

Blood samples from the zoo help predict diseases in humans

July 15 2019



The blood of the 'radiated tortoise' was also examined by bioinformatics professor Andreas Keller and zoo director Richard Francke. Credit: Oliver Dietze

The zoos of Saarbrücken and Neunkirchen are home to penguins, Asian elephants and many other species. Since they come from different

continents, blood samples are regularly taken from the animals to check their health. These blood samples have now been used by bioinformaticians and human geneticists at the University of Saarland to search for biomarkers that can be used to detect diseases at an early stage. The researchers want to use similar genetic patterns, which have been present in the blood of humans and animals for thousands of years, to improve computer-assisted disease prognosis.

The [research project](#) is unusual for bioinformaticians not only because of the cooperation with the zoo. "Measuring the molecular blood profiles of animals has never been done before in this way," explains Andreas Keller, bioinformatics professor at Saarland University. Instead of examining tissue and data from [human patients](#), Keller and Eckart Meese, a human geneticist from Saarbrücken, analyzed [blood samples](#) from 21 animals. Zoo director Richard Francke had collected the blood during routine examinations between 2016 and 2018 and made it available to the scientists. In fact, these scientists normally investigate biomarkers that occur in [human blood](#) in order to identify lung tumors or diseases such as Alzheimer's and Parkinson's earlier and better. "Micro-RNAs are well suited for this," says Andreas Keller.

"These are short sections of specific molecules in ribonucleic acid that play an important role in the control of genes. In order to find these sections, the researchers use modern bioinformatic methods, including machine learning, a method of artificial intelligence. This in turn leads to a challenge in which the animals from the two Saarland zoos can help. "Up to 20 million data points are collected per (human) patient. The [machine learning](#) methods recognize the typical patterns, for example for a lung tumor or Alzheimer's disease. However, it is difficult for artificial intelligence to learn which biomarker patterns are real and which only seem to fit the respective clinical picture." This is where the blood samples of the animals come into play.

"If a biomarker is evolutionarily conserved, i.e. also occurs in other species in similar form and function, it is much more likely that it is a resilient [biomarker](#)," explains Professor Keller. For this reason, the researchers analyzed the residues from the blood samples taken from the animals. A total of 21 samples were taken from 19 animal species, including a coati and a Humboldt penguin. "The new findings are now being incorporated into our computer models and will help us to identify the correct biomarkers even more precisely in the future," explains Keller.

The researchers from Saarbrücken have published their results in the renowned journal *Nucleic Acids Research*. In addition, they have set up a database in which they also enter their current results. So far, scientists have examined the [blood](#) of a total of 40 [animals](#), including an anaconda and a kangaroo. Scientists from all over the world now have access to this data. The research project was financially supported by the state government of Saarland.

More information: Tobias Fehlmann et al, The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals, *Nucleic Acids Research* (2019). [DOI: 10.1093/nar/gkz227](https://doi.org/10.1093/nar/gkz227)

Provided by Saarland University

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