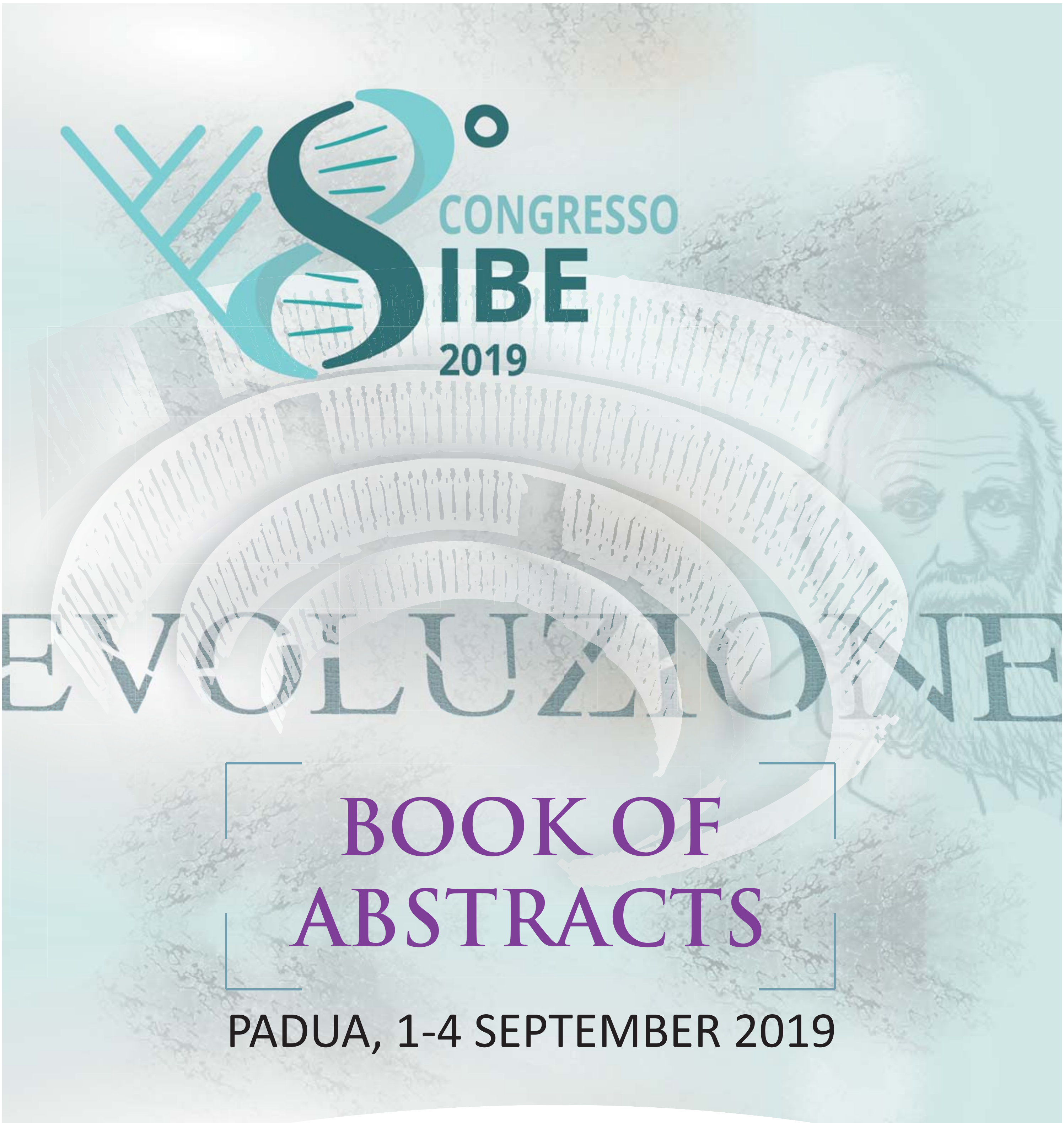

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BOOK OF ABSTRACTS

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Investigating geographic and temporal genetic variation in the black grouse (*Lyrurus tetrix)* in the Italian Alps

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The black grouse (*Lyrurus tetrix*) is a Galliform distributed across northern Eurasia, and is a game bird in most EU countries. Although the species is listed as 'Least Concern' by the IUCN, populations at the western and southern edges of its range are considered 'Vulnerable' due to increasing habitat fragmentation and human disturbance. Between 1995 and 2017, in collaboration with several hunting associations, we collected more than 600 black grouse samples across seven regions of the Italian Alps. Ten microsatellite markers (STRs) and 2442 Single Nucleotide Polymorphisms (SNPs) were analysed in large subsets of the collected data, with the aim of identifying environmental, temporal and anthropic factors that affect the distribution and level of genomic variation. The main factor shaping the genetic distances between populations based on STRs is the geographic distance between them (i.e. isolation-by-distance), but even the populations on the two extremes of our sampling area are very similar (F_{st} between the two regions = 0.053). SNP data supports the STR analysis. However, isolation-by-resistance methods for the larger STR data set show that both higher altitudes and urban areas inhibit movement of grouse between populations. While temporal analysis of STRs for the Trentino-Alto Adige region showed no significant change in the mean number of alleles and allelic size range between the two time frames studied (e.g. mean number of alleles 1995-1999: 8.8, 2009-2010: 8.2), and the expected heterozygosity was high in both time frames (1995-1999: 0.740, 2009-2010: 0.722). While black grouse population size is reportedly decreasing, our results suggest there is no measurable genetic impact from this trend. Hence this dataset provides a basis for future monitoring of genetic diversity in this charismatic alpine species.