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SÉMINAIRE

Analysis of genomic structural diversity in wolf-like canids.

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Structural variation in general, and copy number variants (CNV) in particular, has emerged as an important source of genetic variation. The genetic history and the extraordinary morphological, physiological and behavioral variation of dogs, make them an ideal mammal in which to study the effects of CNV on biology and disease. The dog genome revealed the existence of more than one thousand of CNV that overlap ≈ 400 genes, which are enriched for defense/immunity, oxidoreductase, protease, receptor, signaling molecule and transporter genes. Furthermore, CNV can have significant impacts on a wide range of phenotypes including breed-definiting traits and showed to be appropriate markers to analyze genetic relationships between dog populations. This finding implies that most of the surveyed CNVs were present in the pool of canine breed founders. In order to understand the ancestral dog genome organization, we designed a high density custom 720K probes NimbleGen aCGH chip based on all known dog CNV and segmental duplication and genotyped 15 wolves from 11 populations, with a wide distribution (including Europe, Asia and America), 5 dogs (Dingo, Basenji, Beagle, Boxer and Dachshund) and three outgroups (red wolf, coyote and golden jackal). The dataset analyzed in this study allow us to identify selected CNV during early dog domestication.

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