

# [Introduction variability, that may be useful to](https://assignbuster.com/introduction-variability-that-may-be-useful-to/)

IntroductionIn order to efficiently utilize plant genetic resources andto have effective conservation and management of these resources, an adequateknowledge of existing genetic diversity is of fundamental interest. Theimprovement of crop genetic resources has largely been dependent on modernplant breeding techniques; however, the introduction of material from wildrelatives and local varieties is gaining in popularity. This shift in breedingtechnique in a modern commercial setting is in response to the narrow geneticrange of many crop species. This narrow genetic diversity hinders the abilityto adequately respond to changing climate and commercial needs in a timelyfashion. At the genetic level, natural populations possess high variability (Ahmed, et al.

, 2011, Ballian, et al., 2012, Snoeijs and Potapova, 1998), which enables these populations to adapt rapidly to variable environmentalpressures; and it is this variability, that may be useful to modern plantbreeding systems. Modern plant breeding depends on the assessment andmanipulation of genetic diversity to generate highly productive and resistantvarieties. The genetic diversity, i. e. differing allele frequencies, within genes of crop plant wild relatives havethe potential to reintroduce useful characteristics that may have been lostduring the domestication process. This approach has been used with greatsuccess for example in rice (Bimpong, et al., 2011, McCouch, et al.

, 2012), and in oil seed rape (Johnston, 1974). In tomato allelic differences at the fw2. 2 locus have been implicated in theincrease of fruit size during the domestication process (Frary, et al., 2000). In strawberry varieties, a SNP variant change in a MYB10 gene has been shown to control fruit colour (Hawkins, et al.

, 2016). In Arabidopsis significantSNP relating to salt stress have been identified (Negrao, et al., 2013); and in soybean two cell division genes with insertion/deletionvariants have been implicated in short root phenotypes in Glycine soja as compared with cultivated soybean (Prince, et al., 2015).

It is likely therefore, that any potentialgenetic diversity seen within red clover ecotypes could be used to introgressuseful traits from its wild relatives into current breeding lines. Red clover is a relatively newly domesticated species, andit was not until around the year 1, 000AD that it was first intentionallydomesticated in Southern Spain (Kjærgaard, 2003). Modern varieties are extensively used as silagedue to the growth habit. Many of the varieties currently on the market inEurope originate from a Mattenklee type of plant, with their growth habitcharacterised by tall upright stems. However, natural populations have been reportedto show varied growth habits, characteristically with less dependency on thecentral crown and a more prostrate nature to stem growth.

Under certaintemperature and moisture conditions, stems of these prostrate communities areable to produce nodal root growth (Frame). Potential genes underlying the prostrate growth habit of some red cloverecotypes, as well as the latent disease resistance often associated withnatural populations, could be of considerable use to the IBERS breedingprogram, in terms of furthering the range of climatic and agriculturalconditions suited to red clover growth and use. When plants spread into newecosystems they may encounter new and diverse sets of selective pressures (Perez, et al., 2006, Vannier, 2009), which may lead to changes in growth habit, and morphology and the partitioningof metabolites and disease resistance. This natural diversity in growth habithas enabled red clover ecotypes to adapt to the varied environmental conditionsin which it exists (Taylor and Quesenberry, 1996). The genetic diversity of wild and cultivated populations ofred clover have previously been studied using low throughput methods ofisoenzyme (Mosjidis, et al., 2004), AFLP (Collins, et al.

, 2012), RAPD (Dias, et al., 2008) (Dias, et al., 2008) and SSR markers (Ahsyee, et al.

, 2014). It is now possible to studylarge scale genome wide variation in populations by using next generationsequencing (NGS) technologies. Genotyping by sequencing (GBS) (Elshire, et al., 2011) has become a popular NGStechnique to identify large scale variation both with and without a referencegenome. The use of GBS has allowed researches to identify thousands to millionsof single nucleotide polymorphism (SNP) markers, which can be used to identifygenetic variation within and between study populations. These SNP can be usedin the analysis and dissection of complex traits, especially those involved inadaptive selection. We report here on the genotyping by GBS of 70 wildpopulations of red clover from Europe and Asia and five European elite breedinglines from the seed bank at IBERS. There has been no previous characterizationof the genetic resources of wild ecotypes and landraces held at IBERS.

Therefore, the breeders have not been enthusiastic to exploit this diversity, and the pattern of genetic variation between and within these ecotypes hasremained unknown. We aligned the GBS data to the red clover reference genome (De Vega, et al., 2015). We found a four grouppopulation structure using Cluster and nine potential ancestry groups usingSTRUCTURE.

There was moderate genetic diversity between the groups; and acorrelation of genotype to geography and SNP that correlated to adaptation totheir geography; and from a genome wide association study (GWAS) we identifiedpossible SNP involved in flowering time.