

Epigenetic characterization of horse centromeric domains in different tissues and individuals from the FAANG equine consortium

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The centromere is the locus required for chromosome segregation during cell division whose function is epigenetically specified by CENP-A, the centromere specific histone H3 variant. Although satellite DNA is a common feature of mammalian centromeres, we demonstrated that equid species are characterized by several satellite-less centromeres, making them a suitable model system for unraveling the epigenetic marks related to centromere function.

In the horse, the centromere of chromosome 11 (ECA11) is the only one devoid of satellite DNA. We previously demonstrated that the position of its CENP-A binding domain is not fixed but slides within an about 500 kb region in different individuals, giving rise to positional alleles. These epialleles are inherited as Mendelian traits but their position can slide in one generation.

As members of the equine community of the FAANG consortium, our first goal was to investigate whether centromere sliding can occur during development. To this purpose we characterized the position of the centromeric domains of ECA11 in tissues of different embryonic origin from the two Thoroughbred mares and two Thoroughbred stallions. Our results demonstrated that the centromere is located in the same region in all tissues, suggesting that the position of the centromeric domains is maintained during development.

We then evaluated the epigenetic and transcriptional profile of the centromeric locus, taking advantage of RNA-seq, ChIP-seq and microRNA-seq datasets produced by the consortium. This analysis demonstrated that the ECA11 centromere is transcriptionally silent across tissues and individuals, indicating that transcription is not a key feature of centromeric chromatin.