

Genepool diversity in carrot: molecular and phenotypic variation

Charlotte Allender, Mariateresa de Cesare, and Peter Glen Walley

Rich in beta-carotene, and with a sales value of £290 million, carrots (*Daucus carota sativus* L.) are a nutritionally and economically significant crop in the UK. Existing variation (see Figure 1) in the carrot genepool is a valuable resource for research and plant breeding, but full exploitation of this resources requires an understanding of the scale and pattern of genetic diversity in both cultivated types and in related wild species.



Figure 1. Root diversity in cultivated carrot

The carrot genepool is composed of three subgroups; wild taxa, Asiatic accessions and Western accessions.

A field trial held at Wellesbourne in 2011 also revealed variation in phenotypic traits such as flowering time (Figure 4). Half of the accessions flowered from 10-23 weeks after sowing. This trait was more common in the wild and Asiatic groups.

A set of 87 accessions of cultivated and wild carrot of wide geographical origin were assessed for genome-wide variation using 2770 DArT markers. These data revealed three sub-populations (Fig. 2 and Fig. 3).

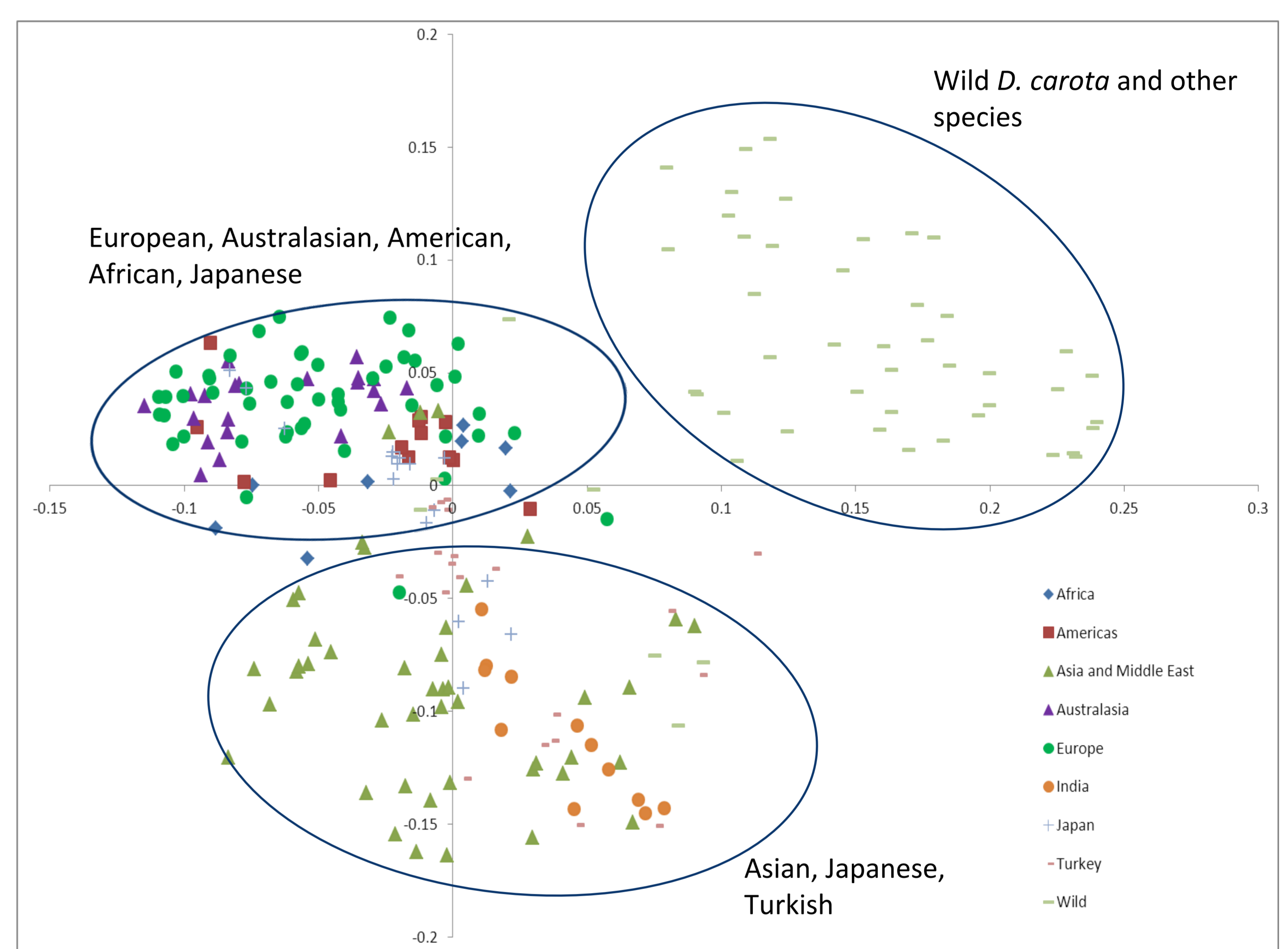


Figure 2. PCO plot of DArT marker data – each individual tested is plotted, the co-ordinates are derived from the marker data. Three sub-groups are clearly visible – wild, Asian and Western material are well separated.

