

Inferring the Evolutionary History of the European Rabbit (*Oryctolagus cuniculus*) from Molecular Markers

NUNO FERRAND

Introduction

The European rabbit (*Oryctolagus cuniculus*) is a well-known species all over the world and occurs in both wild and domestic forms. European rabbits are present in most of Europe, North Africa, parts of South America, Australia and New Zealand, as well as in more than 800 islands, where they occupy a huge variety of ecosystems (Thompson and King 1994). Its domestic counterpart exhibits a remarkable variety of breeds showing variation in colour, size and fertility. Domestic breeds are kept and raised globally for meat, wool and fur, and also as increasing popular pets. However, for most of its history, the European rabbit was confined to the Iberian Peninsula where the species is supposed to have emerged in the mid-Pleistocene. We know this from the analysis of the fossil record that in addition, places also in the Iberian Peninsula the emergence of genus *Oryctolagus* (Lopez-Martinez 2008, this book). The subsequent geographical expansion and successful colonization of multiple territories is as recent as historical times and has been mostly human-mediated. This expansion eventually ended in a domestication process that is unique to Western Europe.

While the fossil record together with much more recent historical documents attesting the origin and recent expansion of the European rabbit provide us with a rough picture of the history of the species, the fact is that in both cases they are represented by scarce and spotty information. This in turn prevents a deeper understanding of the rich and unique evolutionary history of the rabbit species. An alternative way to address questions related to this subject is the analysis of genetic data. In fact, the history of species, including their split from sister taxa, historical population subdivisions, expansions and contractions, and other types of demographic events, leave a signature in their genomes that can be assessed by using a combination of molecular biology tools and statistical inference procedures. This is particularly true in the last few years, which witnessed the dramatic development

CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Campus Agrário de Vairão, 4485-661 Vairão, and Departamento de Zoologia e Antropologia, Faculdade de Ciências, Universidade do Porto, Praça Gomes Teixeira, 4099-002 Porto, Portugal; E-mail: nferrand@mail.icav.up.pt

P.C. Alves, N. Ferrand, and K. Hackländer (Eds.)
Lagomorph Biology: Evolution, Ecology, and Conservation: 47–63
© Springer-Verlag Berlin Heidelberg 2008

of different types of molecular markers able to provide different, but complementary, information on the evolutionary trajectories of species (Avice 2004). In a mammalian species genetic information is typically packed in four different genomic compartments, which different properties will be briefly discussed below and exemplified in the subsequent sections.

The Different Genomic Compartments of a Mammal

The four different genomic compartments of a mammal are represented in Fig. 1. Most of the genetic information is in the autosomes, in which two genes per sex occur. These genes are bi-parentally inherited and can recombine freely at a rate that varies depending on different genomic features. Different from the autosomes is the peculiar X-chromosome that exhibits two copies in females but only one in males, where it is haploid. As a consequence, while

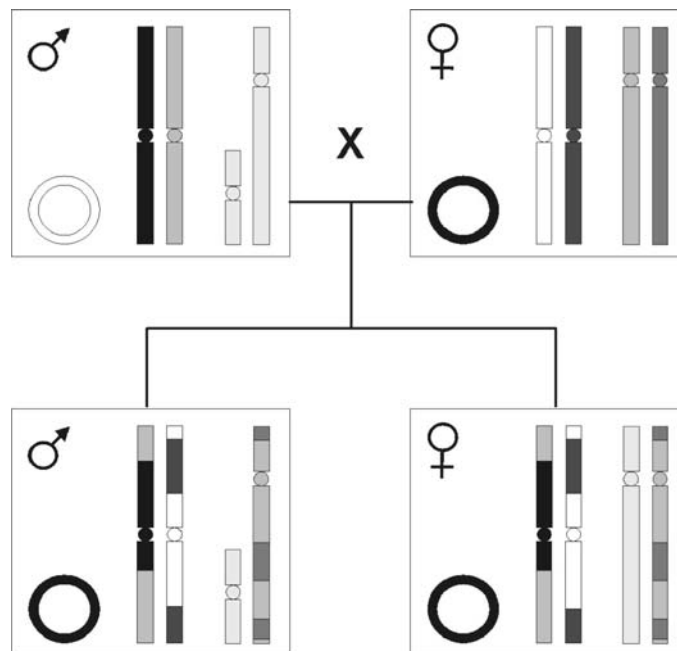


Fig. 1 The four genomic compartments of a mammal. In this two-generation genealogy, the *small circle* represents the mtDNA molecule that is exclusively inherited through the female lineage in spite of being also present in males. The male counterpart is represented by the small Y-chromosome, which occurs only in this sex and defines paternal lineages. In both cases, recombination is absent. The chromosome pair on the left is an example of an autosome, which has two copies in each sex and can recombine in every generation. Finally, the chromosome pair on the right is the peculiar X-chromosome, which has one copy in males and two copies in females, where they are allowed to recombine