

# Immune system study could help conserve endangered species

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(Phys.org) —A study by University of Georgia ecologists has found that diversity in mammal immune system genes may have more to do with the opportunity to choose a mate than with exposure to parasites.

Besides answering a long-standing question in evolutionary ecology, the findings, recently published in the *Proceedings of the Royal Society B*, have implications for the conservation of imperiled species.

For decades, scientists have puzzled over what causes the extreme diversity in genes of the immune system, especially for a group of genes known as the [major histocompatibility complex](#), or MHC. These genes are responsible for recognizing and fighting against the many different pathogens and parasites encountered by hosts. MHC genes can harbor enormous variation, even in [animal species](#) that have very low diversity in the rest of the genome—particularly species that have experienced population "bottlenecks" caused by catastrophic events that reduce the size of the population and its [gene pool](#).

According to lead author Jamie Winternitz, who received her doctorate from the UGA Odum School of Ecology earlier this year, there have been two main competing hypotheses about what causes this variation.

One is that diversity in immune genes is mainly driven by pressure from parasites—the more diversity in immune genes, the more different types of parasites the immune system can recognize and fight. Animal species that encounter many different kinds of parasites would therefore be

expected to have greater immune gene diversity.

The second hypothesis is that [sexual selection](#) to avoid [inbreeding](#) or to choose a compatible mate drives the variation. The immune genes that detect and fight against parasites also affect traits that make animals—including humans—more or less attractive to potential mates. Studies have shown that [prospective mates](#) that smell different—an indicator they have a different MHC [genetic makeup](#)—are more appealing, helping prevent mating between closely related individuals. Animals also might use MHC-based cues to choose partners that will provide "good genes" for their offspring.

To conduct her analysis, Winternitz used MHC genetic sequences for 112 mammal species from GenBank, a repository of genetic data maintained by the National Institutes of Health, and compiled data about those species' behavioral and physical traits from other published databases. She also drew on the Global Mammal Parasite Database compiled by Odum School researchers.

The scope of the information made it possible to compare immune gene diversity across species while exploring both hypothetical drivers of that diversity.

"What the study found, in a nutshell, is that the strength of sexual selection is a much better predictor of MHC immune gene variation than parasitism is," said study co-author Sonia Altizer, an associate professor in the Odum School.

Winternitz added that the findings were "pretty exciting and unexpected," she said. "When I started compiling the data, I had no idea if I would observe any significant associations at all."

Understanding the importance of sexual selection has practical value for

those working to conserve rare and endangered species.

"One relevant situation we had in mind was for managers of conservation genetic programs that use fertilizations to maintain a species' standing genetic stock," said Winternitz. "Our results suggest that the current practice of random assignment of mates might be less than optimal for maintaining variability at functionally important immune genes and that employing some opportunity for mate choice could be more effective."

**More information:** [rspb.royalsocietypublishing.org ... /1769/20131605.short](https://rspb.royalsocietypublishing.org/doi/10.1098/rspb.2013.1605)

Provided by University of Georgia

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