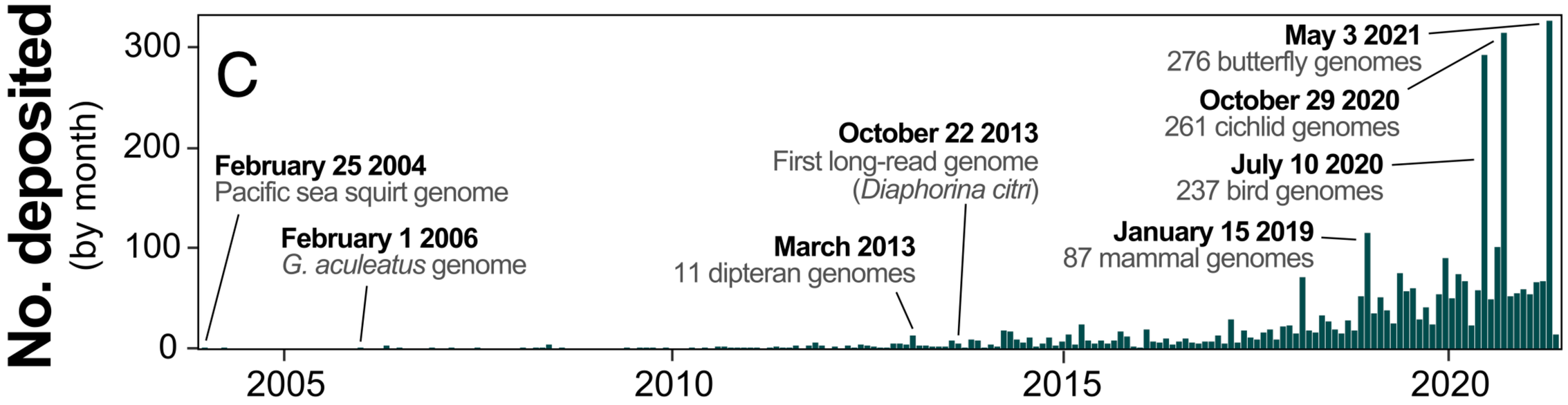
Towards a genome for every animal

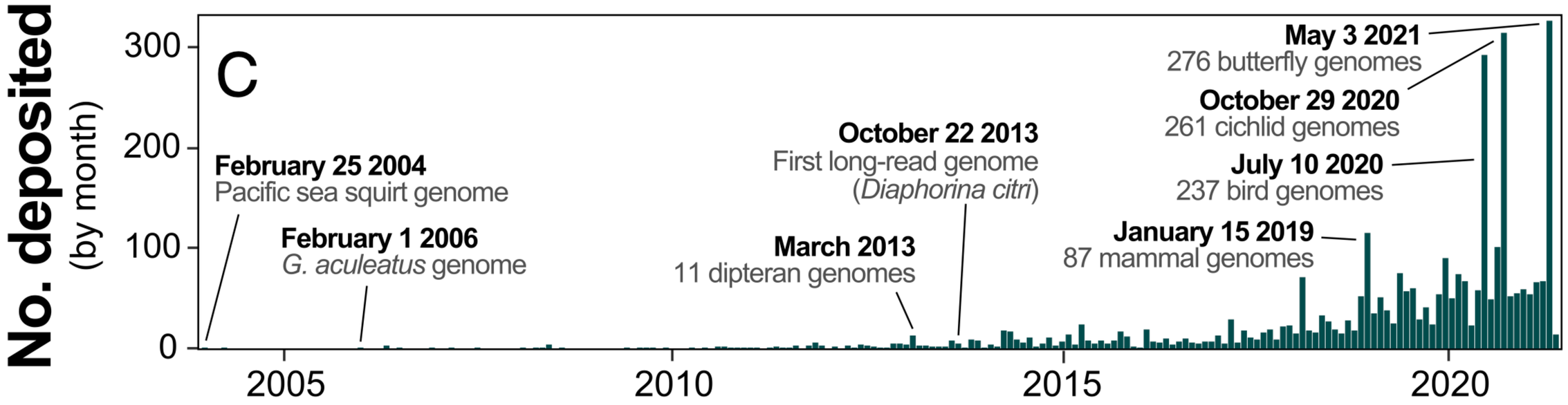
Between 2004 to 2021



PNAS 2021 Vol. 118 No. 52 e2109019118

Towards a genome for every animal

Between 2004 to 2021



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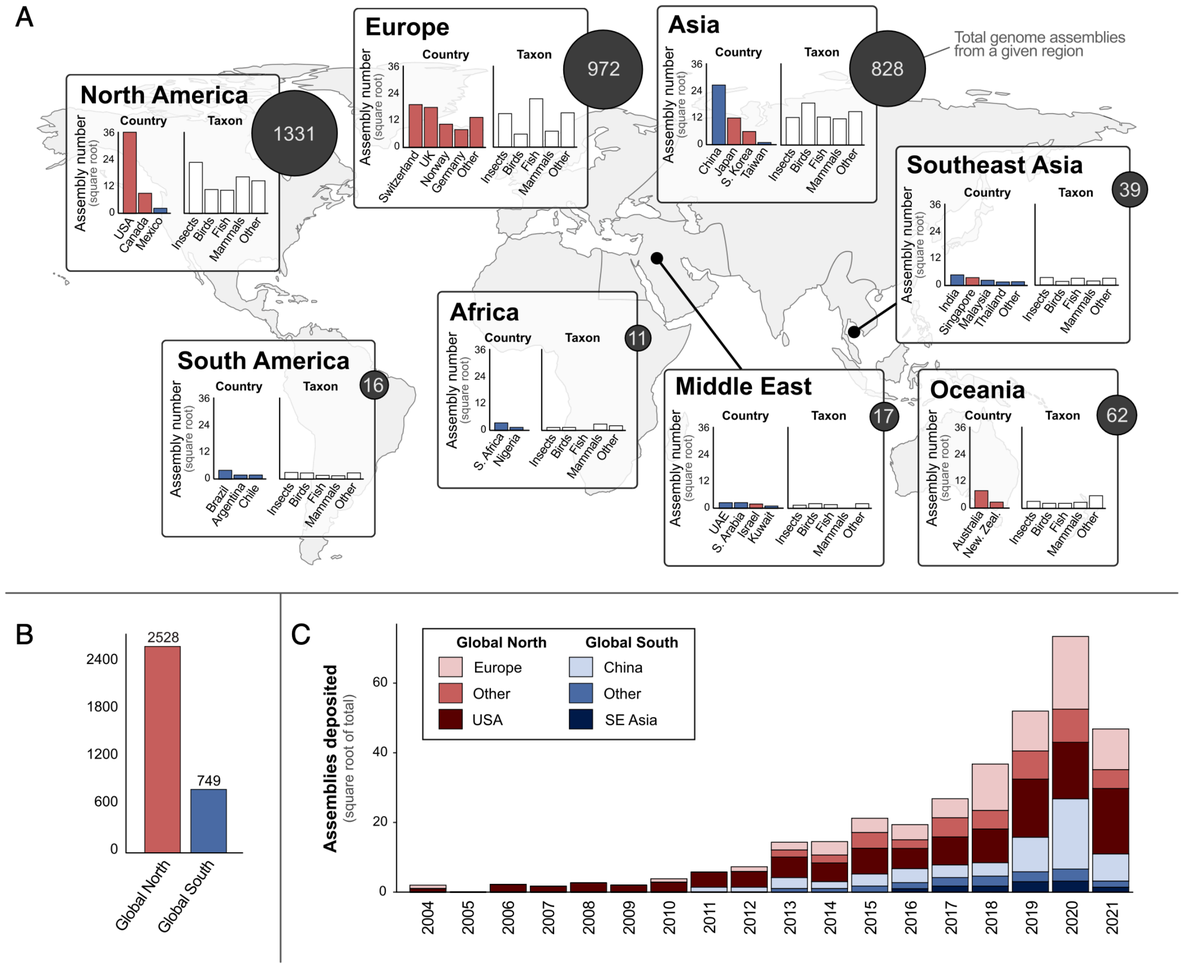
Threatened species with sequenced genomes: 2.4%

PNAS 2022 Vol. 119 No. 4 e2115643118

Loss of biodiversity is a global problem

Yet most genome sequencing studies are performed in the global North



- Few countries led sequencing of animal genomes so far (USA, UK, China)
- Sampling bias (eg, Tree of Life, 70k species in Britain/Irland)
- Parachute science (helicopter research)
- Need for global training of genome scientists and cheaper/mobile sequencing technologies

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Towards a genome for every animal

Where are we now?

