

[Home](#) > [Journal](#) > [Earth & Environmental Sciences](#) > [AS](#)
[Indexing](#) | [View Papers](#) | [Aims & Scope](#) | [Editorial Board](#) | [Guideline](#) | [Article Processing Charges](#)
[AS](#) > Vol.3 No.7, November 2012



## The genetic variation of the backcross modified lines developed from the maize line 08-641 selected by different directions

PDF (Size: 320KB) PP. 918-922 DOI : 10.4236/as.2012.37111

### Author(s)

Lujiang Li, Yaoyu Xiong, Wensheng Chen, Yongjian Liu, Hai Lan, Haijian Lin, Kecheng Yang, Shibin Gao, Guangtang Pan

### ABSTRACT

In this study, two donors CN962 and 8065 were used to improve the resistance to northern leaf blight of the recurrent parent inbred line 08-641 (R08). A total of 79 lines (BC2F4) were developed by a bidirectional selection based on the similarity and dissimilarity in the shape and color of seeds to R08. The genetic variation of these lines were analyzed by 44 pairs of SSR molecular markers, the result showed that a total of 272 alleles were detected in the improved lines and R08, 123 out of them were detected in the modified lines but discarded in R08. The modified line selected based on dissimilarity in the shape and color of seeds to R08 have lower genetic similarity between R08 than that between the lines selected based on similarity in the shape and color of seeds and R08, and the genetic variation of these lines were wider. It concluded that when the backcross breeding were used to improve the maize inbred lines, multidirectional selection based on phenotypic value were contribute to create and keep genetic variation.

### KEYWORDS

Backcross Breeding; Select Direction; Genetic Variation; SSR

### Cite this paper

Li, L. , Xiong, Y. , Chen, W. , Liu, Y. , Lan, H. , Lin, H. , Yang, K. , Gao, S. and Pan, G. (2012) The genetic variation of the backcross modified lines developed from the maize line 08-641 selected by different directions. *Agricultural Sciences*, 3, 918-922. doi: 10.4236/as.2012.37111.

### References

- [1] Ho, J.C., McCouch, S.R. and Smith, M.E. (2002) Improvement of hybrid yield by advance backcross QTL analysis in elite maize. *Theoretical and Applied Genetics*, 105, 440-480. doi:10.1007/s00122-002-0945-x
- [2] Chen, H.M., Zhang, Y.D., Chen, W., Kang, M.S., Tan, J., Wang, Y.F., Yang, J.Y. and Fan, X.M. (2010) Improving grain yield and yield components via backcross procedure. *Maydica*, 55, 145-153.
- [3] Melching, A.E. (1990) Use of molecular markers in breeding for oligogenic disease resistance. *Plant Breed*, 104, 1-9. doi:10.1111/j.1439-0523.1990.tb00396.x
- [4] Hospital, F. and Charcosset, A. (1997) Marker-assisted introgression of quantitative trait loci. *Genetics*, 147, 1469-1485.
- [5] Stuber, C.W. and Sisco, P.H. (1991) Marker facilitated transfer of QTL alleles between elite inbred lines and responses in hybrid. *Process 46th Annual Corn and Sorghum Industry Research Conference, American Seed Trade Association*, 41, 70-83.
- [6] Duvick, D.N. (1974) Continuous backcrossing to transfer prolificacy to a single-eared inbred line of maize. *Crop Science*, 14, 69-71. doi:10.2135/cropsci1974.0011183X001400010021x
- [7] Qiao, S.B., Wang, Y.H., Yang, K.C., Rong, T.Z., Pan, G.T. and Gao, S.B. (2009) Effects contributed by different donor parents and backcross times on R08 improvement. *Acta Agronomica Sinica*, 35, 2187-2196. doi:10.3724/SP.J.1006.2009.02187

- [Open Special Issues](#)
- [Published Special Issues](#)
- [Special Issues Guideline](#)

[AS Subscription](#)
[Most popular papers in AS](#)
[About AS News](#)
[Frequently Asked Questions](#)
[Recommend to Peers](#)
[Recommend to Library](#)
[Contact Us](#)

Downloads:	145,384
------------	---------

Visits:	317,023
---------	---------

[Sponsors, Associates, and Links >>](#)

- [2013 Spring International Conference on Agriculture and Food Engineering \(AFE-S\)](#)

- [8] Smith, J.S.C., Chin, E.C.L. and Shu, H. (1997) An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays* L.): Comparison with data from RFLPs and pedigree. *Theoretical and Applied Genetics*, 95, 163-173. doi:10.1007/s001220050544
- [9] Nei, M. and Li, W.H. (1979) Mathematical model for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences of the United States of America*, 76, 5256-5273. doi:10.1073/pnas.76.10.5269
- [10] Rolf, J.F. (1998) NTSYS—pc2 Numerical taxonomy and multivariate analysis system (CP). Version 2.0