

## Should we care that rabbit genes are different around Australia?

By Dr Amy Iannella

Traditionally, we have pinned the blame for Australia's rabbits squarely on Thomas Austin of Barwon Park in Victoria, whose efforts in importing wild British rabbits lead to widespread plague. Recent work, both historical<sup>1</sup> and genetic<sup>2</sup>, has shown that Australia's rabbits are more likely to come from numerous introductions. Our feral rabbits form six genetic clusters based on their ancestral introduction group, so Mr Austin can probably only take credit for the rabbits around Victoria. That's all very well for the late Thomas Austin, but does it have any impact on the rabbits of today?

The origin of Australia's rabbits influences the genes they carry today, plus or minus a tiny bit of mutation and a lot of natural selection. If one of our rabbit groups just happened to carry a gene variant that helped them to survive the calicivirus (RHDV), then that variant would have become common over time (after all, you need to survive the diseases of adolescence if you want to make lots of rabbit babies and pass on your genes), but only in the areas where that gene was available in the first place. Perhaps this could help us to explain why RHDV works better in some areas than others, or, in the distant future, to release different virus strains in each region based on where they might have the most effect.



So, to figure out whether knowing the ancestry of our rabbits can help us with controlling them, I have been investigating exactly which genes are different around Australia and comparing them to the genes that we think might have a role in RHDV resistance.<sup>3,4,5</sup> Of the 135 possible resistance genes that I tested, just one seems to vary based on rabbit ancestry. That suggests that other factors, like the presence or absence of the benign RCV-A1 virus, might have more impact on modern rabbit genetics than which boat the rabbit's ancestors came in on.



That being said, the one resistance gene that I did find ancestral differences in is a particularly interesting one. The gene, known as MHC class 1, is a major immune gene which helps the body to identify viruses and other infections and target them for destruction. Humans have this gene too, and the particular variants sitting in your genome will impact which virus strains can sneak past your immune system and which get caught before they have a chance to make you sick. Variation in MHC class 1 genes has previously been shown to impact RHDV resistance in rabbits<sup>3</sup>, and likely impacts the effectiveness of myxomatosis too. My research shows that the MHC variants that are common in Western Australia and South Australia are probably very uncommon in the Eastern states, and vice versa. This means there is a decent chance that the effectiveness of any given virus strain will have an East/West divide in Australia's rabbits. The next step is finding some effective ways to put that knowledge to use!

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<sup>1</sup> Peacock, D. and I. Abbott (2013). "The role of quoll (*Dasyurus*) predation in the outcome of pre-1900 introductions of rabbits (*Oryctolagus cuniculus*) to the mainland and islands of Australia." *Australian Journal of Zoology* **61**(3): 206

<sup>2</sup> Iannella, A. et al. (2019). "Genetic perspectives on the historical introduction of the European rabbit (*Oryctolagus cuniculus*) to Australia". *Biological Invasions* **21**(2): 603-614.

<sup>3</sup> Schwensow, N. et al. (2017). "High adaptive variability and virus-driven selection on major histocompatibility complex (MHC) genes in invasive wild rabbits in Australia." *Biological Invasions* **19**(4): 1255-1271.

<sup>4</sup> Schwensow, N. et al. (2017). "Resistance to RHD virus in wild Australian rabbits: Comparison of susceptible and resistant individuals using a genomewide approach." *Molecular Ecology* **26**(17): 4551-4561.

<sup>5</sup> Nyström, K. et al. (2015). "Neofunctionalization of the Sec1 alpha1,2fucosyltransferase paralogue in leporids contributes to glycan polymorphism and resistance to rabbit hemorrhagic disease virus." *PLoS Pathogens* **11**(4): e1004759.