



Assessment of a new strategy for selective phenotyping applied to complex traits in *Brassica napus*

PDF (Size: 456KB) PP. 190-201 DOI : 10.4236/ojgen.2012.24025

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ABSTRACT

The accurate mapping of quantitative trait loci (QTL) depends notably on the number of recombination events occurring in the segregating population. The cost of phenotyping often limits the sample size used in QTL mapping. To get round this problem, we assessed a selective phenotyping method, called *qtlRec* sampling. In order to improve the accuracy of QTL mapping, a subset of individuals was selected to maximize the number of recombination events at putative QTL positions; the usefulness of this subset was compared to a selected sample built to maximize the recombination rate over the whole genome. We assessed this method on the quantitative oil content trait in *Brassica napus*. We showed that the *qtlRec* strategy could allow increasing accuracy (both support interval and position) of QTL location while it maintained a similar power of detection. We then applied this approach to the *B. napus*—*Leptosphaeria maculans* pathosystem for which resistance QTL with minor effect were previously identified. This allowed the validation of the QTL in six genomic regions. The *qtlRec* method is an attractive strategy for validating QTL in multiple year and/or location trials for a trait which requires costly and time-consuming phenotyping.

KEYWORDS

Selective Phenotyping; QTL; Brassica Napus; Leptosphaeria maculans

Cite this paper

Jestin, C. , Vallée, P. , Domin, C. , Manzanares-Dauleux, M. and Delourme, R. (2012) Assessment of a new strategy for selective phenotyping applied to complex traits in *Brassica napus*. *Open Journal of Genetics*, 2, 190-201. doi: 10.4236/ojgen.2012.24025.

References

- [1] Kearsey, M.J. and Farquhar, A.G.L. (1998) QTL analysis in plants: where are we now? *Heredity*, 80, 137-142. doi:10.1046/j.1365-2540.1998.00500.x
- [2] Salvi, S. and Tuberosa, R. (2005) To clone or not to clone plant QTLs: Present and future challenges. *Plant Science*, 10, 297-304.
- [3] Lander, E.S. and Botstein, D. (1989) Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics*, 121, 185-199.
- [4] Lebowitz, R.J., Soller, M. and Beckmann, J.S. (1987) Trait-based analyses for the detection of linkage between marker loci and quantitative trait loci in crosses between inbred lines. *Theoretical and Applied Genetics*, 73, 556-562. doi:10.1007/BF00289194
- [5] Navabi, A., Mather, D.E., Bernier, J., Spaner, D.M. and Atlin, G.N. (2009) QTL detection with bidirectional and unidirectional selective genotyping: Marker-based and trait-based analyses. *Theoretical and Applied Genetics*, 118, 347-358. doi:10.1007/s00122-008-0904-2
- [6] Kimura, T., Kobayashi, T., Munkhbat, B., Oyungerel, G., Bilegtsaikhan, G., Anar D., Jambaldorj, J., Munkhsaikhan, S., Munkhtuvshin, N., Hayashi, H., Oka, A., Inoue, I. and Inoko, H. (2008) Genome-wide association analysis with selective genotyping identifies candidate loci for adult height at 8q21.13 and 15q22.33-q23 in Mongolians. *Human Genetics*, 123, 655-660. doi:10.1007/s00439-008-0512-x

