

# Unlocking the Potential of Genebank Carrot Collections: Creating a Carrot Diversity Set as a Research and Pre-Breeding Resource

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## Abstract

Plant genetic resource collections such as the carrot collection held at the Warwick HRI Genetic Resources Unit are extremely useful assets for both crop improvement programmes and research. However, it is not practical to screen or assay all accessions within such collections for traits of interest; the Warwick HRI GRU holds over 1600 accessions of carrot and related wild species, which is too great a number for most screening programmes to handle. In order to make the diversity present in the collections more available, we have constructed a Carrot Diversity Set which samples the global carrot gene pool in terms of geographical origins and root morphology. We chose 77 accessions from the Warwick HRI GRU collection, and supplemented these with experimental lines such as the parents of genetic mapping populations kindly donated by other researchers. We will also include eight modern elite varieties for comparison in trait screening and genetic studies. The diversity set represents a snapshot of the global carrot gene pool held in a manageable format which will be made available to interested parties and allow collation of data from future studies.

## Introduction

In recognition of the fact that the production of many important crops depended on the performance of a relatively small number of elite varieties derived from a small part of the crop gene pool, much effort in recent decades has been put into the collection, conservation and management of plant genetic resources. Material representing older varieties, traditional landraces and populations of related wild species has been collected, catalogued and placed into long-term storage. For carrot, these resources are seed collections held at various institutions across the world including a globally significant collection at the Warwick HRI Genetic Resources Unit. However, the sheer number of accessions in these seed collections may make easy access for plant breeders or researchers difficult, and with so many accessions to choose from it is easy to see how data from different studies cannot be compared if different accessions were used as starting material. The number of carrot accessions available in two major combined collections can be seen in Table 1.

These and similar collections of carrot genetic resources may contain traits and alleles which would be of use in crop improvement programmes, such as novel pest and disease resistances and tolerance of water and nutrient stresses. In order to locate such novel traits, it is necessary to adopt a structured screening approach, as it is not feasible to look at >5000 accessions in trials and experiments. 'Core collections' have been designed for other crops such as *Brassica oleracea* (cabbage, cauliflower, broccoli)

etc) where the range of diversity of cultivated and wild types has been maintained in a structured subset of all the available accessions (Leckie et al, 1996).

Our aim was to develop a 'diversity set' for carrot which represents the diversity of the carrot gene pool but has a more tractable number of accessions to allow for easier use in trials and experiments. We wanted to include accessions which have already been used by other researchers as we hope the diversity set will enable data to be pooled from different studies, adding to its value.

**Table 1.** Summary of carrot accessions (*Daucus carota* including both wild and cultivated subspecies) available in two major collections in Europe and the USA. These collections include weedy, hybrid and breeding material in addition to the wild, landrace and cultivars listed in the table.

Source	EURISCO <sup>1</sup>	ARS-GRIN <sup>2</sup>
Total <i>Daucus carota</i> accessions	4379	882
Wild material	379	154
Landraces	845	207
Cultivars	1552	116

<sup>1</sup> Data downloaded from the EURISCO database at <http://eurisco.ecpgr.org>. EURISCO is a web-based catalogue that provides information about *ex situ* plant collections maintained in Europe, including that of the Warwick HRI GRU

<sup>2</sup> Data downloaded from the Genetic Resources Information Network (<http://www.ars-grin.gov>), a program within the United States Department of Agriculture's Agricultural Research Service

## Methods

We have selected a total of 77 accessions from the carrot collection held at the Warwick HRI Genetic Resources Unit, one of the most comprehensive collections of carrot germplasm in the world. Although some molecular marker studies have found the carrot gene pool to be unstructured (Bradeen et al, 2002) we selected our accessions on the basis of root type and colour and geographical origin to make sure we had a good representation of all types. We obtained input and advice on the composition of the set from the wider carrot research community, and attempted to overlap with sets of accessions used by other researchers where possible. Emphasis has been put on landrace accessions as these may be pools of useful diversity as they have been locally selected over many generations to perform well in particular ecogeographical environments. We have concentrated on *Daucus carota* accessions which include some related subspecies to sample the wild gene pool at the same time as facilitating crossing into cultivated types. We have also included some representatives of more distant relatives of carrot such as *D. capillifolius*. This wider gene pool has already been the source of useful traits such as enhanced resistance to carrot fly (Ellis et al, 1993). A list of the accessions selected for the diversity set can be downloaded from the website for the Vegetable Genetic Improvement Network (VEGIN) at [www.warwick.ac.uk/go/vegin](http://www.warwick.ac.uk/go/vegin).

In order to facilitate research into the genetic control of traits of interest, we also wanted to include parental lines from as many genetic mapping populations as possible. This will allow the best mapping population for further investigation to be identified at the time of the initial diversity set screen/trial rather than having to carry out follow-up

investigations. Parental lines were very kindly donated by P. Simon (University of Wisconsin, Madison) and T. Nothnagel (Julius-Kühn-Institut). We have also included space for several modern elite cultivars so that direct comparisons of performance can be made.

Our diversity set is based on open-pollinated accessions with varying levels of intra-accession diversity. This is useful as it reflects the pattern of diversity in the carrot gene pool but has drawbacks when it comes to comparing the results of genetic studies on different individual plants. We are structuring each accession in the diversity set to attempt to address this problem, whilst delaying the onset of inbreeding depression that can be observed in highly selfed lines. Each accession in the diversity set will be represented by seed collected individually from ten intercrossed plants. This will result in 10 'half sib' families, each derived from an individual maternal plant. We will also self pollinate an additional individual so that a more homozygous line is available for each accession if required.

We are currently producing seed according to the design described above through the use of isolation cages and blowfly pollinators in polytunnels. We have prepared a DNA extract of each parental plant for future use. We are also quantifying the genetic diversity of the whole set through sampling a subset of each accession using DArT markers (Jaccoud et al, 2001) which can detect genomic wide variation. This will allow comparisons of inter-and intra-accession diversity and indicate where the greatest amounts of genetic variation lie within the set.

### **Summary**

Our Carrot Diversity Set is based on the carrot collection held in the Warwick HRI GRU, together with parental lines of genetic mapping populations and modern elite varieties for comparison. We have tried to make the best use of available data by selecting accessions that have already been screened in other projects.

We anticipate that the carrot diversity set will be a useful tool for bringing new traits as rapidly as possible into crop improvement programmes and to that end we plan to make the Carrot Diversity Set available to all interested users. Small quantities of seed will be made available on either a collaborative basis or for a small charge to cover costs. Samples of the DNA extracts for each of the eleven plants per accession will also be made available.

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