Combining Indigenous knowledge and population genomics to understand the diversity and distribution of a staple food source used throughout the Western Desert of Australia



Figure 1 *Solanum diversiflorum* (*Wamula*) flowering in greenhouse at Bucknell University.

Since their forced removal, the Martu people have returned back to their lands. The Martu people practice a mixed-based economy lifestyle that includes foraging and hunting. These practices are aiding in the increase of taxa diversity and abundance, as well as the facilitation of ecosystem recovery.



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Project Goal

To understand how the Martu people have shaped *Solanum diversiflorum/Wamula*'s distribution, diversity patterns, and dispersal.

Background

The continent of Australia is a vast island that is home to estimates of ~70% of plants and animals that have yet to be identified [Chapman 2009]. Nearly one third of the continent is classified as desert. Although rainfall is low, this area is rich in floral and fauna. Indigenous foragers of Australia's Western Desert, known as the Martu people, have a deep connection to this landscape. They have culturally significant pathways of movement used for traveling from centralized settlements to foraging and hunting sites and for Dreaming: the rich ceremonial and philosophical foundations of Aboriginal homelands [Bird et al. 2013] (Fig 1-2). Along these pathways staple and nutrient-rich food sources, such as Solanum diversiflorum – locally known as Wamula, are harvested and processed (Fig 5). Seeds are discarded along the movement corridors or in processing sites, allowing for the next generation of *Wamula* to grow. Along with the Martu people, we are interested in the genetic diversity and population structure patterns of Wamula within the Martu lands and outside of the Martu lands. We are also interested in elucidating the role humans, being one of the best long distance dispersal agents, have on gene flow and plant distributions across Australia's Western Desert.



Figure 2 S. diversiflorum (Wamula) fruit in Western Desert.

Figure 4 Map of *S. diversiflorum* (*Wamula*) collections. The red area shows the Martu title lands and gold triangles within this area are classified as such. The collections outside of the title lands fall into three major natural areas: Great Northern Highway, Bunda Station, and Wolfe Creek.

Key Findings

Wild populations of *Wamula* are distinct from Martu title land populations. Wild populations also have a higher F_{ST} , signifying more population differentiation. Inbreeding rates (F_{IS}) are also higher when compared to the Martu populations. We are on our way to Australia to increase sampling, especially among wild populations, and learn more from the Martu

Methods

- DNA extraction and quality controls were done for 154 S. *diversiflorum* specimens. Specimens were from two groups: within Martu title lands and others from assumed wild populations outside of the Martu title lands (Fig 4).
- A genotype-by-sequencing (GBS) approach was done at the University of Wisconsin's Biotechnology Center.
- Sequences were assembled using a *de novo* approach in ipyrad.
- All population genomics analyses done in R using such packages as hierfstats, LEA, and adegenet.

Results

• We had over 9,800 loci, ~20,000 alleles, and less than 7% missingness to assess genomic structure.





people!



Figure 5 A group of Martu women and children with *S. diversiflorum* (*Wamula*) fruits at a processing site. Photo: Chloe McGuire.

Implications

Indigenous peoples and their stewardship of the land can have profound impacts on species distributions. Understanding the relationship between the biogeography of plants in the Western Desert and the people who have lived and used these plants for thousands of years will give new insights into ethnobotany, biogeography, anthropology, and help in our efforts to conserve species.

Overall F_{ST} was 0.0836, which indicates there is not a lot of population differentiation among these specimens.
Overall F_{IS} was 0.1770, showing evidence for low levels of inbreeding.
Low levels of genetic diversity. H_E was greater than H_O for all populations (Overall: H_E = 0.1083 and H_O = 0.0817)
PCA and STRUCTURE analyses showed similar results, distinguishing Martu title land populations from wild

distinguishing Martu title land populations from wild populations (Fig 3).

Figure 3 STRUCTURE results showing (A) wild populations clustering together (blue) and Martu title land populations clustering together (orange and green). Zooming into the Martu title lands (B) populations are clustering along two distinct genetic units. The Martu populations are also clustering along known travel routes.

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