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A mitogenic view on the evolutionary history of the Holarctic freshwater gadoid, burbot (*Lota lota*)

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Climatic oscillations during the Pleistocene epoch had a dramatic impact on the distribution of biota in the northern hemisphere. In order to trace glacial refugia and postglacial colonization routes on a global scale, we studied mitochondrial DNA sequence variation in a freshwater fish (burbot, *Lota lota*; Teleostei, Gadidae) with a circumpolar distribution. The subdivision of burbot in the subspecies *Lota lota lota* (Eurasia and Alaska) and *Lota lota maculosa* (North America, south of the Great Slave Lake) was reflected in two distinct mitochondrial lineages (average genetic distance is 2.08%). The *lota* form was characterized by 30 closely related haplotypes and a large part of its range (from Central Europe to Beringia) was characterized by two widespread ancestral haplotypes, implying that transcontinental exchange/migration was possible for cold-adapted freshwater taxa in recent evolutionary time. However, the derived mitochondrial variants observed in peripheral populations point to a recent separation from the core group and postglacial recolonization from distinct refugia. Beringia served as refuge from where *L. l. lota* dispersed southward into North America after the last glacial maximum. Genetic variation in the *maculosa* form consisted of three mitochondrial clades, which were linked to at least three southern refugia in North America. Two mitochondrial clades east of the Continental Divide (Mississippian and Missourian clades) had a distinct geographical distribution in the southern refuge zones but intergraded in the previously glaciated area. The third clade (Pacific) was exclusively found west of the Continental Divide.