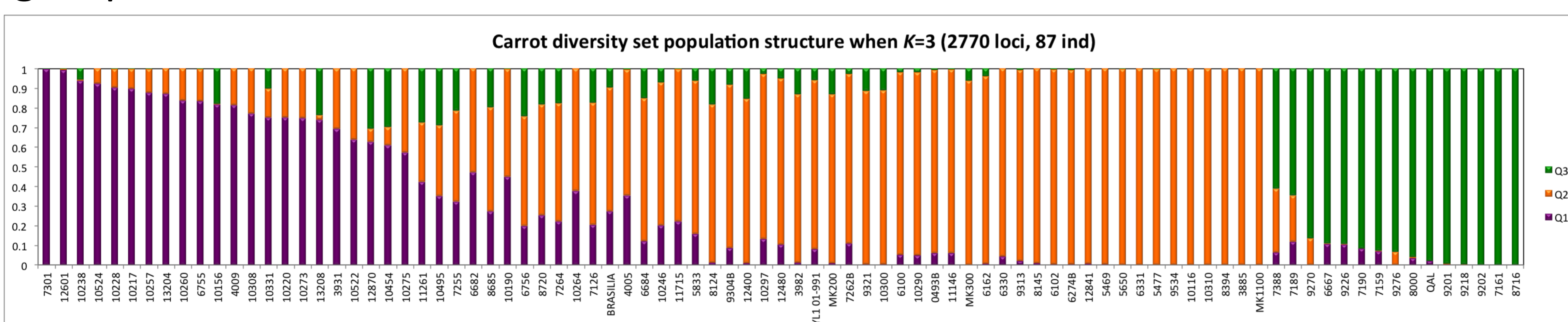


Figure 3. Classification of the 87 accessions into the three sub-populations identified using Structure software. For each accession, the different colours represent the proportion of the genome classified as belonging to each of the three groups; Asiatic (purple), Western (orange) and wild (green).

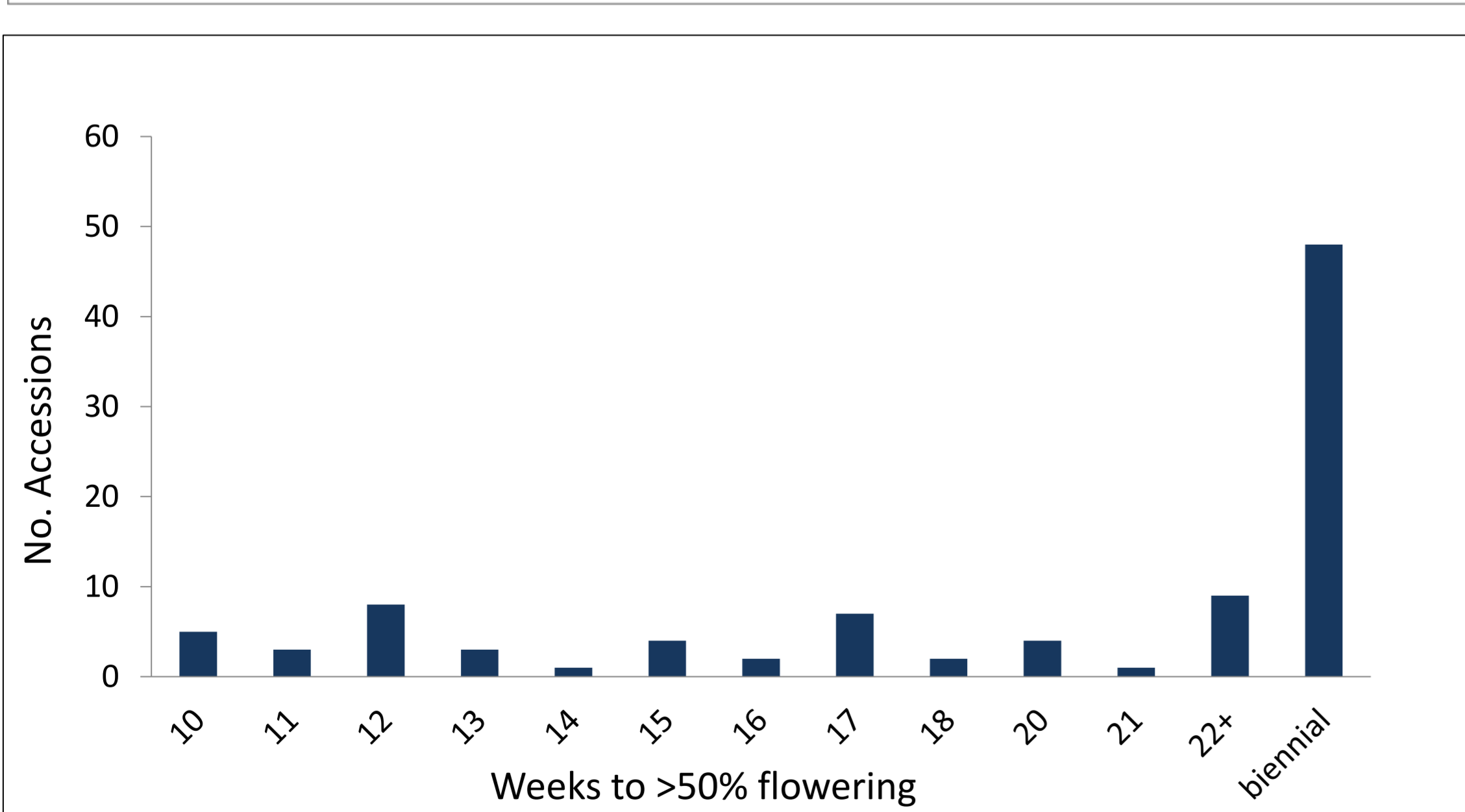


Figure 4. Range of flowering behaviours observed in the 87 accessions in the field trial. Accessions with > 50% of individuals in flower were scored. Accessions which never reached this threshold were classed as biennial.

This work was carried out as part of the Vegetable Genetic Improvement Network funded by Defra, and forms the basis of future studies of trait genetics aimed at developing pre-breeding resources for carrot.

Vegetable Genetic Improvement Network

