Reconstructing the phylogeography of an invasive species: tracing invasion routes of norway rats using mtDNA control region.

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The norway rat, *Rattus norvegicus*, is a cosmopolite invasive species that moves especially following human routes. It is considered one of the worst pest, since it may be dangerous for native species and responsible for of the spreading of pathogens to man and animals. The norway rat reached Europe during XVIII century from Asia, but little is known concerning its invasion history and population structure in this area. Here we used the mtDNA control region to study pattern of invasion of *Rattus norvegicus* by a phylogeographic approach. We used 372 rat sequences, 211 from GenBank and 161 collected from Europe, Africa, and Middle East. Despite the very recent invasion of Europe, preliminary results show an unexpected high genetic diversity. Twenty-six haplotypes were identified. Among them, two are predominant and included in two haplogroups showing a star-like structure. This preliminary result, corroborated by mismatch distribution, Tajima'S D and Fu's Fs neutrality test, suggest a recent sudden expansion of the species. The two haplogroups found in Europe are apparently unrelated each other, suggesting the occurence of two different invasion events of Europe possibly along two different colonization routes. Further deepened analysis are necessary to better understand the phylogeographic pattern of this invasive species.