The Vertebrate Genomes Project (VGP): a project of the G10K Consortium, aims to generate near error-free reference genome assemblies of ~70,000 extant vertebrate species.

The Earth BioGenome Project (EBP): a *moonshot* for biology, aims to sequence, catalog and characterize the genomes of all of Earth's eukaryotic biodiversity over a period of ten years.

Global Invertebrate Genomics Alliance (GIGA): Over 95% of all metazoan (animal) species comprise the "invertebrates," but very few genomes from these organisms have been sequenced.

The Threatened Species Initiative (TSI) aims to improve conservation practices through the use of cutting-edge genomics technology and advanced computational biology to transform the way the conservation industry manages wildlife recovery programs.

Towards a genome for every animal

Where are we now?

https://www.dnazoo.org/

DNA Zoo Consortium: A global network with >60 collaborating partners across 8 countries for comprehensive worldwide sampling of biological diversity with the participation of geographically localised communities (academic labs, zoos, museums)


10 May 2007 | www.nature.com/nature
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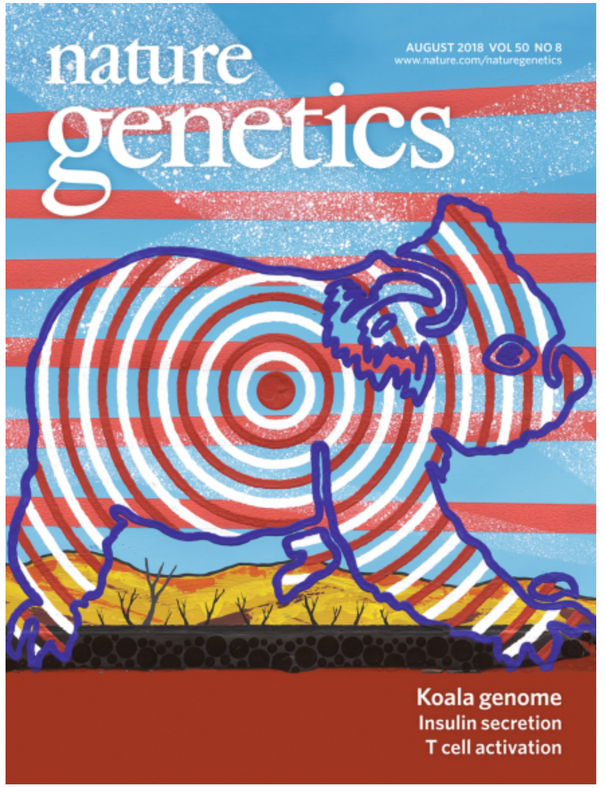

nature genetics
AUGUST 2018 VOL 50 NO 8
www.nature.com/naturegenetics
Koala genome
Insulin secretion
T cell activation

The Tasmanian devil

worlds largest marsupial carnivore

- Member of the marsupial family: with kangaroo, koala, opossum, possum, wombats, wallabies, bandicoots
- Tasmania devils weight 5-10 kg and live up to 5 years
- Up to 4 breedings per life: 20-30 newborns, but only few survive (females have only 4 nipples)
- Newborn stay 100 days in the mothers pouch and become independent after 9 months

The Tasmanian devil

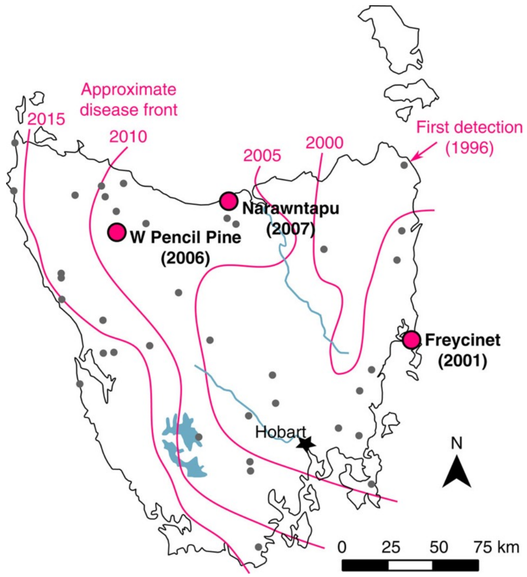
now an endangered species

- Formerly present throughout Australia
- Extinct in Australia since 3,500 years ago
- Now only present on the Island of Tasmania
- Possible reasons: dingos, humans, climate change
- Now an Endangered species

