

Spotting the genetic differences in barn owls

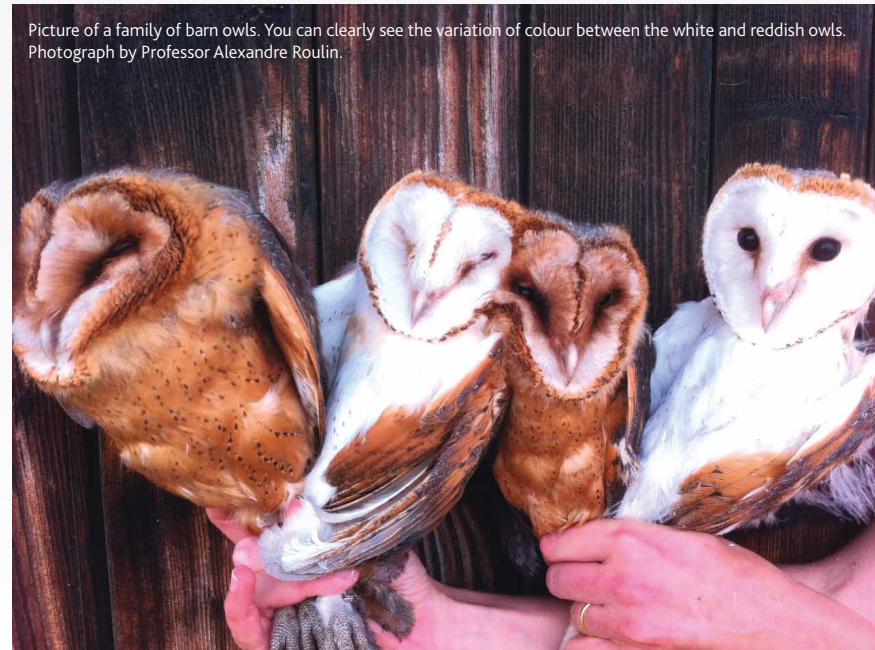
- ★ The number and size of black spots on barn owls varies significantly, while major differences have also been observed in their colouration. We spoke to **Professor Alexandre Roulin** and **Professor Jérôme Goudet** about their work in investigating the genetic basis of this variability, research which could open up new avenues of investigation in several different fields.

A female barn owl typically has larger black spots on its feathers than males, which is associated with a number of qualities that increase resistance to stressful factors, helping to improve their overall survival rate. By contrast, the opposite is the case for male barn owls, which have much smaller spots, an example of what is called sexually antagonistic selection. "The key idea here is that the two sexes share and express the same trait, but the males are selected in one direction, and the females in the other," explains Alexandre Roulin, Professor of Behavioural and Evolutionary Biology at the University of Lausanne. As the Principal Investigator of an SNF-funded research project, Professor Roulin aims to investigate the genetic basis of this variation in barn owls. "We aim to identify the genes that underlie the expression of these large spots. We think that this might be related to genes that have pleiotropic effects," he continues.

Pleiotropic effects

This means a gene that acts on several different traits. For example, a specific gene might be involved in the production of the black spots, while also being responsible for a number of other physiological traits. "So there is a link between the size of the spots and the physiology of the owl," outlines Professor Roulin. The aim now in the project is to explore melanin-based colouration in barn owls. "There are two forms of melanin – eumelanin is black melanin and pheomelanin is red melanin. What's interesting in the owl is that both of these two are expressed," says Professor Jérôme Goudet, a specialist in population genetics also based at the University of Lausanne. "The barn owl varies in the degree of reddishness in colouration, which is related to pheomelanin. They vary also in the number and size of black spots, which is related to eumelanin."

These two traits have different functions, with colouration in barn owls varying between white and a sort of dark-reddish colour, which is thought to be associated with predator-prey interactions. For example, barn owls may use their plumage to stun prey at



Picture of a family of barn owls. You can clearly see the variation of colour between the white and reddish owls. Photograph by Professor Alexandre Roulin.

certain stages of the lunar cycle. "Moonlight is reflected by the white plumage, and the prey are scared by this reflection. They panic and they freeze for longer, so white-coloured birds have a hunting advantage when there is a full moon," explains Professor Roulin. The size of the spots however is related more to sexual selection, which is why Professor Roulin believes it's important to study the genomics

arrive at a position where the research team have sequences from telomere to telomere for each chromosome. "Each genome has its own particularities. The genome of the barn owl is specific in that we can get the big chromosomes, but the small chromosomes are very difficult to get. This is one of the issues we are trying to tackle with these new sequencing methods," he outlines. "With

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in this area to build a fuller picture. "We have been able to find some genes associated with the reddishness, with natural selection, and some genes which are associated with the black spots, so sexual selection," he says.

