

# MEDIA RELEASE

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## Vital clues to devil's survival in genome sequence

US-based researchers have today reported the genome sequence of the Tasmanian devil, a development that could have a significant impact on conservation management of this threatened species.

The work, published in the *Proceedings of the National Academy of Sciences*, represents “an important advance in our understanding of the devil and its battle against devil facial tumour disease (DFTD)”, according to a leading Australian researcher, Associate Professor Greg Woods of the Menzies Research Institute Tasmania.

Assoc Prof Woods is one of four members of the Save the Tasmanian Devil Program who contributed to the study. The research was led by Profs Webb Miller and Stephan Schuster of Pennsylvania and Vanessa Hayes of the Children's Cancer Research Institute Australia. Prof Hayes is now at the J. Craig Venter Institute in San Diego, California. The other authors are Dr Menna Jones from the University of Tasmania's School of Zoology, Dr Alex Kreiss of the Menzies Research Institute Tasmania and Dr Stephen Pyecroft of Department of Primary Industries, Parks, Wildlife and Environment

As new findings come to light the Save the Tasmanian Devil Program works closely with researchers and UTAS to identify how relevant findings can be integrated into the program.

The genome is the entirety of an organism's hereditary information. In the case of animals, it is encoded in DNA.

Dr Jones said the genome provided much more detailed markers for understanding the genetic diversity of devils.

“We can use the detailed information in the genome to design captive insurance populations that better represent wild populations. We are also better placed to monitor changes in wild populations.

“Devils could become inbred and lose further genetic diversity in the wild as populations will be at very low levels for decades to come,” she explained. “They are also responding to the extreme mortality from the disease. The genome will enable us to study the way in which it is adapting.”

Assoc Prof Woods added: “The devil genome will contain vital clues to help resolve how DFTD avoids recognition and destruction by the devil’s immune system.

“Interrogating the genome sequence will produce new tools to answer a number of questions about the tumour.”

The researchers obtained the sequence by sequencing the genomes of two devils from geographically isolated areas of Tasmania; the north-west and the south-east.

“The idea is to save a species, not to do a ‘post-mortem’ on it,” Prof Schuster said in a statement.

UTAS is part of the Save the Tasmanian Devil Program – the official response to the threat to the survival of the Tasmanian devil. The program is an initiative of the Australian and Tasmanian governments.

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