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A survey of the genetic diversity in
populations of White Clover,
Trifolium repens with a focus on
South-Western Europe

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Roanna Richards 2011



Trifolium repens, white clover

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Abstract

Trifolium repens (white clover), is an allotetraploid, formed from the cross of putative parents *T. pallescens* and *T. occidentale*. The purpose of this study was to analyse intra-species genetic diversity of *T. repens* among and within populations from the Mediterranean, UK, continental Europe, North Africa, and the near East. This allowed light to be shed on the origins and radiation of the species. It was hypothesized from current distributions of the putative parents, and *T. repens* that an origin for the species was within South-Western Europe.

A survey of genetic diversity was conducted through PCR and direct sequencing of the chloroplast trnL intron, and a chloroplast internal repeat region (IRB21NE) (300 plants) and from the nuclear rDNA, ITS regions of the nucleolar organizing region, (NOR), (327 plants). The interpretation of results was complicated by the spread of commercial varieties over the top of natural populations of *T. repens*.

Diversity was greater for ITS pattern types (45) than for chloroplast pattern types (5). Maximum chloroplast diversity was found in Portugal/Spain. Pockets of ITS diversity were observed in, Portugal/Spain, North Africa, UK (Kent landrace) and Northern/North-Western Europe. Within the natural distribution zone for the species two chloroplast lineages and three main nuclear lineages described the majority of the observed variation. However a novel nuclear lineage was observed in north/north-western Europe. Spain and Portugal differed in their predominant ITS lineages, as did Morocco and Algeria from each other.

The diversity in chloroplast data was consistent with an origin in Portugal and Spain. ITS diversity also supported this, but the presence of other areas of ITS diversity, gave a complex pattern that requires further study.

Abbreviations

PCR: Polymerase chain reaction

ITS: Internally transcribed spacer region

NOR: Nucleolar organising region

IRB21NE: Internal repeat region 21, NE- Nick Ellison.
(a shortened version of the full length IRB21)

FISH: fluorescence *in situ* hybridization

rDNA: ribosomal DNA

TCS (version 1.2.1): a software program that does phylogenetic estimation by using statistical parsimony, (Clement et al., 2000).

Table of Contents

Abstract	1
Abbreviations	2
Table of Contents	3-6
1 Literature review	1-21
1.1 <i>T. repens</i> or White Clover	1-7
1.1.2 <i>T. repens</i> : a rare hybrid of the Trifolium genus	
1.1.3 Parentage of <i>T. repens</i>	
1.1.4 Morphology of white clover	
1.1.5 Self incompatibility	
1.1.6 Diversity in white clover DNA	
1.1.7 Distribution of white clover	
1.1.8 Breeding history of <i>T. repens</i>	
1.2 Clover in general	7-10
1.2.1 The Trifolium genus	
1.2.2 Origins of clover	
1.2.3 Spread of clover	
1.2.4 Agricultural use	
1.3 Appropriate Genetic markers for phylogeny & diversity	10-17
1.3.2 Polyploidy	
1.3.3 Polyploid models for comparison to white clover	
1.3.4 Concerted Evolution, an influence on DNA sequence diversity	
1.3.4.2 Bidirectional Concerted Evolution	
1.3.4.3 Factors affecting the observation of and effect of concerted evolution	
1.3.5 Reticulate evolution	
1.4 Glaciations and affect on species and populations	17-21
1.4.2 Glacial hypotheses	
1.4.3 Interpreting species genetic diversity in relation to glaciations	

1.5	Hypotheses and aims	22
1.5.1	Aims	
1.5.2	Hypotheses	
2	Methods	23-43
2.1	Accession selection and growing of plants	23-30
-	A list of used accessions and numbers of surviving plants	
-	Seed germination techniques	
-	Growing conditions and methods	
2.2	PCR	31-33
-	Reagents and kits used in PCR	
-	PCR primers	
-	Gel purification protocol	
2.3	Sequencing	34-37
-	Reagents for sequencing	
-	Sequencing protocol	
2.4	Chromatogram analysis and contig assembly	37-39
2.5	Diversity analysis	39
2.6	Morphology study	40-42
2.7	Comparison of DNA and morphology	43
2.8	Novel Algerian accession C20859	43
3	Results from DNA sequence data	44-125
3.1	Results from chloroplast perspective	44-60
-	Universal CD primers (<i>trn L</i> intron)	
-	Modified IRB21(NE) primers	
3.2	Results from ITS nuclear pattern types	61-89
-	EC1/EC2 (ITS) primers	
3.3	Results for the combined pattern types generated from the combination of the chloroplast and nuclear pattern types	90-104
3.4	TCS Analyses of pattern types	105-118

3.5	Combined Results and Morphological characteristics	119-125
4	Discussion DNA sequence data	126-167
4.1	Observations of chloroplast sequences	126-137
4.1.1	Geographic distributions of chloroplast sequences	
4.1.2	Comments on chloroplast sequence variation from selected ecotypes, ecotype selections and mixed cultivars	
4.1.3	Comparison of chloroplast diversity in Zone 1 to Zone 2	
4.1.4	Relationships between observed chloroplast pattern types	
4.1.5	Chloroplast pattern type origins	
4.2	Observations of Nuclear ITS sequences	138-152
4.2.1	Geographic distributions of nuclear ITS sequences	
4.2.2	Discussion of main and variants of main nuclear ITS pattern types	
4.2.3	Infrequently observed Nuclear ITS pattern types	
4.2.4	Hypotheses of dispersal and origin with a focus on common ITS types	
4.2.5	Parental or Biparental inheritance of nuclear ITS pattern types in <i>T. repens</i> ?	
4.3	Discussion of the combined perspective	153-160
4.3.1	Geographic distributions of combined (<i>trn L</i> , IRB21NE, and ITS) pattern combinations.	
4.3.2	Chloroplast & nuclear results do they agree: or disagree?	
4.3.3	Diversity and models of origin, from a combined perspective	
4.3.4	Discussion of the perspective gained from TCS networks	
4.3.5	Discussion of Combined DNA sequence pattern types and Morphology	
4.4	Discussion of the perspective gained from TCS networks	161-162
4.5	Discussion of Combined DNA analyses and Morphology	162-163
4.6	Concluding remarks	163
4.7	Limitations of the study	163-164
4.8	Future directions, extensions from this work	164-166
4.8.1	Extension of the sampled area	
4.8.2	Single copy markers	
4.8.3	Chromosome specific markers	
4.8.4	Phylogenetic analysis	

4.9 Conclusion	167
5 Novel Algerian species C20859	168-177
- Introduction	
- results	
- Discussion	
References	178-187

Appendices

A: Chloroplast DNA sequence data	188-199
B: Nuclear DNA sequence data	200-217
C: Combined chloroplast and nuclear DNA sequence data	218-229
D: Combined DNA sequence data and morphology scoring	230-241
E: TCS analyses	242
F: Chi Squared analyses	243-251

Alignments

1. <i>trn L</i> alignment (universal CD primers)	252-299
2. IRB21NE alignment (IRB21NE primers)	300-338
3. ITS alignment (EC1/EC2 (ITS) primers)	339-392