



Original Investigation

Preservation of genetic diversity in a wild and captive population of a rapidly declining mammal, the Common hamster of the French Alsace region

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ABSTRACT

The Common hamster (*Cricetus cricetus*) faced massive population declines throughout its western range margin. In France, relict populations remained in the Alsace region. By comparing allelic diversity using microsatellite analysis over a time span of 12 years we investigated if this population decline led to genetic erosion in a French relict population of the species. Genetic diversity was moderate but comparable to other populations from Western Europe. Interestingly, no decline of allelic variation was revealed between 1999 and 2012 in the study region (expected heterozygosity = 0.51 in 1999 and 0.5 in 2012, respectively), suggesting a sufficiently high effective population size of ~500 (179–956 SD). While several alleles were lost in a captive breed maintained for restocking purposes in the region, expected heterozygosity was comparably high (=0.5). Our results show that genetic diversity has been effectively maintained in a relict population of French Common hamsters despite of massive range loss. We recommend the maintenance of intense in situ conservation effort, along with regular monitoring of genetic diversity and effective population size.

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Introduction

The Common hamster *Cricetus cricetus* faced massive population declines in the western margin of its Eurasian distribution over the past few decades and is now considered a highly endangered species throughout Western Europe (Nechay, 2000; Weinhold, 2009). Despite intensive conservation efforts, formerly stable populations decrease rapidly, most likely as a result of agricultural intensification and landscape fragmentation (Ulbrich and Kayser, 2004; Meinig and Boye, 2009; Weinhold, 2009).

Compared with populations from the central species range in Europe (e.g., Eastern Germany, Czech Republic, Poland) where the species is generally considered to be more abundant (but see Ziomek and Banaszek, 2007; Tkadlec et al., 2012), western Common hamster populations display low levels of genetic diversity. There is a marked decline in genetic diversity from east to west (Neumann et al., 2004, 2005; Banaszek et al., 2010). Neumann et al. (2004) for instance, found the lowest allelic diversity among Common hamster populations in Netherlands-Limburg and Belgium-Flanders.

It remains unclear, however, if the low genetic variation is due to historic founder events or recent anthropogenic population bottlenecks. In Belgium, the Netherlands and North-Rhine Westphalia (BNN region), however, genetic comparisons of historic vs. recent samples document a recent loss of allelic diversity due to anthropogenic bottlenecks (Smulders et al., 2003; La Haye et al., 2012).

In the most western edge of its range, hamster populations showed a particular critical decline over the past years, leading to intensive conservation action, such as conservation breeding, reintroductions and habitat restoration (Villemey et al., 2013). The failure of halting this dramatic decline has recently led to the condemnation of France by the Court of Justice of the European Union on the 9th of June 2011 for a lack of measures to strictly protect the habitat of the species (case C-383/09). It is thus of crucial importance to identify potential reasons for population decline in western and particular French Common hamsters and to elaborate effective strategies for population recovery. One potential key factor which could explain the failure in restoring Common hamsters in its western range is inbreeding and low genetic diversity. Demographic bottlenecks are usually accompanied by loss of genetic variation and increased inbreeding due to lowered effective population sizes (Frankham, 2005). A potential contribution of genetic factors to the dramatic situation of Common hamsters in France

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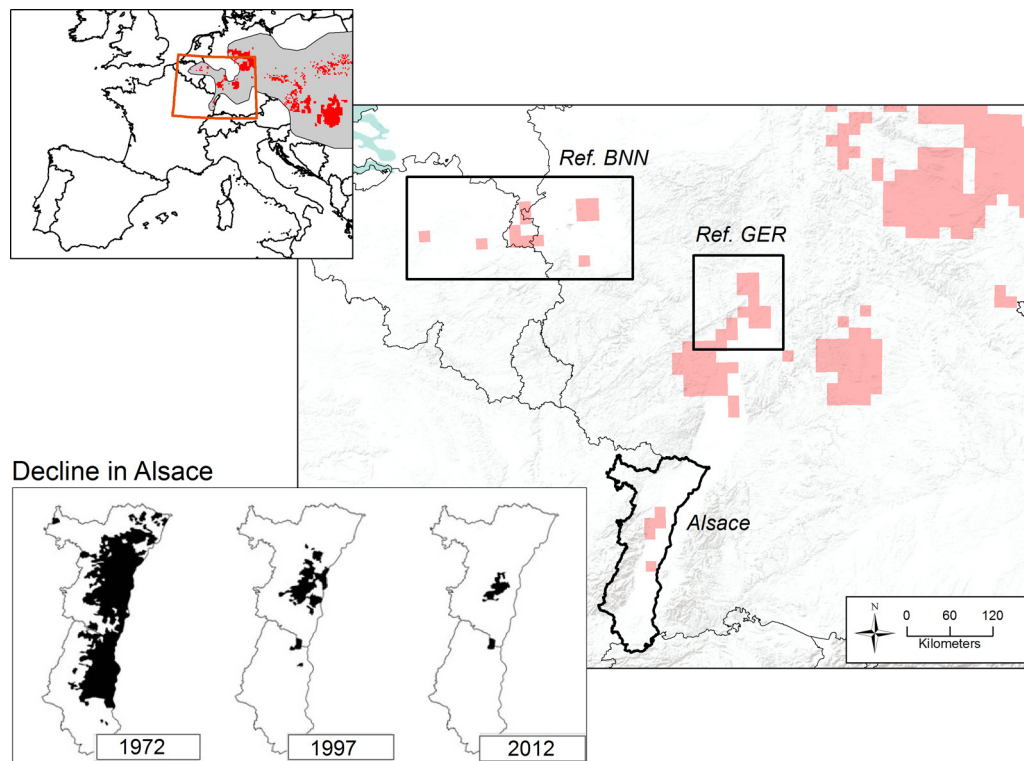