Devil Facial Tumor Disease (DFTD)

A transmissible cancer and new threat for devils

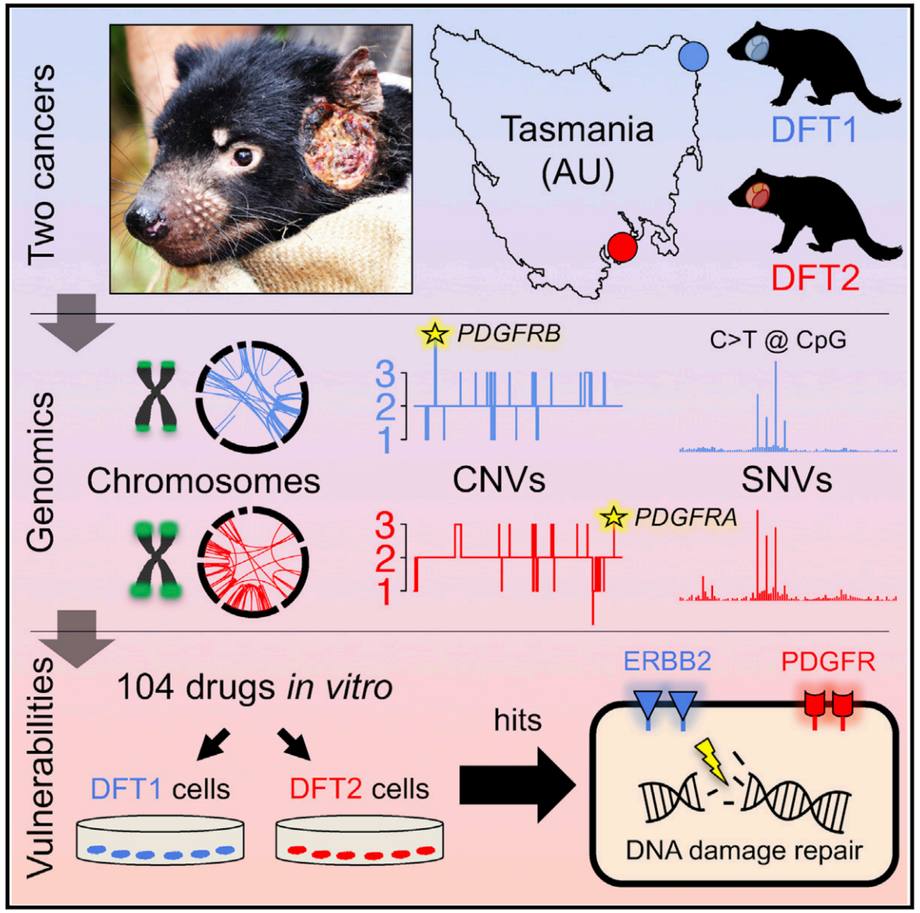
- **DFTD** is a contagious, non-viral cancer affecting Tasmanian devils, manifesting as tumors around the mouth.
- **Transmissible cancer**: the disease spreads primarily through biting, with live cancer cells transferred through the saliva; other transmission methods include sharing food or consuming infected carcasses.
- **Impact on population**: since its discovery in 1996 in north-east Tasmania, DFTD has caused a dramatic decline of Devils (80% in less than 20 years).
- **Conservation efforts**: there is no cure yet; ongoing efforts include breeding programs, research on vaccines, and monitoring disease-free pockets in Tasmania.



Nat Commun. 2016 Aug 30;7:12684.

DFTD cancer genomics

Origins and therapeutic vulnerabilities



- Two independent origins (DFT1 and DFT2): one from a female (DFT1, common clone) and one from a male (DFT2, rare clone; confirmed in only 11 devils).
- Currently no explanation for the independent origin yet no signs of exogenous exposures or viruses from genome studies
- Somatic DNA copy number alterations in receptor tyrosine kinase (RTK) genes detected in both tumors (PDGFRA, PDGFRB, PDGFA, PDGF)
- Drug screen suggests vulnerability against RTK inhibitors

