

INNOVATION IN VARIETY TESTING

To be marketed in the UK all new agricultural varieties must pass DUS and VCU (Value for Cultivation and Use) tests and be added to the UK's Variety Lists (also known as National Lists). DUS testing is essential for the awarding of Plant Breeders' Rights (PBR), the intellectual property rights over a plant variety in the UK.

- Distinctness (D): must be sufficiently different from existing varieties
- Uniformity (U): plants within the variety must have consistent features
- Stability (S): all plants should remain consistent across subsequent generations.

DUS testing ensures that new varieties are unique and that they are 'true to type'. Distinctness is determined by visually comparing a new variety against the reference collection, and a standard test involves two years of growing trials. Differences between some varieties can be easy to detect but others may be far more subtle.

focus on NIAB research

In a Defra-funded research project, NIAB is exploring the use of genetic data to screen new barley candidates against the reference collection to identify the most similar varieties to include in the growing trials. The goal is to identify similar varieties earlier in the testing process to give more opportunity for assessment, increasing the speed and efficiency of testing.

The genetic data is also being explored to identify a smaller subset of DNA markers to be used for varietal identification and seed stock authentications.

Barley is an important crop for the UK so it is essential that the testing system is relevant and effective. The aim is to facilitate and encourage the development of new plant varieties for farmers and end users, to meet the challenges and opportunities of a changing world.

Wheat and barley DUS trials at NIAB Park Farm



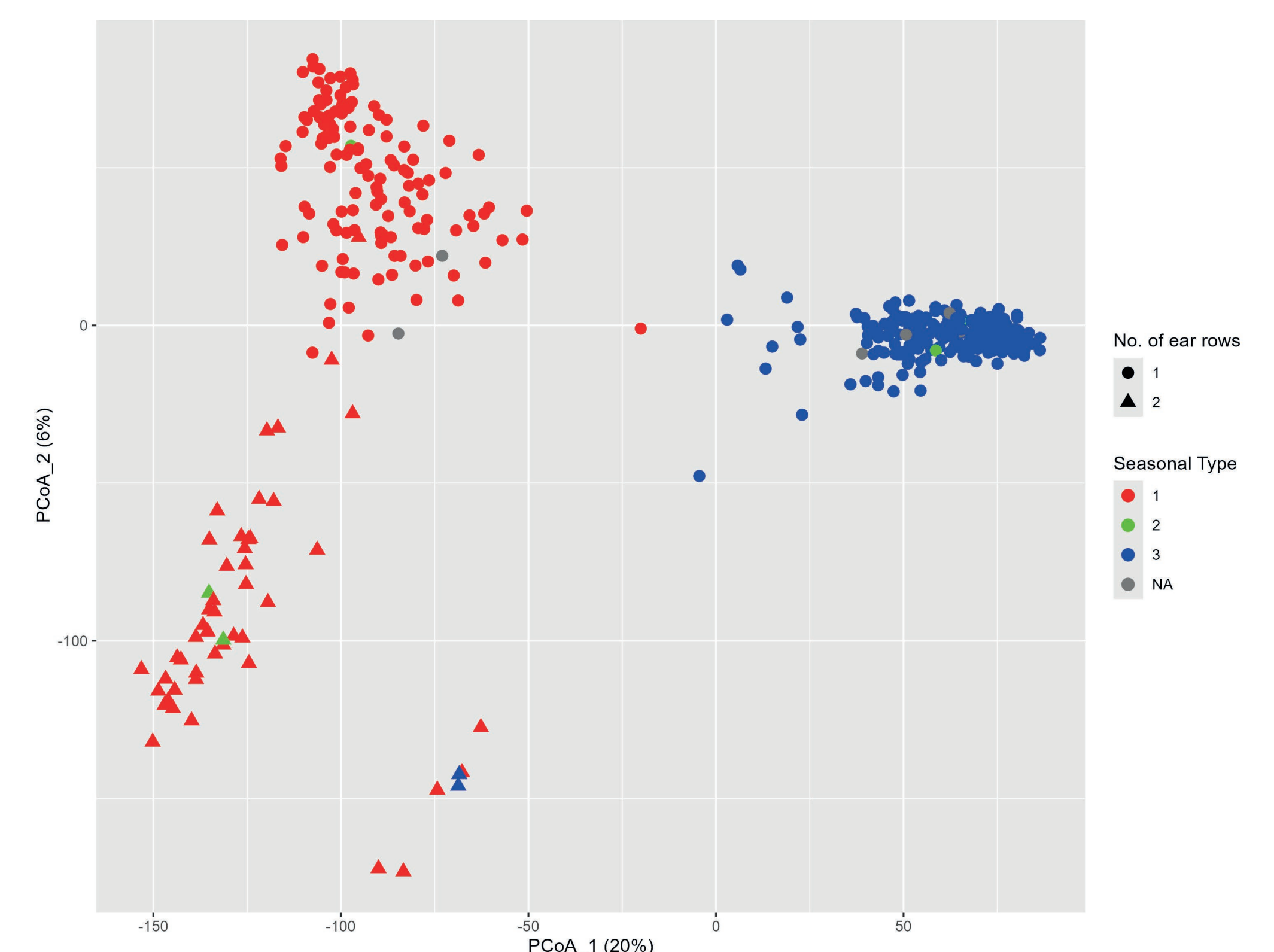
Barley rachilla hair type – long and short



Barley pigmentation – present and absent



Principal Coordinate Analysis for genotypes with different ear row number and seasonal habit



Correlation plot of phenotype and genotype distances

