
Unravelling the worldwide invasion history of the highly invasive red swamp crayfish *Procambarus clarkii*

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Abstract

Biological invasions are one of the most devastating threats to global biodiversity. Propagule pressure (i.e., the size and number of introduction events) is thought to be one of the key elements driving invasion dynamics. Over the last 45 years, European freshwaters have been widely invaded by the red swamp crayfish, *Procambarus clarkii*. It is generally reported that European invasion was originated from only two large crayfish batches, legally introduced from Louisiana (US) to southern Spain in 1973 and 1974. In order to confirm this "official" history, we aim to: (1) determine whether there have been unrecorded introductions into Europe and where they came from; (2) establish the genetic structure of European populations; and (3) compare their genetic diversity to that of the native area. To do this, 1416 crayfish from 122 sampling sites in the Northern Hemisphere (22 native populations) were analysed using the mitochondrial gene (COI). Some genetic structuring was found in the native area allowing us to putatively identify Louisiana as the main area of origin for introduced populations worldwide. Diverse hotspots in some invaded areas, such as South-Western Spain (Extremadura and Andalusia) or Central Italy (Tuscany) did not show strong bottlenecks, likely due to the high propagule pressure (either large size inoculum, many introduction events or both). Our results showed some genetic homogeneity across Europe, suggesting multiple secondary events mediated by humans. The finding of one haplotype only present in Northern Europe, but not in Spain, also suggests additional translocations of crayfish. These mitochondrial results will be compared to microsatellite results from the same dataset. Any additional *P. clarkii* introductions have, so far, not been well-documented in the literature.

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