

**PROJECT TITLE**

Mapping ionic parameters in an Arabidopsis thaliana island model

**CONSORTIUM**

P 1	Angela Hancock		
P 2	Emmanuel Tergemina		

# SUMMARY OF THE REPORT

Understanding how plants adapt to living in harsh environments with strong selection pressures is useful not only to clarify the mechanisms of the evolutionary process, but also for producing crops that can withstand harsh conditions. But traits are interconnected at the molecular level, so that understanding only one or two dimensions of this adaptive process is insufficient. Rather, to understand how plants survive and thrive under resource limitation or harsh climates we must examine the multidimensional ways that these organisms adapted.

Much work has been conducted on Eurasian populations of the primary model plant, *Arabidopsis thaliana* (Durvasula et al., 2017; Fulgione et al., 2017; The 1001 Genomes Consortium, 2016). However, the genetic structure of this population is extremely complex and allelic and genetic heterogeneity are common, which impede efforts to localize causative variants. In an alternative approach, we have collected accessions and developed mapping populations from natural island populations from the Cape Verde archipelago, which are the product of strong selection to a harsh environment. This is a very simple natural system, analogous to a mutational screen across the natural environment. The CVI populations are ideal for trait mapping and evolutionary analyses because they have an extremely tractable history and clear climatic divergence from the ancestral habitat in Morocco.

The Cape Verdean archipelago takes its origin from volcanism as it lies over a hotspot (Helffrich et al., 2010). While the last eruption in Santo Antão is estimated at 90 +/- 30 kya (Plesner et al., 2003), the volcano in Fogo is still active (last eruption in 2014). As a result, while both islands have soil with divergent properties relative to the mainland including limitations in several micronutrients, topsoils from Fogo are more extreme in many aspects.

Here, we map loci underlying variation in elemental processing in collaboration with Prof. Dr. David Salt and Dr. Paulina Flis at the University of Nottingham. For this, we used the panels of natural accessions we have collected in Cape Verde. From this project, we will identify novel natural variants involved in elemental processing, and learn how these evolved in nature and how they influence other traits. We identified several candidates and examine the genetic architecture of the individual traits.