

Genetic and phenotypic diversity of Swiss red clover landraces

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Introduction: Mattenlee landraces are persistent and locally adapted Swiss red clover populations. About 100 populations are preserved and may represent a significant yet poorly characterised genetic resource for temperate regions. Genetic characterisation is important in order to improve cultivars, manage genetic resources and to maintain or restore biodiversity. The objectives of this study were to analyse genetic diversity, investigate potential ancestry and to elucidate the congruence of phenotypic and genetic structure of Mattenlee landraces.

Materials and methods Eighty-nine Mattenlee landraces and 31 populations of five additional red clover groups (Swiss wild clover populations, Mattenlee cultivars, field clover cultivars, Dutch landraces, Dutch wild clover populations) were analysed using bulked AFLP (amplified fragment length polymorphism) analysis with twelve primer combinations. AFLP analysis was performed on two bulked samples per population consisting of twenty plants each. In addition, eight phenotypic characteristics were determined for a subset of 33 Mattenlee landraces and the Mattenlee cultivar Milvus (Table 1).

Results Genetic distances among red clover groups, expressed as co-ancestry coefficients derived from analysis of molecular variance, ranged from 0.06 to 0.25. Swiss wild clover populations revealed the largest genetic distance to any of the five groups investigated. In addition, principal coordinate analysis based on two bulked samples clearly separated Swiss wild clover populations from all other populations. Average Euclidean squared distances among the 33 Mattenlee landraces for which phenotypic characteristics were determined ranged from 12 to 52 with an average of 27.8 (Table 1). The 33 Mattenlee landraces investigated showed a broad variation for phenotypic characterisation as well as for AFLP marker diversity. Although average agronomic performance of phenotypic characteristics of Mattenlee landraces was lower compared to the cultivar Milvus, there was, for most of the traits, at least one Mattenlee landrace which showed a better performance (Table 1). Cluster analysis based on 212 polymorphic AFLP markers and phenotypic characteristics yielded dendrograms of largely different topologies. However, redundancy analysis using the eight phenotypic characteristics as explanatory variables revealed that the three characters "dry matter yield, first production year", "stem length" and "length of medial leaflet" had a significant influence on AFLP diversity ($P < 0.05$).

Table 1 Phenotypic characteristics and AFLP marker diversity for 33 Mattenlee landraces and the Mattenlee cultivar Milvus

	Milvus	Mattenlee landraces		
		Mean	Highest value	Lowest value
Phenotypic characteristic				
Dry matter yield, first production year	155.66	141.63	158.54	118.92
Dry matter yield, second production year	110.27	87.18	108.55	74.50
Anthraxnose disease score (1=healthy)	2.74	4.82	7.15	2.02
Downy mildew disease score (1=healthy)	2.31	4.55	5.97	3.62
Stem length (cm)	90.71	86.27	94.26	79.58
Time of flowering (days after 30 th April)	29.66	27.80	30.71	25.27
Length of medial leaflet (mm)	49.54	47.89	51.13	43.54
Width of medial leaflet (mm)	28.56	28.60	30.47	26.86
AFLP marker diversity				
Euclidean squared distances	33.55	27.80	52.00	12.00

Conclusions Mattenlee landraces are a distinct genetic resource with considerable variation in AFLP marker diversity as well as in phenotypic characteristics. Swiss wild clover populations were clearly separated from Mattenlee landraces, which in turn grouped closely to Dutch germplasm. Multivariate analyses indicated a significant effect of three key characteristics on AFLP marker diversity. This study shows that Mattenlee landraces may serve as a valuable gene pool for red clover improvement and may contribute to the restoration of biodiversity in pastures and meadows. In addition, the ancestry of Mattenlee landraces is found more in introduced cultivars than in natural wild clover populations.