Hedgehogs of the genus *Erinaceus* are key models for studying population genetics, phylogeography, and speciation in the Western Palearctic. This thesis integrates genome-wide data to reconstruct phylogenetic relationships within the Erinaceidae family, revealing that the divergence of *E. europaeus*, *E. roumanicus*, *E. concolor*, and *E. amurensis* occurred during the Pleistocene, driven by climatic fluctuations. Phylogeographic analyses highlight the role of glacial refugia in shaping postglacial expansions, with distinct mitochondrial lineages corresponding to the Iberian, Apennine, and Balkan refugia. A newly identified Asian lineage of *E. roumanicus* suggests a Ponto-Caspian refugium. Contact zones between *E. europaeus* and *E. roumanicus* in Central Europe and the Russian-Baltic region demonstrate asymmetric gene flow and limited hybridization, likely constrained by reproductive barriers. In populations in sympatry we identified skull size reduction, suggesting competitive interactions andconvergent character displacement. Additionally, landscape genetics reveals fine-scale population structure influenced by geographic barriers and anthropogenic factors. These findings contribute to a deeper understanding of hedgehog evolutionary history, speciation processes, and the impact of environmental and genetic factors on population differentiation.