



# Cryptic but important genetic differences within species

Across the range of a species, populations experience different environments that can cause local adaptation. For example, the skin colour of our human ancestors was selected for by the latitude they lived at: higher sun intensities at low latitudes selected for darker skin tones as protection against the damaging effects of UV rays; lower sun intensities at high latitudes selected for lighter skin tones to ensure sufficient UV exposure for vitamin D production. Some differences among populations can also be cryptic, i.e. not apparent to the naked eye. Again, taking a human example, the enzyme lactase is produced by infants to break down the sugar lactose present in breast milk. In many modern human populations, lactase production does not continue into adulthood as it is no longer required. However, in descendants of populations that shifted from a hunter-gatherer to an agricultural lifestyle, where the farming of cattle provided milk as an extra food source for human adults, selection has resulted in a life-long tolerance of lactose through continued lactase production.

As well as adaptive differences between populations due to selection, neutral or non-adaptive genetic differences can also accumulate. Geographic isolation between populations can reduce or prevent breeding between individuals. This reproductive isolation means that genes are not shared among populations. Over time, random mutations in neutral (non-functional) regions of the genome will accumulate (a process known as genetic drift) resulting in distinct genetic signatures within each population. These neutral genetic differences can provide important insights into historical colonisation processes and are the basis for commercial human ancestry tests that can inform on your ethnic make-up.



Figure 1 The narrow-leaf hopbush, *Dodonaea viscosa* ssp. *angustissima*

Researchers at the University of Adelaide carried out an assessment of genetic diversity and differentiation in an endemic Australian shrub, the narrow-leaf hopbush (*Dodonaea viscosa* ssp. *angustissima*). By sampling populations from Kangaroo Island in the south, through the Flinders Ranges, and up to the Gammon Ranges in the north (~700 kms away) the research team developed a picture of how closely related the populations are. Using a novel genotyping technique, they analysed a set of neutral genetic markers that were common among the sampled populations. This analysis gave a measure of how genetically similar individual plants are within populations (the genetic diversity of the populations) as well as between the different sampling sites (how genetically differentiated the populations are).

The results showed that the 17 sampled populations could be grouped into three genetically distinct clusters: a Kangaroo Island cluster, a Flinders/Gammon Ranges cluster, and a cluster of populations from the eastern portion of its range. The Kangaroo Island cluster appears simple enough to explain, with the geographic separation between the island and mainland populations reducing the capacity for pollen and/or seed migration and leading to genetic isolation.

The distinction between populations from the Flinders/Gammon Ranges ranges and the eastern portion of the species range was a more surprising result. The authors offer two potential

explanations. They suggest that the difference in environmental conditions between the two areas (with lower temperatures and higher rainfall on the Ranges) may have led to isolation-by-environment: where plants in the two different clusters may have adapted to their local conditions, resulting in them having a genetic makeup only suitable for those conditions. So, even if pollen and seed is transferred between the Eastern and Flinders/Gammon Ranges populations, any resultant offspring will most probably not survive or at least will be less competitive than offspring from local parent plants. This is akin to a lactose intolerant person having to survive in a land where milkshakes and cheese are the dominant foodstuffs – they just do not have the genetic disposition to do well in this environment.

Alternatively, the different genetic signatures may reflect the hidden historical origins of the contemporary populations: During past ice ages, species retreated to southern regions of the Australian continent to escape the arid conditions of more central areas. This resulted in the formation of refugia: areas that acted as safe havens for species, providing suitable environmental conditions and buffering them from climatic change. There are thought to have been many refugial areas along the southern coastline of Australia during the ice ages, where more mesic conditions were maintained. In inter-glacial periods, like we are in now, species expand out from these refugia as other areas become suitable for them to inhabit. The Flinders Ranges has been identified as one such refugium, for plant and animal species, and the high genetic diversity of the populations in the Flinders Ranges identified in this study suggests that it may also have played a refugial role for the hopbush in the past. Under this scenario, the eastern populations may represent the edge of an ancient expansion from a south-eastern refugium that occurred millennia ago. If this second hypothesis is correct then it is no wonder that these two sets of populations demonstrate such distinct genetic signatures.

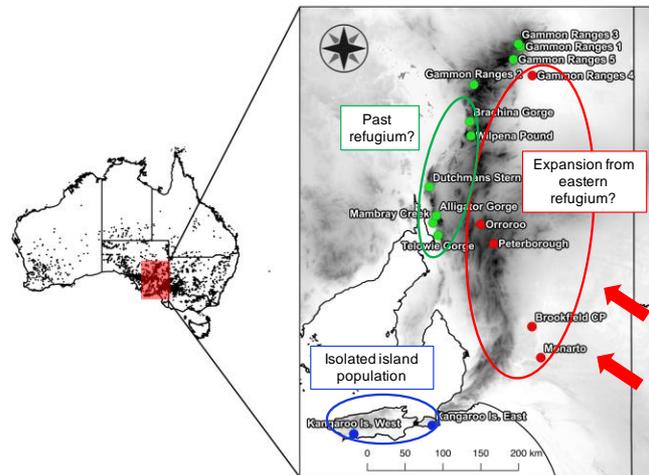


Figure 2 Map of the study region and sampling sites. Is the eastern cluster an expansion from the east?

And why are these findings important? Well, the Australian continent has experienced unprecedented land use change since the arrival of the first Europeans. Swathes of land have been cleared for agriculture, resulting in the destruction and fragmentation of native habitats. There are now increasing efforts to protect and restore areas of native vegetation. Restoration efforts require sources of good-quality native seed and the seed needs to be from plants that will thrive in the restored area. The hopbush is commonly used in restoration throughout South Australia and is a dominant understorey species in many habitats. By getting a clearer understanding of the genetic connectivity of populations across the region, better informed decisions can be made as to where to source seed from for restoration. For example, the movement of seed between the Flinders ranges and the drier eastern regions should be avoided as the resultant plants may not be well adapted to the different environmental conditions, compromising well meaning restoration efforts.

This study has been published in the journal *Nature Scientific Reports* and is available open-access [here](#):  
 Christmas et al. 2017 Targeted capture to assess neutral genomic variation in the narrow-leaf hopbush across a continental biodiversity refugium. *Scientific Reports*, DOI: 10.1038/srep41367.