

Contents

1. Introduction.....	1
1.1 The importance of rapeseed.....	1
1.2. The genetic background of important traits in rapeseed.....	2
1.3. QTL mapping.....	4
1.4. Intervarietal substitution lines.....	5
1.5. QTL mapping using intervarietal substitution lines.....	7
1.6. General Objective.....	8
2. Materials and Methods.....	9
2.1. Plant materials.....	9
2.1.1. Mapping population.....	9
2.1.2. ISL populations.....	9
2.1.2.1. A cross between ‘Express’ and the resynthesized line ‘RS239’ (‘ExRS239’).....	9
2.1.2.2. A cross between ‘Mansholt’ x ‘Samourai’ (‘MxS’).....	10
2.2. Microspore culture and ploidy analysis.....	12
2.3. Acclimatization and vernalization.....	12
2.4. Colchicine re-treatment.....	12
2.4.1. Root immersion method.....	12
2.4.2. Cutting immersion method.....	12
2.5. DNA extraction and AFLP analysis.....	13
2.6. Genetic linkage map construction.....	14
2.7. Field trials and trait analysis.....	15
2.8. Statistical analysis.....	17
2.9. QTL localization.....	17
3. Results.....	20
3.1. Construction of a genetic linkage map in the cross of ‘ExRS239’.....	20
3.2. Detection of duplicated regions in the linkage map.....	25
3.3. Development of the ISLs by doubled haploid plants production from BC ₄ plants of the cross ‘ExRS239’.....	25

3.3.1. Effect of colchicine treatment at microspore culture stage.....	25
3.3.2. Effect of colchicine re-treatment.....	28
3.3.3. Number of ISLs generated.....	30
3.4. Molecular analysis of the ISLs generated from the cross ‘ExRS239’.....	30
3.5. Phenotypic analysis of the ISLs generated from the cross ‘ExRS239’.....	32
3.5.1. Seed quality trait.....	32
3.5.2. Plant height and phenological traits.....	36
3.6. QTL analysis in the ISLs generated from the cross ‘ExRS239’.....	37
3.6.1. Seed quality trait.....	37
3.6.2. Plant height and phenological trait.....	49
3.7. Molecular analysis of the ISLs generated from the cross ‘MxS’.....	51
3.8. Phenotypic analysis of the ISLs generated from the cross ‘MxS’.....	52
3.8.1. Seed quality trait.....	52
3.8.2. Plant height and phenological trait.....	56
3.9. QTL Analysis in the ISLs generated from the cross ‘MxS’.....	58
3.9.1. Seed quality traits.....	58
3.9.2. Plant height and phenological traits.....	62
3.10. Comparison of QTL detected in the ISLs and F ₁ DH population generated from the cross ‘MxS’.....	64
4. Discussion.....	72
4.1. The genetic linkage map developed from the cross ‘ExRS239’.....	72
4.2. Distorted segregations.....	74
4.3. Detection of duplicated regions.....	75
4.4. Effect of colchicines re-treatment in increasing the frequency of doubled haploid plants production.....	76
4.5. Characterization of the donor segments in the ISLs.....	77
4.6. Detection of interesting QTL for rapeseed breeding in the ISLs from the cross ‘ExRS239’.....	79
4.7. Undetected QTL in the ISLs of the cross ‘ExRS239’.....	81
4.8. Comparison of QTL and their effect detected in the ISLs and the corresponding F ₁ DH population from the cross ‘MxS’.....	82
4.7.1. The confirmed QTL.....	82
4.7.2. The undetected QTL.....	84

4.7.3. The detection of new QTL.....	84
4.7.4. The false positive QTL.....	85
4.9. Fine mapping.....	86
4.10. Pleiotropy versus closely linked QTL.....	87
4.11. Comparison of QTL in the ISL populations.....	88
5. Summary.....	90
6. Zusammenfassung.....	93
References.....	96
Appendix.....	107
Acknowledgements.....	108