Fig. 1. (Top left) Species range in Western and Central Europe according to IUCN (gray) and current distribution (red). (Central) *C. cricetus* distribution in 2009–2012 in the western range margin is marked in red. Origin of reference samples (Ref. BNN and Ref. GER) is highlighted. (Bottom left) Recent Common hamster distribution and decline in Alsace since 1972 (Eidenschonck and Grandadam, 2012). (For interpretation of the references to color in figure legend, the reader is referred to the web version of the article.)

would have important consequences for conservation, implying that habitat restoration alone might be insufficient for population recovery. In the French Alsace region, the Common hamster range declined to less than 10% of the former range within the past 40 years (329 municipalities in 1972 vs 19 in 2012). This loss of range was accompanied by decline in population size within the last 12 years (1167 burrows in 2001 vs. 206 in 2012; semi-exhaustive consensus (Eidenschonck and Grandadam, 2012)) (Fig. 1), suggesting genetic bottleneck effects. As urban development is increasing in the region loss of genetic diversity and increased inbreeding seems unavoidable.

In order to test if the ongoing decline of Common hamster populations in the Alsace has led to a significant decrease in overall genetic diversity, we reassessed the allelic diversity of the main Alsatian Common hamster population sampled in 2012 and compared it to a sample of the same region from 1999 (Neumann et al., 2004), when hamsters were more abundant than today (1167 burrows in 2001 vs. 206 burrows in 2012; semi-exhaustive consensus) (Eidenschonck and Grandadam, 2012). Moreover, we collected samples from Common hamster breeding stations in France which maintain captive population originating from the same region from around the year 2000. Genetic diversity of the native Alsace population in 1999 and 2012 was compared with the diversity in the breeding units in order to quantify the effectiveness of maintaining intraspecific diversity in ex situ hamster breeding programs.

Specifically, we aimed to answer the following questions:

- i) Did the rapid and ongoing large-scale decline lead to a genetic erosion of genetic diversity in the Central Alsace relict population of the Common hamster?
- ii) Did the captive breeding strategy result in an effective preservation of genetic diversity compared to the field population?

Material and methods

Study area and breeding units

Common hamsters are still present in three regions of the Alsace, two areas near Strasbourg in the north and one southern area (Fig. 1). According to the spring burrow consensus of 2012 the “Central” area near Strasbourg comprises 80% of the Alsatian population and highest burrow densities are reached there. In this study only the “Central” population from the area near Strasbourg was sampled. In 2012, 206 burrows were found there during spring consensus. In addition to the wild living individuals, Common hamsters from the region are kept in captivity in four breeding units. Population sizes in the units range from 80 to 300 animals with a total of more than 700 captive bred hamsters. Animals are annually exchanged in a random manner between the three units run by Sauvegarde Faune Sauvage (SFS). These units also receive some animals from the Centre national de la recherche scientifique (CNRS) every year. Wild founder animals of CNRS as well of SFS breeding stations originated from the “Central” area near Strasbourg caught between 1996 and 2002 (Losinger and Labouesse, 2002).

Sampling and storage

Samples from free-living hamsters were collected using hamster-specific hair-traps (Reiners et al., 2011a) (Fig. 2). Hair-traps were placed in burrow entrances in the late afternoon and surveyed for hairs early next morning. Samples were stored dry in 125 ml vials (Sarstaedt®) equipped with packages of silica gel (Wisepac®). In total 75 samples were collected in 2012 which had sufficient number of hairs (>10 hairbulbs) (=Alsace 2012). In addition, 71 animals from the four breeding units were sampled (=Alsace Breed). Due to the fact that animals are exchanged yearly between these breeding units these were pooled in one dataset. Hairs from

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