Cancer Cell (2018) 33, 607–619

Genomics-informed recovery of Tasmanian devils

Insurance populations and maintenance of genetic diversity

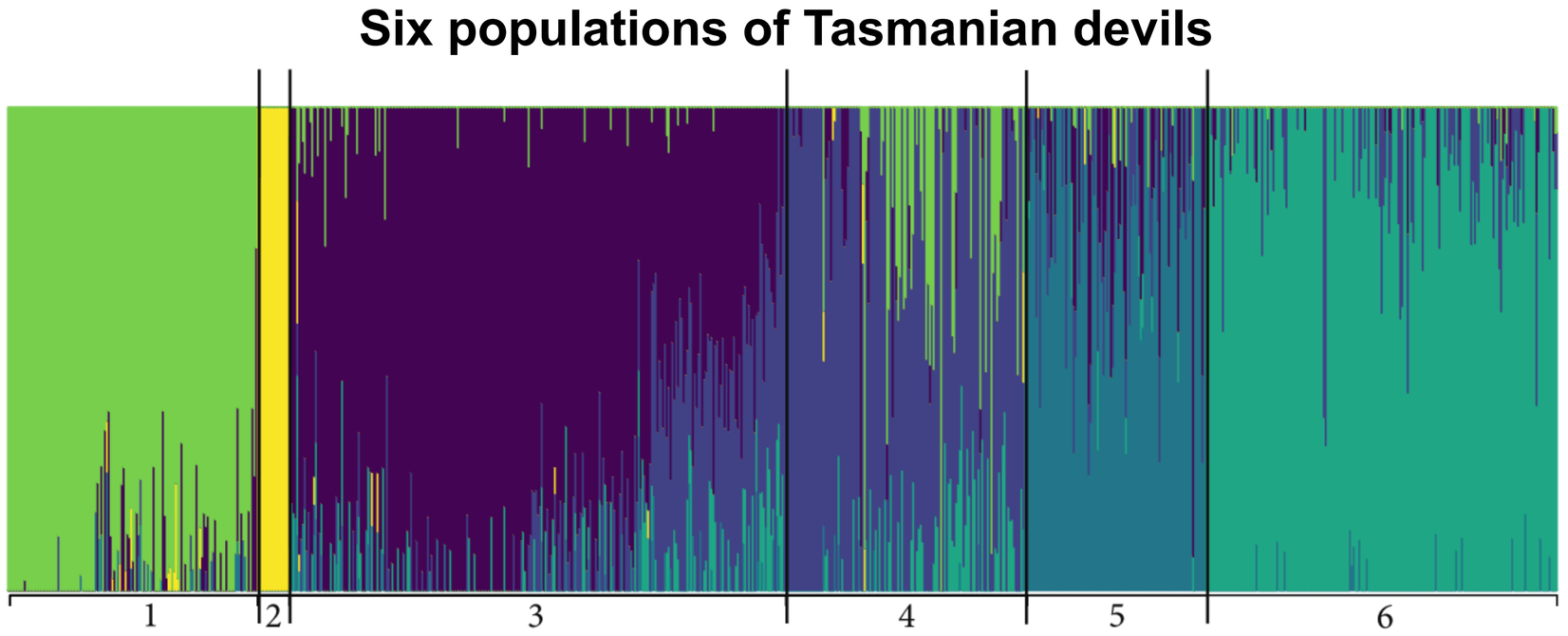
- Insurance population: captive breeding of DFTD-free animals
- Ex situ programs need to maintain genetic diversity (=adaptive potential) and decrease risks of genetic bottlenecks
- Devil genome sequencing studies help to identify wild Devil populations, track genetic diversity of insurance populations, population sizes, and success of release of individuals into existing wild populations

IUCN SSC Conservation Planning Specialist Group

More than 100 healthy devils have been released into disease-free areas, and the insurance population has grown to more than 600 animals strong.

