

Title: “Assessing dog introgression through structural variants in European refugial wolf populations”

European wolves have recently undergone a remarkable demographic recovery, however the potential conservation implications of wolf-dog hybridization across a broad range of genomic variation remains unclear. For example, wolf-dog hybridization can alter the adaptive potential of wild wolf populations, yet its genomic consequences have been inferred from single nucleotide polymorphisms (SNPs) alone. Here, we tested whether structural variants (SVs) capture patterns of admixture and introgression between wolves and dogs in three European wolf populations from glacial refugia (Dinaric-Balkan, Iberian, and Italian), where wolf-dog hybridization has been relevant over the last 30 years. Moreover, we included a broad representation of domestic dogs, plus Karelian wolves and three outgroup species to infer introgression. Admixed and non-admixed individuals were first identified using genome-wide SNP-based analyses, providing an independent reference to assess SV-based signals. Then, we characterized deletions, duplications, and inversions and implemented tailored dual approaches to identify putative recent and historical dog introgression separately within each wolf population and SV category. Deletions and duplications captured broad-scale population structure and revealed signatures of genome-wide admixture, although with lower resolution than SNPs, whereas inversions only distinguished wolves from dogs. We identified both putatively recent and historical dog introgression, highlighting heterogeneous dynamics across refugia. Gene ontology analyses of candidate introgressed SVs suggested potential functional roles that might have shaped physiology, behavior and ecology during population evolution and following recent admixture. Overall, our results show that SVs provide a complementary perspective to SNPs, adding an additional layer for disentangling the genomic impacts of wolf-dog hybridization.

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