Chromosomal speciation in wild house mice

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View of part of the Aeolian Archipelago. Credit: Dr Paolo Franchini

Alterations to chromosomes are considered important in speciation (the process by which new species are formed). This is because several chromosomal rearrangements can make the genome of a few individuals

in a population so different that they cannot successfully interbreed with the rest of the population. It is believed that, over time, this can lead to the evolution of two distinct species with different karyotypes (i.e. different sets of chromosomes making up the genome). In-depth testing of these ideas is now possible with advanced molecular technologies, which allow researchers to sequence DNA across entire genomes.

In a new paper in the journal *Molecular Biology and Evolution*, researchers from the University of Konstanz, Harvard University and La Sapienza University of Rome, study wild house mice (Mus musculus domesticus) from several islands in the Aeolian archipelago off the coast of Sicily, Southern Italy. Their findings provide empirical support to the idea that a specific type of large-scale chromosomal rearrangements called "Robertsonian (Rb) fusions" play an active role in speciation.

Elucidating the role of chromosomal rearrangements in speciation

Chromosomal rearrangements are mutations within the genome of an individual, a population, or an entire species where large pieces of the genome change, for instance through duplication (where an entire chunk of a chromosome is duplicated) or inversion (where a part of a chromosome changes its orientation relative to the rest of the chromosome). "The most common type of chromosomal rearrangement to occur in the natural house mouse populations of Western Europe are Robertsonian fusions," explains Dr. Paolo Franchini, first author on the study and a researcher in the University of Konstanz's zoology and evolutionary biology research group led by Professor Axel Meyer.

Robertsonian fusions are large-scale chromosomal rearrangements where two entire chromosomes fuse to form one very large metacentric (X-shaped) chromosome. "This type of rearrangement is known to play a

considerable role in speciation," says Franchini. "And it happens to be very common in wild house mice, which makes them a perfect study system. The added advantage with the Aeolian mice is that these populations are very small and genetic mutations are likely to spread rapidly through the population of a given island."

The wild house mouse populations in the Aeolian archipelago, which consists of seven small islands of volcanic origin, have different karyotypes characterized by different combinations of Robertsonian fusions. One of the main goals in studying these populations was to understand how these karyotypic distributions evolved—that is, to reconstruct their evolutionary history.

Single origin vs multiple independent origins

"The main issue in this context is the origin of these distributions," Franchini explains. Interestingly, three of the Robertsonian chromosomes found in Aeolian island populations are also found in mice from central Italy. A previous study had therefore suggested that the mice from central Italy colonized the islands alongside human settlers, concluding that this is why these three Robertsonian fusions can be observed now in the Aeolian islands.

This is what is referred to as the "single origin hypothesis." It postulates that these Rb fusions happened just once—in central Italy—and spread from there. "What we were able to show in our paper is that the same chromosomal fusions can happen in different locations and independently from one another," says Franchini. Since Robertsonian fusions are known to play an active role in chromosomal speciation, understanding their origin and establishing whether they are occurring frequently and in different geographic locations or not can provide insights into the dynamics of speciation: "If the same chromosomal fusions occur much more readily than previously thought, then this

would support a high mutation rate and, indirectly, a greater chance of Robertsonian rearrangements playing an active role in speciation."

To distinguish these two hypotheses—"single origin" and "multiple-independent origins"—it is necessary to dig deeper into the genetic sequence of these Robertsonian chromosomes. Therefore, the researchers in this new study traced the origins and evolutionary history of the three identical Robertsonian chromosomes found in the island and mainland populations. Applying phylogenetic and population genetic approaches to genetic markers spread across the whole genome, they were able to show that this particular set of chromosomes originated at least twice in two different geographic locations—in the islands and in central Italy. This supports the "multiple-independent origins" hypothesis.

Interplay of Robertsonian fusions and hybridization events

The team were further able to show that some of the karyotypes observed in the island populations are in fact a product of hybridization events involving different mice with different sets of Robertsonian or standard chromosomes. "Ultimately, it is this interplay between the fixation of newly formed Robertsonian chromosomes and such hybridization events that shaped the distribution of karyotypes in the Aeolian archipelago," concludes Paolo Franchini.

Whether these genomic mutations have an impact on the phenotypes of these mouse populations remains unknown. "This is the next step," says Franchini. "We know that, most of the time, mutations do something. Some Robertsonian fusions are very common across Europe, which suggests that some sort of selection in favour of these mutations might take place. This in turn suggests that these mutations could even be

beneficial." However, what exactly the advantage of these fusions may be remains an open and fascinating question.

More information: Paolo Franchini et al. Reconstructing the evolutionary history of chromosomal races on islands: a genome-wide analysis of natural house mouse populations, *Molecular Biology and Evolution* (2020). DOI: 10.1093/molbev/msaa118

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