Genomics-informed recovery of Tasmanian devils

Insurance populations and maintenance of genetic diversity

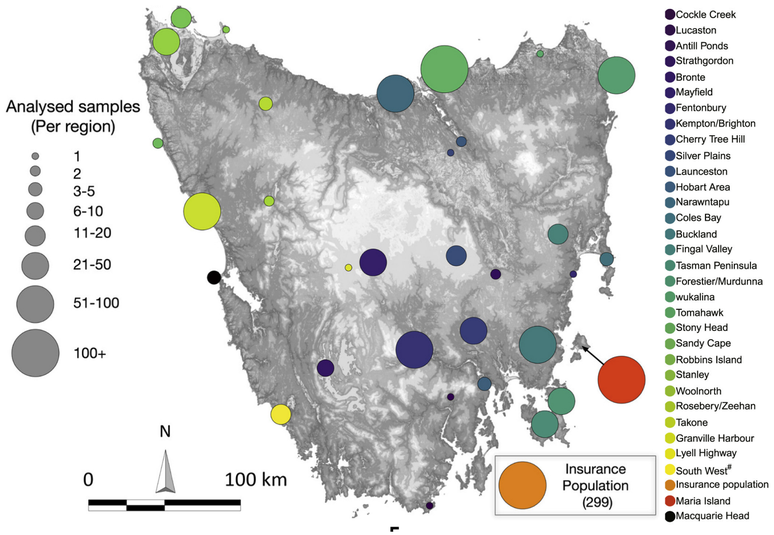


Farquharson et al., iScience 25, 104474 (2022)

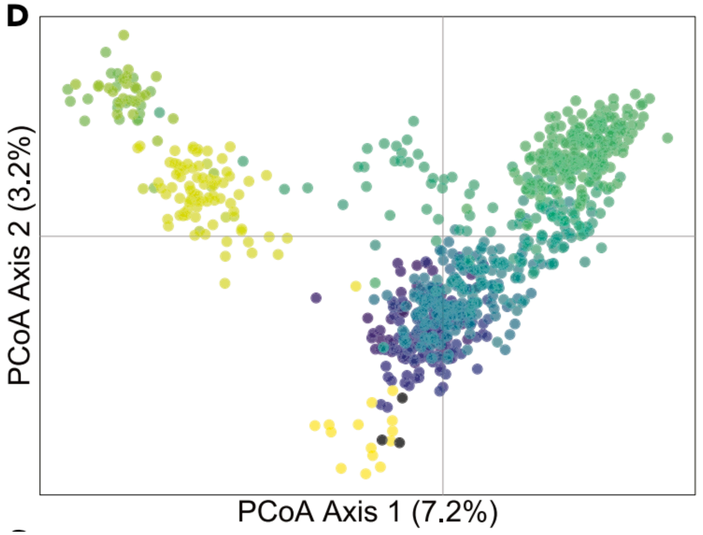
Genomics-informed recovery of Tasmanian devils

Insurance populations and maintenance of genetic diversity

Wild Devil sampling sites

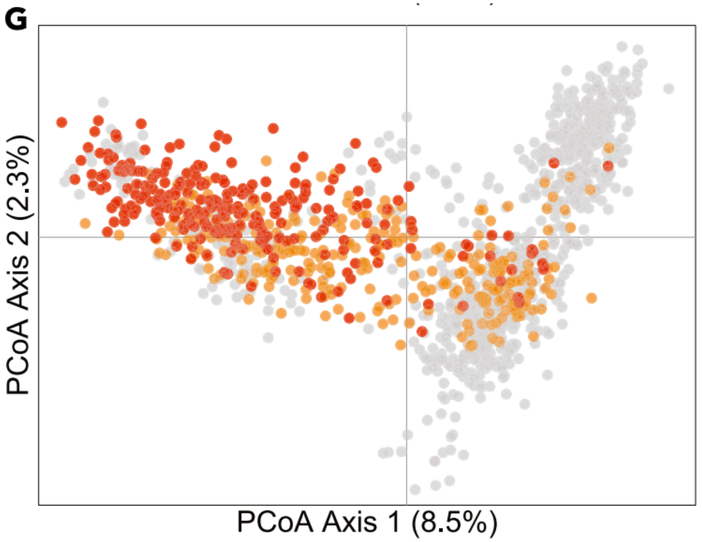


Wild Devil populations



West vs East variation
North vs South variation

Insurance populations (IP)



IP more representative
of Western Devil populations

Farquharson et al., iScience 25, 104474 (2022)

Genetic basis of resistance to DFTD in Tasmanian Devils

Discovery of SNPs for genetic monitoring and conservation management

- 50% of variation in being infected by DFTD is due to genetic variation in Tasmanian devils
- 34% of variation in being transmissible is due to DFTD genomic variation
- Devil-DFTD genomic coevolution explains disease susceptibility
- Few Devil genomic regions with large effect sizes (2 SNPs explain 19% of variance in infection)
- Targeted SNP genotyping for conservation monitoring

*Nature Communications, **7**, 12684 (2016)*
PNAS, 121, e2307780121 (2024)