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- [7] Sun, Y., Wang J., Crouch, J.H. and Xu, Y. (2010) Efficiency of selective phenotyping for genetic analysis of complex traits and potential applications in crop improvement. *Molecular Breeding*, 26, 493-511. doi:10.1007/s11032-010-9390-8
- [8] Brown, D. and Vision T. (2000) Software for selective mapping and bin mapping. <http://www.bio.unc.edu/faculty/vision/lab/mappop>
- [9] Xu, Z.L., Zou, F. and Vision, T.J. (2005) Improving quantitative trait loci mapping resolution in experimental crosses by the use of genotypically selected samples. *Genetics*, 170, 401-408. doi:10.1534/genetics.104.033746
- [10] Simon, M., Loudet, O., Durand, S., Berard, A., Brunel, D., Sennesal, F.S., Durand-Tardif, M., Pelletier, G. and Camilleri, C. (2008) Quantitative trait loci mapping in five new large recombinant inbred line populations of *Arabidopsis thaliana* genotyped with consensus single-nucleotide polymorphism markers. *Genetics*, 178, 2253-2264. doi:10.1534/genetics.107.083899
- [11] Vales, M.I., Schon, C.C., Capettini, F., Chen, X.M., Corey, A.E., Mather, D.E, Mundt, C.C., Richardson, K.L., Sandoval-Islas, J.S, Utz, H.F. and Hayes, P.M. (2005) Effect of population size on the estimation of QTL: A test using resistance to barley stripe rust. *Theoretical and Applied Genetics*, 111, 1260-1270. doi:10.1007/s00122-005-0043-y
- [12] Birolleau-Touchard, C., Hanocq, E., Bouchez, A., Bauland, C., Dourlen, I., Seret, J.P., Rabier, D., Hervet, S., Allienne, J.F., Lucas, P., Jaminon, O., Etienne, R., Baudhuin, G. and Giauvret, C. (2007) The use of MapPop1.0 for choosing a QTL mapping sample from an advanced backcross population. *Theoretical and Applied Genetics*, 114, 1019-1028. doi:10.1007/s00122-006-0495-8
- [13] Barchi, L., Lefebvre, V., Sage-Palloix, A.M., Lanteri, S. and Palloix, A. (2009) QTL analysis of plant development and fruit traits in pepper and performance of selective phenotyping. *Theoretical and Applied Genetics*, 118, 1157-1171. doi:10.1007/s00122-009-0970-0
- [14] Jin, C., Lan, H., Attie, A.D., Churchill, A.G., Bulutuglo, D. and Yandell, B.S. (2004) Selective phenotyping for increased efficiency in genetic mapping studies. *Genetics*, 168, 2285-2293. doi:10.1534/genetics.104.027524
- [15] Jannink, J.L. (2005) Selective phenotyping to accurately map quantitative trait loci. *Crop Science*, 45, 901-908. doi:10.2135/cropsci2004.0278
- [16] Charcosset, A. and Gallais, A. (1996) Estimation of the contribution of quantitative trait loci (QTL) to the variance of a quantitative trait by means of genetic markers. *Theoretical and Applied Genetics*, 93, 1193-1201. doi:10.1007/BF00223450
- [17] Orgogozo, V., Broman, K.W. and Stern, D.L. (2006) High-resolution quantitative trait locus mapping reveals sign epistasis controlling ovariole number between two *Drosophila* species. *Genetics*, 173, 197-205. doi:10.1534/genetics.105.054098
- [18] Delourme, R., Falentin, C., Huteau, V., Clouet, V., Horvais, R., Gandon, B., Specel, S., Hanneon, L., Dheu, J.E, Deschamps, M., Margale, E., Vincourt, P. and Renard, M. (2006) Genetic control of oil content in oilseed rape (*Brassica napus* L.). *Theoretical and Applied Genetics*, 113, 1331-1345. doi:10.1007/s00122-006-0386-z
- [19] Fitt, B.D.L., Brun, H., Barbetti, M.J. and Rimmer, S.R. (2006) World-wide importance of phoma stem canker (*Leptosphaeria maculans* and *L. biglobosa*) on oilseed rape (*Brassica napus*). *European Journal of Plant Pathology*, 114, 3-15. doi:10.1007/s10658-005-2233-5
- [20] West, J.S., Kharbanda, P.D., Barbetti, M.J. and Fitt, B.D.L. (2001) Epidemiology and management of *Leptosphaeria maculans* (phoma stem canker) on oilseed rape in Australia, Canada and Europe. *Plant Pathology*, 50, 10-27.
- [21] Delourme, R., Chèvre, A.M., Brun, H., Rouxel, T., Balesdent, M.H., Dias, J.S., Salisbury, P., Renard, M. and Rimmer, S.R. (2006) Major gene and polygenic resistance to *Leptosphaeria maculans* in oilseed rape (*Brassica napus*). *European Journal of Plant Pathology*, 114, 41-52. doi:10.1007/s10658-005-2108-9
- [22] Rimmer, S.R. (2006) Resistance genes to *Leptosphaeria maculans* in *Brassica napus*. *Canadian Journal of Plant Pathology*, 28, S288-S297. doi:10.1080/07060660609507386
- [23] Pilet, M., Duplan, G., Archipiano, M., Barret, P., Baron, C., Horvais, R., Tanguy, X., Lucas, M.O., Renard, M. and Delourme, R. (2001) Stability of QTL for field resistance to blackleg across two genetic backgrounds in oilseed rape. *Crop Science*, 41, 197-205. doi:10.2135/cropsci2001.411197x

- [24] Pilet, M.L., Delourme, R., Foisset, N. and Renard, M. (1998) Identification of loci contributing to quantitative field resistance to blackleg disease, causal agent *Leptosphaeria maculans* (Desm.) Ces. et de Not., in Winter rapeseed (*Brassica napus* L.). *Theoretical and Applied Genetics*, 96, 23-30. doi:10.1007/s001220050704
- [25] Foisset, N., Delourme, R., Barret, P., Hubert, N., Landry, B.S. and Renard, M. (1996) Molecular-mapping analysis in *Brassica napus* using isozyme, RAPD and RFLP markers on a doubled haploid progeny. *Theoretical and Applied Genetics*, 93, 1017-1025. doi:10.1007/BF00230119
- [26] Lombard, V. and Delourme, R. (2001) A consensus linkage map for rapeseed (*Brassica napus* L.): Construction and integration of three individual maps from DH populations. *Theoretical and Applied Genetics*, 103, 491-507. doi:10.1007/s001220100560
- [27] Delourme, R., Piel, N., Horvais, R., Pouilly, N., Domin, C., Vallée, P., Falentin, C., Manzanares-Dauleux, M.J. and Renard, M. (2008) Molecular and phenotypic characterization of near isogenic lines at QTL for quantitative resistance to *Leptosphaeria maculans* in oilseed rape (*Brassica napus* L.). *Theoretical and Applied Genetics*, 117, 1055-1067. doi:10.1007/s00122-008-0844-x
- [28] Wang J., Lydiate, D.J., Parkin, I.A.P., Falentin, C., Delourme, R., Carionand, P.W.C. and King, G.J. (2011) Integration of linkage maps for the amphidiploid *Brassica napus* and comparative mapping with *Arabidopsis* and *Brassica rapa*. *BMC Genomics*, 12, 101. doi:10.1186/1471-2164-12-101
- [29] Lincoln, S., Daly, M. and Lander, E. (1992) Constructing genetic linkage maps with Mapmaker/Exp 3.0: A tutorial and reference manual. 3rd Edition, Whitehead Institute Technical Report.