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MOLECULAR APPROACHES TO SUPPORT DUS TESTING

Document prepared by experts from the United Kingdom

INTRODUCTION

1. This paper provides an overview of work aiming to explore and implement the use of molecular methods to improve the efficiency and quality of DUS testing in the United Kingdom. For example by (i) developing the use of marker-informed similar variety selection models to allow side-by-side phenotypic comparison at an earlier stage in the testing procedure (ii) identifying characteristic-specific molecular markers with the potential to replace resource intensive phenotyping and (iii) using markers for authentication of seed stocks, allowing early identification of potential problems. The research is at an early stage in the planned work programs and the research highlights so far will be presented focusing on wheat (*Triticum aestivum* L.), barley (*Hordeum vulgare* L.) and raspberry (*Rubus idaeus* L.).

Wheat

2. The wheat breeding industry is highly active in the United Kingdom, with an increasing number of varieties under DUS test and an ever-expanding reference collection. Work has been conducted to advance the understanding of the genetic control of DUS characteristics in wheat.

3. Genotypic and DUS data from a panel of over 400 elite wheat varieties (predominantly United Kingdom, French and German varieties), has been used in an association genetics analysis. Significant genetic loci and markers were identified for a number of DUS traits. For example, on Chromosome 7A for coleoptile color, Chromosome 2A for grain coloration with phenol and Chromosome 1A for glume hairiness.

4. Work is ongoing to further explore molecular marker approaches in wheat DUS testing within the Horizon 2020 INVITE project (Grant agreement ID: 817970).

Barley

5. Spring barley is a high priority crop group for the United Kingdom, with approximately 50 new applications per year. The standard DUS test is two years, but often an additional third year of test is required for closer comparison with similar varieties.

6. The main aim of the project is to explore the use of molecular marker information to inform the selection of similar varieties at the beginning of the test. This could improve trial design and reduce the need for the additional test year.

7. Over 500 varieties from the United Kingdom barley reference collection, sampled from across the DUS trait diversity space, have been genotyped using the 50k iSelect array within the project. This dataset is being integrated with existing 50k variety data to expand the number of varieties analyzed. A variety of statistical approaches including genomic prediction methodologies will be explored to improve marker-based predictions and an analysis pipeline developed to select similar variety subsets for inclusion in the growing trials.

8. The project also aims to determine and experimentally validate a smaller marker set to be used for seed sample authentications and varietal identity checks. The open-source software “Uniqueness”

(https://www.upov.int/edocs/mdocs/upov/en/bmt_18/bmt_18_11.pdf) is being utilized to identify a subset of molecular markers, able to discriminate between the varieties tested, for experimental validation.

9. To facilitate the implementation of these approaches our existing DUS database structure is being modified to enable the inclusion of the genotypic data and associated passport information.

Raspberry

10. The aim of this work is to explore Artificial Intelligence modelling approaches to identify genomic markers with the potential to distinguish between red raspberry varieties. Work is currently underway to obtain representative raspberry material for genotyping.

Future prospects

11. These research projects are intended to provide proof-of-concept for the use of molecular markers to support DUS growing trials in the United Kingdom. Based on the research outcomes, recommendations for future implementation will be made including consideration of cost, practicality and effectiveness.

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13. The wheat data was generated via the BBSRC funded (Biotechnology and Biological Sciences Research Council) WAGTAIL (Wheat Association Genetics for Trait Advancement and Improvement in Lineages) project (BB/J002542/1).

14. For more information on these projects please contact: vanessa.mcmillan@niab.com

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