assortative mating and barriers to reproduction in the host (mate preference based on olfaction cues) acting as magic traits.

S2.O.3

The *Brachypodium pangenome* reveals differently evolved drought responsive dehydrin genes within its species

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Dehydrins (DHNs) belong to group 2 LEA (Late-Embryogenesis-Abundant) proteins which play an important role in plant responses to abiotic stresses. DHN data was retrieved from Phytozome and Ensembl Plants and used to perform comparative evolutionary analysis of dehydrin genes in four *Brachypodium* species, 54 B. distachyon ecotypes and five cereal crops (*Aegilops tauschii, Hordeum vulgare, Sorghum bicolor, Oryza sativa* and *Zea mays*). DHN domain analysis across the four *Brachypodium* species dehydrins (Bdhn) revealed eight architectures. The most common architecture was YSK2. In addition, some upstream cis-elements related to exogenous and endogenous stresses were detected. B. distachyon (Bdis) drought-tolerant ecotypes contain a slightly lower number of dehydrins (4 vs. 9), and some of them have a distinct sequence composition. Chromosome distribution of Bdhn genes differ among Bdis ecotypes as well as the number of DHNs in each chromosome. Seven out of nine Bdhn genes are located in Bdis chromosomes 3 and 4 and one gene each in chromosomes 1 and 2. Phylogenetic analysis of DHN sequences show a general evolutionary trend of early diverging B. stacei and its derived (sister) B. hybridum–S subgenome Bdhns, followed by those of B. distachyon and sister B. hybridum–D subgenome Bdhns, and those of *B. sylvaticum*. However *B. sylvaticum*, a moist-environment perennial species, contains nine DHNs, four of which diverge from any of the nine DHNs present in the annual dry-environment

Brachypodium species. Further analysis of orthologous sequences shows that only Bdhn1 and 2 are present in every grass studied.

S2.O.4

Genomic structure, demographic histories and differential introgression in two distant populations of African golden wolf

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The recently recognized African golden wolf (Canis lupaster) is widely distributed across the Sahara and Sahel of Africa. Large distribution and diversity of habitats have been shown to drive population differentiation in other related canids such as the gray wolf (Canis lupus) but not in others like coyotes (Canis latrans). Also, there is potential for introgression among canids which could affect genetic diversity and adaptation in local populations. Since African golden wolves may act as top predators in several ecosystems in Africa, understanding the demographic history of the species could inform changes across entire ecological networks. We have used several bioinformatic tools to test for divergence, genetic diversity and introgression from other canids in seven whole genome sequences of African golden wolves from the extremes of their distribution. We have detected different demographic histories in two well-defined groups of this species in Northwestern and Eastern Africa that provide evidence of interconnection during Pleistocene and Holocene climatic changes. We have detected a higher co-ancestry of Ethiopian wolves (Canis simensis) in Eastern than in Northwestern African golden wolf populations, and a clear hybrid ancestry with gray wolves and/or dogs (Canis familiaris) in an Egyptian African golden wolf. Finally, we have found different patterns of genome-wide heterozygosity across the range of the African golden wolf. Our results aim to aid the conservation of these little known carnivores, which could play a pivotal ecological role across huge areas in Africa.