

Regions in the genome cause infertility in some hybrids of house mouse subspecies

December 10 2014



The distribution of the house mouse subspecies cuts across Central Europe: *Mus musculus musculus* lives to the east, *Mus musculus domesticus* to west. In the border region, the two sub-species mix. Credit: MPI for Evolutionary Biology/ B. Harr

Three from one: Half a million years ago, the house mouse, *Mus musculus*, split into three subspecies, two of which are native to Europe.

Within a transition zone, the two European forms interbreed to produce hybrids that are less fertile than their purebred kin. Two scientists at the Max Planck Institute for Evolutionary Biology in Plön have now identified sections in the genomes of such hybrid mice that reduce the animals' fertility. The genes control testicular gene activity and testicular weight. The researchers' analysis uncovered a complex web of interactions between various gene regions that can suppress reproduction between the hybrids in the course of evolution. Consequently, the mouse forms continue to diverge until the two subspecies give rise to entirely distinct species.

Biological science has proposed a number of different species concepts. One thing is certain though: evolution is an ongoing process, and we only observe a brief snapshot of it. A species that exists today can soon split into two subtypes. The process of speciation is particularly easy to study in emerging species: Before the flow of genes is completely interrupted, hybrids are often produced that are viable but are largely or fully infertile.

Male fertility is often related to testicular weight and size. Changes in gene regulation in the testicles can also lead to infertility. Bettina Harr and Leslie Turner of the Max Planck Institute for Evolutionary Biology therefore looked for regions in the genotype of mice that affect testicular weight and testicular [gene activity](#). To this end, they studied normal and partially sterile hybrid mice in a genome-wide association analysis. "The study shows that many different gene regions play a role in the fertility of hybrid males, some of which have never previously been associated with fertility," explains Turner.

Once the researchers had identified specific areas in the genome, they looked for interactions between them. Many theories suggest that impaired fertility in hybrids is due to interactions between the genes originating from the different subspecies forms. "With one exception, all

the loci we identified interact with at least one other region. Most have multiple interaction partners," says Bettina Harr.

Hence, an intricate web of interactions exists that reduces the reproductive capacity of hybrid [mice](#) within the hybrid zone. It is not yet clear precisely which genes lead to altered gene activity or testicular size, but the Max Planck scientists have already made progress in narrowing down the search. Some of the genome sections identified contain fewer than ten genes and therefore present some promising candidates.

More information: "Genome-Wide Mapping In A House Mouse Hybrid Zone Reveals Hybrid Sterility Loci And Dobzhansky-Muller Interactions." *eLIFE* doi: [dx.doi.org/10.7554/eLife.02504](https://doi.org/10.7554/eLife.02504)

Provided by Max Planck Society

Citation: Regions in the genome cause infertility in some hybrids of house mouse subspecies (2014, December 10) retrieved 27 April 2024 from <https://phys.org/news/2014-12-regions-genome-infertility-hybrids-house.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--