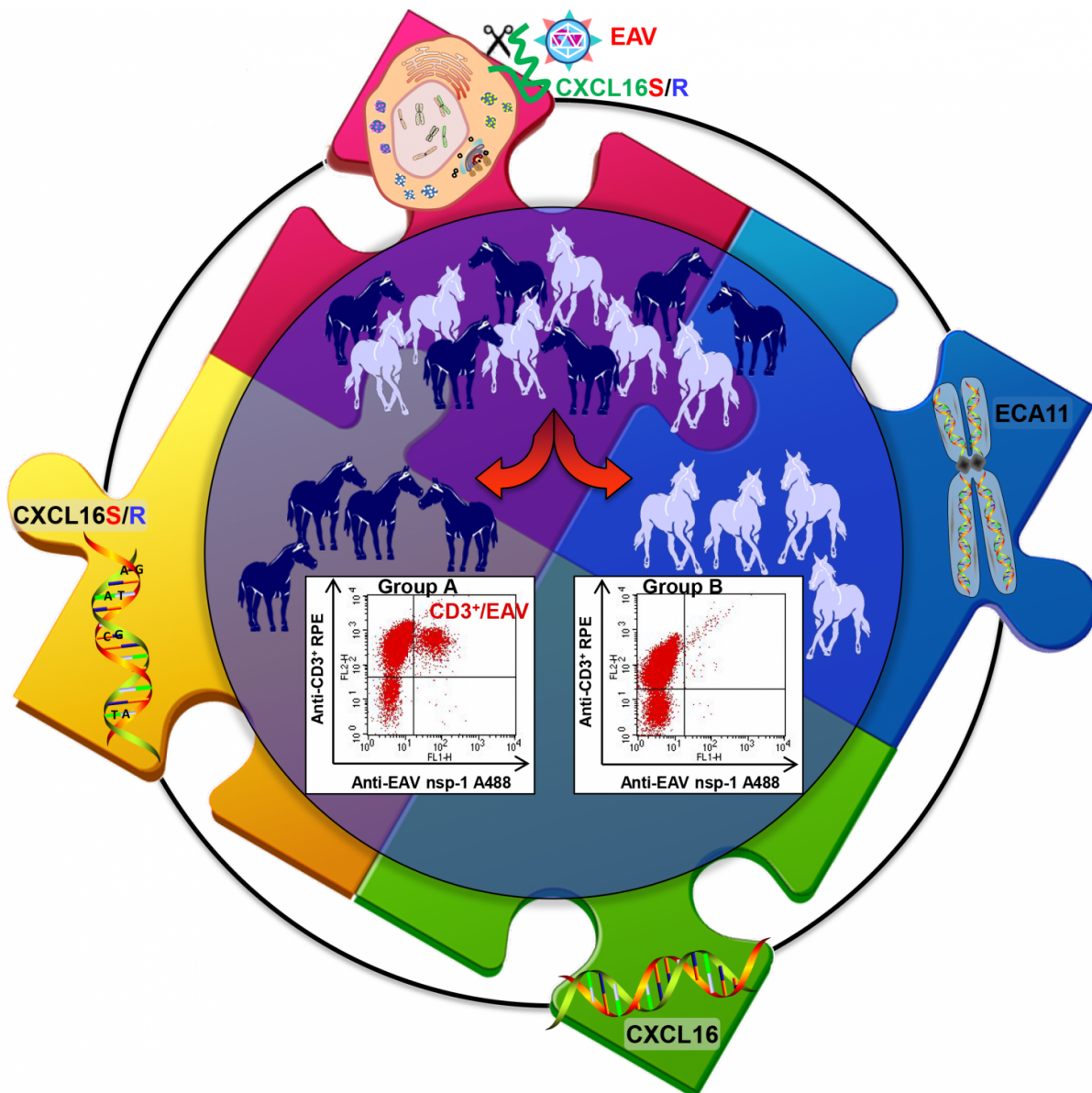


Genetic variant determines if stallions become carriers of equine arteritis virus

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Identification of CXCL16 as a determinant of equine arteritis virus persistent infection in the stallion. Credit: Udeni B. R. Balasuriya and colleagues

Following natural infection equine arteritis virus (EAV) establishes a long-term carrier state in the reproductive tract of stallions without any evidence of clinical signs. These carrier stallions maintain and perpetuate the virus in the equine population between breeding seasons. Sexual transmission of the virus can lead to outbreaks of equine viral arteritis characterized by abortion and respiratory disease in horses.

The change of just four nucleotides in the CXCL16 gene is all that is necessary to determine whether or not stallions are likely to become long-term carriers of EAV. Sanjay Sarkar, Ernest Baily and Udeni Balasuriya of the University of Kentucky, Lexington, and colleagues report these findings December 8th, 2016 in *PLOS Genetics*.

EAV [infection](#) is a serious problem for horse breeders because it can result in 10-70% of infected stallions becoming long-term carriers that can spread the [virus](#) in their semen for months or many years. In previous studies, the scientists discovered that some stallions have subpopulations of CD3+ T lymphocytes - a type of [white blood cells](#) - that are susceptible to EAV infection in lab experiments and are also associated with being carriers. To follow up on these findings, the researchers performed a genome wide association study to find gene alleles that correlate with persistent EAV infection. They identified alleles of the CXCL16 gene that code for two slightly different proteins, one associated with susceptibility to long-term infection, and the other associated with resistance to becoming a long-term carrier. Studies performed in cell culture suggest that the susceptible form of the protein acts as an entry receptor for the virus and is more effective at seeking out and binding the virus compared to the resistant form.

The study describes the specific biological mechanisms that underlie resistance to lasting EAV infections in intact sexually matured male horses. It also adds to our general understanding of host-virus interactions and the evolution of resistance to infectious diseases. The results will likely have a significant impact on horse breeding industries, which can experience considerable economic hardship due to EAV infection. Findings from this study will enable development of a genetic test to identify the stallions at most risk for becoming EAV carriers and will help elucidate the mechanisms involved, the understanding of which could lead to development of treatment strategies to clear the infection. In the meantime, preferentially breeding for the "resistance" allele may help to limit persistent EAV infections in stallions.

More information: Sarkar S, Bailey E, Go YY, Cook RF, Kalbfleisch T, Eberth J, et al. (2016) Allelic Variation in CXCL16 Determines CD3+ T Lymphocyte Susceptibility to Equine Arteritis Virus Infection and Establishment of Long-Term Carrier State in the Stallion. *PLoS Genet* 12(12): e1006467. DOI: [10.1371/journal.pgen.1006467](https://doi.org/10.1371/journal.pgen.1006467)

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