Differences in genetic structuring of populations of the Argentine hemorrhagic fever reservoir, the rodent *Calomys musculinus*, from endemic and non endemic zones

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Abstract

We estimated the effective population size and genetic structuring within populations of the rodent reservoir of Argentine Hemorrhagic Fever, *Calomys musculinus*, from zones with different epidemiologic condition (non endemic, historic and epidemic). We found that populations from epidemic zones presented higher effective sizes, higher differentiation among subpopulations and higher levels of internal relatedness than in non-endemic zones. These results would explain the maintenance of the virus in populations from epidemic zones and the patchy distribution of infected rodents.

Keywords: Argentine Hemorrhagic Fever, *Calomys musculinus*, endemic area, genetic structure, non endemic area, population effective size

Introduction

Calomys musculinus (Rodentia, Cricetidae, Sigmodontinae) is one of the most abundant native rodent species in agro-ecosystems of central Argentina, and the reservoir of Junin virus (JV; Arenaviridae), the etiological agent of Argentine Hemorrhagic Fever (AHF). This serious disease is endemic in a large part of central Argentina, where most of the agricultural and cattle production activities of the country concentrates. Since the discovery of the disease, the endemic area has been expanding gradually; however, the expansion rate has been considerably slower in the last years, suggesting some limiting mechanism (Mills and Childs, 1998; Sabattini and Contigiani, 1982). JV is transmitted horizontally among rodents, mainly during the breeding period so it can be enhanced by high effective sizes and high levels of gene flow among reservoir populations, which favor the close contact among infected and non infected individuals. Therefore, in order to contribute to understand the progression of the disease, in this work we estimate the effective size and genetic differentiation among individuals in populations from zones with different epidemiological situation: non endemic zones, epidemic areas (where the incidence of the disease is high), and historic areas (former epidemic zones where the incidence has declined to sporadic cases).

Materials and methods

C. musculinus individuals were captured using Sherman-like live traps in 13 geographic populations located in non-endemic (n=3), historic (n=4) and epidemic (n=6) zones in central Argentina. In each population, traps were arranged in two groups (subpopulations) of 3 lines of 20 traps, separated by 2 to 5 km. A total of 211 rodents were genotyped for 6 microsatellite loci following Chiappero et al. (2005). Population effective sizes (N_e) were calculated using the Bayesian method implemented in the web-based program OneSamp (Tallmon et al., 2008). The genetic differentiation among pairs of rodents from different subpopulations within populations was estimated by the â statistic (Rousset, 2000); values were averaged by population and means were compared among populations by a Friedman non-parametric test. Additionally, we estimated the internal relatedness (IR; Amos et al., 2001) of individuals, which measures the relatedness of an individual's parents. Mean IR values for the epidemic, historic and non endemic areas were compared using a Friedman test.

Results

Population effective sizes for all populations are shown in Figure 1. N_e was lower in non-endemic populations compared to epidemic ones. Populations from the historic area showed different behaviors: BRA (located in the central historic area) and PEC (limiting geographically with the epidemic area) show

high N_e, while ALS and LAL (that limit with the non-endemic area) present low N_e. Mean â values were significantly higher in populations from the non endemic area than in populations of the epidemic and historic areas (p<0.001), while IR was significantly lower in the non-endemic area populations (p=0.012).
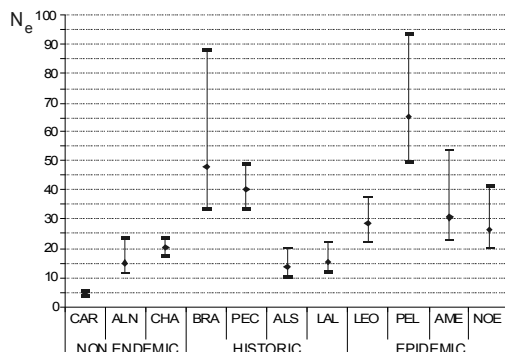

Fig. 1   Effective sizes estimates (filled diamonds) and 95% credible intervals (vertical bars) in 13 populations of *C. musculinus* from non endemic, historic an epidemic zones of Argentine Hemorrhagic Fever.

Discussion

Since the discovery of AHF, the endemic area has been expanding gradually, but prevalence of infection in reservoir populations can be very high in some localities and very low or absent at nearby sites. Within an epidemic locality, infected animals are clustered in a restricted area (focal distribution), yielding a patchy distribution of the JV (Calderón, 2004). We found that populations of the reservoir show a higher effective size, higher differentiation among subpopulations and higher levels of internal relatedness in epidemic areas than in non-endemic ones, which would be in line with the proposal of focal distribution of infected specimens. Polop et al. (2007) reported that the population abundance of *C. musculinus,* and also the relative abundance of this species with respect to other species of the rodent assemblage, is higher in endemic sites compared to non-endemic ones. The high IR values found in endemic sites could be the result of mating occurring mostly among nearby individuals given the high levels of abundance in those sites which would, in turn, increase the genetic distance between subpopulations. The high effective size in epidemic populations would be enough to maintain the virus-cycle infection; on the contrary, populations with low effective sizes (non endemic areas) would be more prone to clear eventual infections, diminishing the probability of transmitting the virus to other conspecific rodents.

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