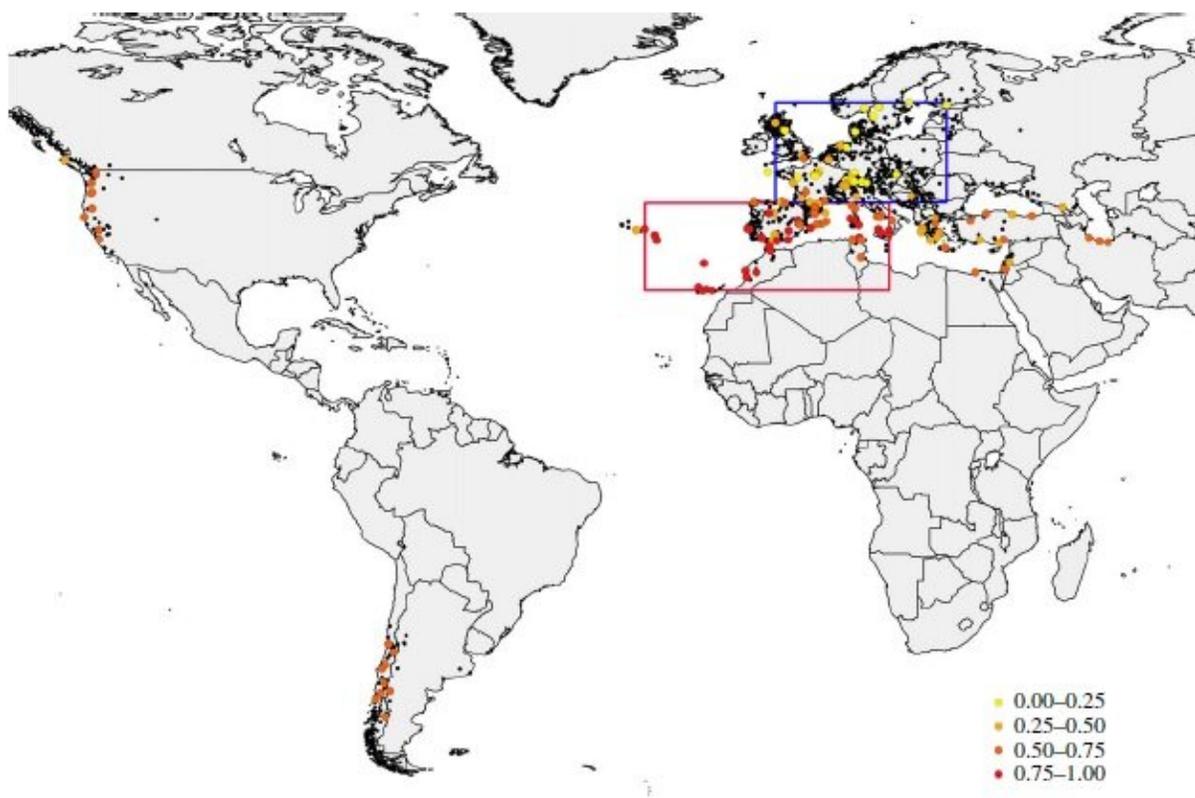


Adaptive genetic markers identify the origins and dispersal of invasive species

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The study confirms the hypothesis that marks the Mediterranean basin as the original place for the *Drosophila subobscura* colonizer individuals. Credit: University of Barcelona

The western area of the Iberian Peninsula could be determinant in the origin of the ancestral population of *Drosophila subobscura*, an invasive

