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**Presenter Information**

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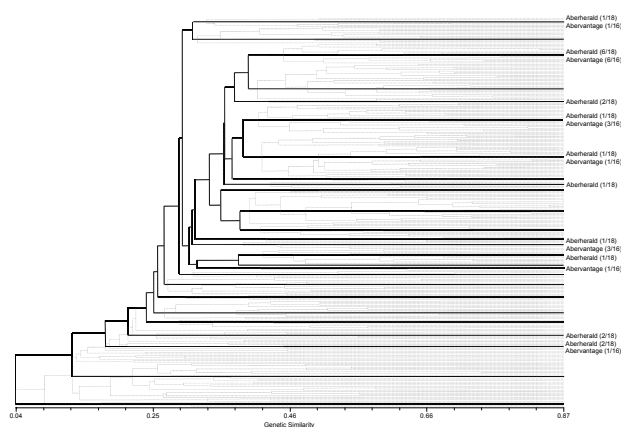
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**Introduction** White clover (*Trifolium repens* L.) is a key important temperate pasture legume. Due to the obligate outbreeding nature of white clover, individual genotypes within cultivars are highly genetically heterogeneous. Genetic diversity has been assessed within and between 16 elite cultivars derived from Europe, North and South America, New Zealand and Australia.

**Materials and methods** Each cultivar was represented by c.15 plants, to a total of 235 individuals. Sixteen simple sequence repeats (TRSSR) markers that had been previously used to construct a white clover reference genetic map were chosen on the basis of single, co-dominant locus status and polymorphic information content (PIC), based on previous studies. Genetic diversity among individuals was measured using the method of Tomiuk and Loeschcke (1991). Phenograms were constructed with the resulting genetic distance matrix using the unweighted pair group method of arithmetic averages (UPGMA). The single dose fragment (SDF) principle was used to score the data for analysis of molecular variance (AMOVA).

**Results and discussion** High levels of genetic variation were detected within and between white clover accessions. AMOVA showed variation within accessions. Most of the cultivars did not separate into distinct clades in the phenogram, but were rather distributed throughout the phenogram. There was no obvious genetic distinction between Mediterranean the cultivars AberHerald and AberVantage. Both AberHerald and AberVantage contain Swiss ecotypic material from similar localities and were each bred in the UK from a selection of 15 parents. These cultivars showed a similar pattern of distribution across the phenogram (Figure 1). Although the number of parental lines used for selection in the breeding program may be expected to influence the levels of genetic diversity in cultivars, no such correlation was observed. The overall level of intra population variation provides a greater understanding of the complexity of domesticated white clover germplasm. This knowledge is being exploited for improved parental selection for the construction of trait specific mapping families. In addition, the data will assist in the construction of larger scale germplasm collections for the design of population samples for linkage disequilibrium (LD)-based genetic analysis. The development of candidate gene-based marker systems for white clover will allow comparison of anonymous and functionally associated genetic diversity.



**Figure 1** The overall white clover UPGMA genetic diversity dendrogram, demonstrating the influence of breeding history on genetic diversity, as exemplified by cultivars AberHerald and AberVantage. The identifiers of individual plants from these varieties are shown adjacent to their locations within the structure. Framework taxa are shown in bold lines, while the remaining accessions are indicated as dotted lines.