

## CASE STUDY 3

### Understanding the structure of Dutch horse populations using a genomics approach: implications for conservation

**Leading IMAGE partner:** WR (Centre for Genetic Resources, the Netherlands)

**Other IMAGE partners involved:** WU

**Other non-IMAGE partners and actors involved:** SLU - Sweden and UU – the Netherlands, Horse breed associations

**IMAGE WP and Task:** WP2 / Task 2.3 – case studies

#### Objectives and expected results/output:

In total nine equine populations in the Netherlands were sampled and genotyped, five of these populations are part of the Dutch gene bank collection. The ultimate aim of our research is to make implications for conservation. Questions that we aim to answer are: which population(s) harbor unique genetic diversity and which population(s) have unique alleles? Various methods will be applied to be able to answer these questions (see section below). Two scientific manuscripts are anticipated, one on inbreeding, structure, relationships and diversity, the other on selection (e.g. selective sweeps). A presentation was made at 12thWCGALP conference (February 2018, Auckland, NZ) with focus on inbreeding, structure and relationships.

#### Material and methods

In total nine equine populations in the Netherlands were sampled and genotyped with either the 50k or 70k equine SNP chip. Five of these populations (Friesian horses, Gelder horses, harness horses, draft horses and Groninger horses) are part of the collection of the Dutch gene bank. About 300 Friesian horses have been genotyped and a few have been sequenced, as part of GWA studies and identification of mutations. From the other populations about 20 individuals per population were sampled and genotyped with a focus on the genetic diversity. To be clear, genotyped individuals are not part of the gene bank collection. For our study, typical analyses were performed (mainly using PLINK software) e.g. calculating inbreeding (based on expected and observed homozygosity, based on ROHs), identifying relationships between and within population, performing Eding method to identify population(s) that harbor unique genetic diversity, identifying selective sweeps to identify population(s) with unique alleles, etc.

Publication: Genes 2019, 10(6), 480; <https://doi.org/10.3390/genes10060480>

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