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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references at the end of each chapters.
Nota di contenuto	Introduction -- Distribution of length of ancestral chromosomal segments in admixed genomes -- Exploring population admixture dynamics via distribution of LACS -- Genome-wide search for signatures of natural selection in African Americans -- Complex selective forces shaping the genes underlying human diseases -- Materials and Methods.
Sommario/riassunto	In this thesis, Dr. Jin presents the distribution of ancestral chromosomal segments in the admixed genome, which could provide the information needed to explore population admixture dynamics. The author derives accurate population histories of African Americans and Mexicans using genome-wide single nucleotide polymorphisms (SNPs) data. Mapping the genetic background facilitates the study of natural selection in the admixed population, and the author identifies the signals of selection in African Americans since their African ancestors left for America. He further demonstrates that many of the selection signals were associated with African American-specific high-risk diseases such as prostate cancer and hypertension, suggesting an important role these disease-related genes might have played in

adapting to their new environment. Lastly, the author reveals the complexity of natural selection in shapinghuman susceptibility to disease. The thesis significantly advances our understanding of the recent population admixture, adaptation to local environment and its health implications.