Researchers already have data on the full genome of over 100 birds across Europe, and are now using genomic tools called Illumina and PacBio to generate even higher quality sequences. By using these sophisticated genomic tools, Professor Goudet hopes to

PacBio sequencing, we can get fragments of 15-20 kilobases sequenced almost perfectly, and we do this at a high coverage so we can then match them."

The length of the genome is constructed through a step-by-step process, resulting in contigs, short components of the assembly. These contigs are then mapped and chained together in a scaffold. "This is how we get to the chromosome-level assembly. We are also using other techniques to help us

to fill any gaps that are still present," says Professor Goudet. This genomic data can then be analysed, from which researchers hope to gain deeper insights. "We have data on the phenotype of individuals – the black spots, the number and the size. By doing classical genome-wide association studies, we can then find which gene connects with a strong signal associated with the size of the spots," explains Professor Goudet. "There, we will be able to use the pedigree data that Alex has accumulated over the last 20 years or so."

Pedigree data

By analysing the pedigree and the phenotype data, and drawing links between them, researchers hope to identify which genes are responsible for variation in both colour and the number of spots.

Once a specific gene has been identified, Professor Roulin says he and his colleagues can then revisit the pedigree data and look to draw wider inferences. "We have blood samples of thousands of individuals, which is a valuable research resource once we know the gene, to calculate how strong the selection is. We can also look at data from other continents, to see what the picture is at a higher level," he outlines. Alongside the barn owl, researchers have also analysed other avian genomes, and a common feature has been identified. "One thing that characterises avian genomes is a high synteny," explains Professor Goudet.

This means essentially that the order of the genes on chromosomes is maintained to a high degree in birds, and the improved quality of the new genome will help in terms of placing the barn owl in the phylogeny. While the project itself has centered on the barn owl, this research holds implications beyond this specific species, which Professor Roulin intends to explore further in future. "The genes associated with these black spots are known to be important from a biomedical point of view. Melanin is highly conserved in all vertebrates, and we expect the genes are also important in humans," he says. One major topic of interest is the



Professor Alexandre Roulin holding a barn owl. Photograph by Séverine Rijken

melanocortin system. "This is a system with five melanocortin receptors. The melanin-stimulating hormones bind to these receptors – they are the same in all animals, including humans – and many diseases are associated with these hormones," continues Professor Roulin.

By combining ecological information on different organisms with the wider picture of population genetics, Professor Roulin and Professor Goudet hope in future to gain new insights into the role of these genes. At this stage however, the immediate priority is to finish the assembly of the genome.

"We want to get a much better, high-quality genome, then it will be easier to find out which genes underly the plumage traits," says Professor Roulin. Another set of data relates to the history of barn owl colonisation of Europe after the last ice-age, a topic of great interest to Professor Goudet. "This is a very interesting project. We published a paper a couple of years ago in which we suggested that the barn owl re-colonised Europe in a ring-like manner, around the Mediterranean Sea. We are looking at these scenarios in genomics," he continues.

THE GENOMICS OF SEXUALLY ANTAGONISTIC SELECTION

Project Objectives

Using genomic tools, we are looking for the genes involved in variation in melanin-based color in the barn owl. This will help us understand why plumage color is associated with physiology, behaviour and predator-prey interactions, but also how coloration could help barn owls to spread over the globe.

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Alexandre Roulin Jérôme Goudet



Alexandre Roulin is a full professor of biology at the University of Lausanne, Switzerland. For already two decades he is studying barn owls to answer evolutionary and ecological scientific questions. His main scientific interests are the adaptive function of melanin-based coloration and negotiation processes taking place in animal societies.

Jérôme Goudet is an associate Professor of Ecology and Evolution at the University of Lausanne, Switzerland. His research uses genomic data in order to understand the interplay of population structure, trait architecture, and selection. For this, he uses different approaches, from theory and the development of statistical tools to field observations.



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