

# Genetic structure of the invasive coastal weed *Euphorbia paralias* (sea spurge) in Australia

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**Summary** Sea spurge (*Euphorbia paralias*) is an herbaceous perennial native to coastal environments of Europe and northern Africa. Sea spurge plants produce buoyant seeds capable of surviving extended periods afloat on ocean currents and seeds are believed to have been accidentally introduced to Australia through ships ballast during the early twentieth century. Since its introduction, sea spurge has progressively invaded many beaches along Australia's southern coastline resulting in dense infestations that reduce the public amenity of beaches. Little is known regarding the genetic complexity of sea spurge in Australia or its possible invasion routes. The aim of this study was to use informative genome-based markers to elucidate the genetic structure and diversity of sea spurge within Australia. To do this, single nucleotide polymorphisms (SNPs) were identified from 374 sea spurge samples from 51 populations across the Australian distribution of the weed using the

DArTseq genome complexity reduction technology. Following several filtering steps, several hundred SNP loci were identified for population genetic analyses. Principal component analysis indicated no clear separation or clustering of sea spurge and multi-locus genotypes appeared to be randomly distributed across the Australian range. Genetic structure analysis did however suggest that Australian sea spurge populations were derived from at least two different genetic sources. At a State level, genetic diversity values of sea spurge are low to moderate with diversity of South Australian sea spurge slightly higher than those of other States. Analyses are ongoing but these initial results suggest that ocean currents and possibly anthropogenic movement of propagules have led to a mixing of sea spurge across Australia and that no particular genotype(s) of the weed dominates.

**Keywords** Euphorbiaceae, invasion biology, weed population genetics