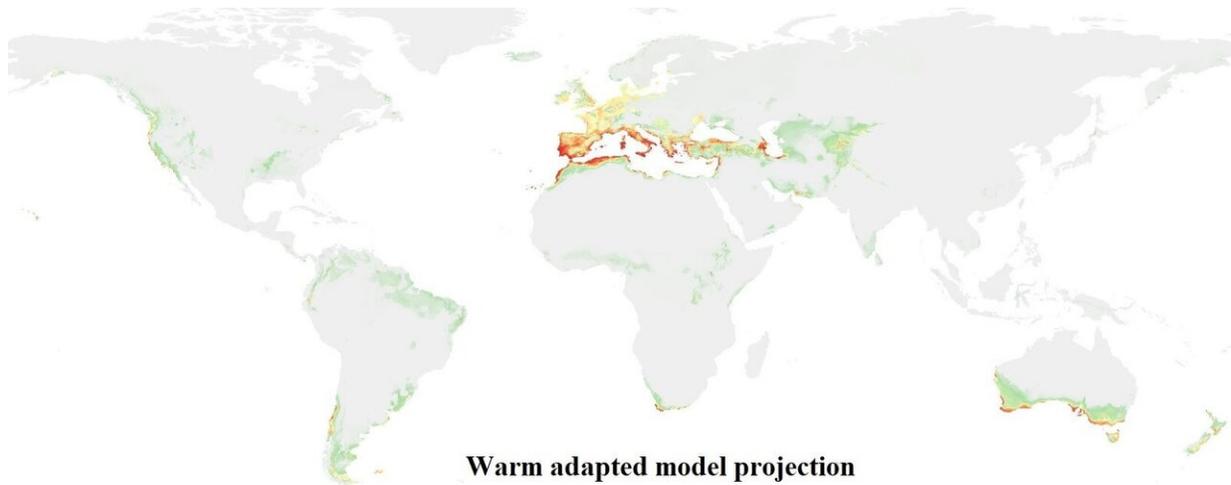
species widely spread across multiple latitudes. This is the conclusion of a study of adaptive genetic markers now published in the journal *Proceedings of the Royal Society B*, which was led by Marta Pascual from the Faculty of Biology and the Biodiversity Research Institute (IRBio) of the University of Barcelona.

The study supports the use of adaptive genetic markers combined with genetically informed environmental niche modeling as the scientific methodology to determine the potential areas of [origin](#) of the colonizer [species](#). Moreover, these indicators could be useful to define areas that are not yet colonized. The study counts on the participation of experts from the University of Oporto (Portugal) and the University of Washington and National Science Foundation (United States), among others.

Drosophila subobscura: from the Mediterranean basin to the American continent

The study confirms the hypothesis that marks the Mediterranean basin as the origin of the *D. subobscura* colonizer individuals, a [native species](#) from the palearctic area, which colonized the American continent in the late 1970s. Like other invasive species, an anthropic environment (freight traffic, etc.) would have made it easier for the species to spread.

According to the experts, during the colonizing process of *D. subobscura*, North and South America underwent a bottleneck effect, and both hemispheres were colonized in a sequential manner. The study confirms the influence of the origin and the genetic composition of the founding individuals in the dispersal of the species. Compared to previous modeling studies on the potential distribution of the species, this study model considers the existence of local adaptations that can allow greater adaptation to certain environmental conditions.



The model that better predicts the colonized region by *D. subobscura* is the one based on populations with a high frequency of warm chromosomal arrangements. Credit: University of Barcelona

"Genetic data enabled determining that chromosomal arrangements of the species are adaptive—in particular, to cold and warm environments—and their frequencies vary quickly depending on the environment," says Pascual, lecturer at the Department of Genetics, Microbiology and Statistics of the UB.

The current distribution in the American continent could not be completely explained if the origins of the colonizers were in northern Europe, whereas if they were from the south, there would be a better explanation, according to the authors. Therefore, the model that better predicts the colonized region by *D. subobscura* is the one based on populations with a high frequency of warm chromosomal arrangements.

Apart from inferring potential areas of origin of the colonizers, the

distribution models of the species combined with adaptive genetic markers can contribute to identify future situations of introduction and spread of a new invasive species.

"If the colonizers come from a specific area, we can predict the potential distribution of the species. If they come from different environments, the dispersal potential can be very powerful. With this knowledge, measures could be taken to prevent [invasive species](#) from reaching certain areas of the world. Once they colonize an environment, it is very hard to remove them," says Pascual.

More information: Neftalí Sillero et al. Distribution modeling of an introduced species: do adaptive genetic markers affect potential range?, *Proceedings of the Royal Society B: Biological Sciences* (2020). [DOI: 10.1098/rspb.2020.1791](#)

Provided by University of Barcelona

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