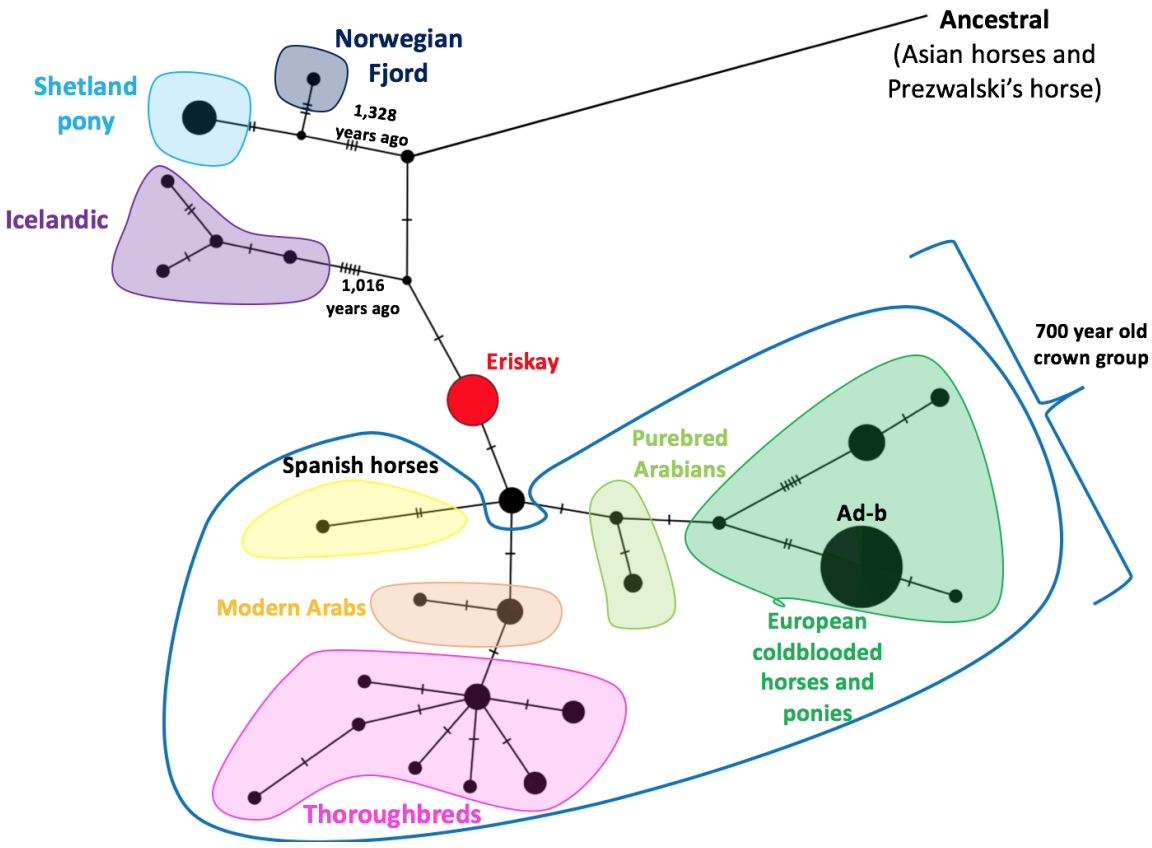

Figure 1: Male sex chromosome network displaying the origin of male lineage groups adapted from Wallner et al., (2017)