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ESSENTIAL DERIVATION AND DIVERSITY ISSUES IN WINTER WHEAT

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## ESSENTIAL DERIVATION AND DIVERSITY ISSUES IN WINTER WHEAT.

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## ABSTRACT

1. A set of c.500 winter wheat varieties have been assessed to quantify any flux in genetic diversity over the past 50 years, using three marker systems (SSR, SSAP and NBS). In terms of diversity flux over time, statistical analyses showed that comparable and consistent results were achieved for each marker system studied. This was not the case when the same data were utilised in a simulated essentially derived variety (EDV) context where previous recommendations (based on barley and lettuce) were confirmed – namely, that systems should be developed on a crop by crop basis, with specific use of targeted, well chosen markers. The data set of winter wheat varieties offers potential to evaluate the usefulness of PREDIP.

Genetic Diversity:

2. A recently completed EU-funded research project (GEDIFLUX), co-ordinated by NIAB and with partners from the United Kingdom, France, Germany and the Netherlands, assessed changes in the genetic diversity of wheat, barley, potato and maize varieties, using germplasm from the years 1950-2000 and a range of molecular markers. For winter wheat, over 270 varieties were selected to represent established commercial varieties grown in Europe over the past 5 decades, with a balance in terms of breeders (and hence gene-pools), and country of origin. These varieties were taken as an estimate of genetic diversity exploited in commercial terms and are designated the “RL” set. A further 229 varieties were analysed that had been National Listed in the 1980s and 1990s, but had not necessarily achieved commercial importance. This latter set of varieties was taken to represent the wider genetic diversity available, but not necessarily exploited and are designated the “NL” set. Data from 40 SSR loci were analysed as pattern profiles, and pair-wise similarity coefficients computed by Euclidean algorithm. In addition, 70 SSAP bands and 70 NBS bands were available and, as the bands are present/absent, the pair-wise similarities were generated by the Jaccard method.

3. The presentation will show that:-

- By treating the 499 varieties as a single variety pool, pair-wise similarities were input into a PCO analysis, which illustrated the partitioning into the “RL” and “NL”;
- No major bottle-necking/expansion in decadal flux in genetic diversity was shown by any of the marker systems assessed.
- In conjunction with morphological records, this data set could be further utilised in an Option 2-type approach, possibly using PREDIP.

Essential Derivation:

4. To simulate an EDV situation from the computed matrices of pair-wise similarities/distances, the following steps were taken. Firstly the RL material only was utilised to establish a framework whereby varieties are distinct, but potential EDV cases may occur. All pair-wise similarity coefficients were collated, ranked and the value corresponding to a threshold value ( $THV_{RL}$ ) of the top 5-percentile determined (this potential threshold was based on previous work with barley). This was repeated for matrices from each marker system. The set of NL pair-wise similarities were then compared to the THV established by

the RL varieties as defined above. Statistics were then computed for the percentage agreement between the marker systems in terms of the identification of possible EDV cases.

5. The presentation will show that:-

- Over 80% of the pair-wise similarity coefficients were below the respective  $THV_{RL}$  using all markers studied, and can be considered unlikely to be possible EDVs;
- The remaining 20% were considered to be potential EDVs by one, two or all three markers;
- There were differences between the markers in the level of flagged EDV “potential”;
- Only 0.47% of the total number of pair-wise similarity coefficients were identified by all three markers. This represents 2.4% of pairs of varieties flagged as a potential EDV by one or more markers.

6. The results will be discussed in the framework of developing and evaluating models for the determination of EDV status.

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