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Germplasm improvement in pasture legumes by developing core collections

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Introduction One of the strongest candidates for new crops suited to the style of agriculture in southern Australia is the annual pasture legumes belonging to the genus *Trifolium* L . (clover) . *T.spumosum* L . (bladder clover) , a species from mediterranean region is only one of several species considered to be fulfilling this need in southern Australia (Loi et al . 2003) . *T.subterraneum* L . (subterranean clover) is the most widely sown annual pasture legume species in southern Australia (Sandral et al . 1997) Little effort has been given to evaluating and characterizing the genetic diversity available within the former species while the latter species has one of the largest pasture legume seed collections in the world . The creation of a core collection assists in future development of cultivars in the two species (Van hintum et al . 2000) . Ecogeographical and molecular data are combined to generate the most representative core collections for the species .

Materials and methods Missing passport data were found using Google Earth , as well as ArcGIS v .9 and Encarta softwares . This information was further confirmed using Global Gazetteer Version 2 .1 on the web . Principal component and hierarchical cluster analyses were used to detect the most diverse accessions in the two collections (Ghamkhar et al . 2007) . Four of the most diverse accessions of bladder clover were screened using fluorescent Amplified Fragment Length Polymorphisms (fAFLPs) to find the right number of repeats within each accession . A core collection was developed for each species using combined ecogeographical and molecular data and maximising strategy (Schoen and Brown 1993) .

Results The distribution maps of the accessions of the original collection were prepared in ArcGIS (Figure 1) . The gaps and over-representations in both collections were detected based on climate and vegetation match studies . Using DNA fingerprinting of the the ecogeographical subsets , 32 accessions for bladder clover and 270 accessions for subterranean clover were selected as core collections . These cores covered maximum ecogeographic and genetic diversity of the original collections . This diversity was then validated using agro-morphological data . The genetic profiles of the preliminary core has been scored and recorded in a database with ecogeographical data for bladder clover and will be recorded for subterranean clover in the same way .

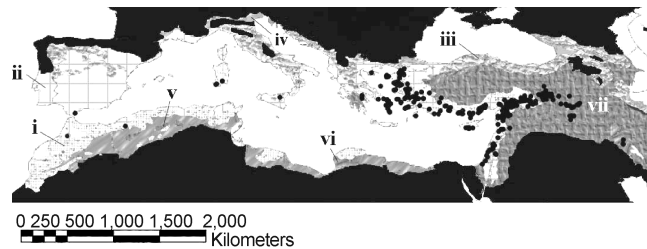


Figure 1 Ecogeographic sub-regions (i-vii) within the Mediterranean and Irano-Turanian ecoregions used to assess the genetic diversity and identify gaps within the germplasm collection of two *Trifolium* species .

Conclusions The present study hopes to demonstrate that a tested methodology for developing core collection using DNA markers and ecogeographical data in a small to medium collection can be applied to much larger collections . This can result in desirable results for breeders and germplasm managers without need for costly and time consuming agro-morphological evaluations . Core collection studies using ecogeographical data also help in finding the gaps in the current collections . This will save time and resources in future targeted collecting missions .

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