

Publications

- 1.) *Publications in refereed journals*
- 2.) *Conference contributions*

1.) Publications in refereed journals

- (50) Falke, K.C., and **M. Frisch**. 2010. Power and false positive rate in QTL detection with near-isogenic line libraries. *Heredity*, in press.
- (49) Shiringani, A.L., **M. Frisch**, and W. Friedt. 2010. Genetic mapping of QTL for sugar-related traits in a RIL population of *Sorghum bicolor* L. Moench. *Theoretical and Applied Genetics* 121:323–336.
- (48) Fu, J., A. Thieman, T.A. Schrag, A.E. Melchinger, S. Scholten, and **M. Frisch**. 2010. Dissecting grain yield pathways and their interactions with grain dry matter content by a two-step correlation approach with maize seedling transcriptome. *BMC Plant Biology* 10:63.
- (47) **Frisch, M.**, A. Thiemann, J. Fu, T.A. Schrag, S. Scholten, and A.E. Melchinger. 2010. Transcriptome-based distance measures for grouping of germplasm and prediction of hybrid performance in maize. *Theoretical and Applied Genetics* 120:415–427.
- (46) Schrag, T.A., J. Möhring, A.E. Melchinger, B. Kusterer, B.S. Dhillon, H.-P. Piepho, and **M. Frisch**. 2010. Prediction of hybrid performance in maize using molecular markers and joint analyses of hybrids and parental inbreds. *Theoretical and Applied Genetics* 120:451–461.
- (45) Thiemann, A., J. Fu, T.A. Schrag, A.E. Melchinger, **M. Frisch**, and S. Scholten. 2010. Correlation between parental transcriptome and field data for the characterization of heterosis in *Zea mays* L. *Theoretical and Applied Genetics* 120:401–413.
- (44) Schrag, T.A., **M. Frisch**, B.S. Dhillon, A.E. Melchinger. 2009. Marker-based prediction of hybrid performance in maize single-crosses involving doubled haploids. *Maydica* 54:353–362.
- (43) Falke, K.C., Th. Miedaner, and **M. Frisch**. 2009. Selection strategies for the development of rye introgression libraries. *Theoretical and Applied Genetics* 119:595–603.
- (42) Prigge, V., A.E. Melchinger, B.S. Dhillon, and **M. Frisch**. 2009. Efficiency gain of marker-assisted backcrossing by sequentially increasing marker densities over generations. *Theoretical and Applied Genetics* 119:23–32.
- (41) Schrag, T.A., J. Möhring, H.P. Maurer, B.S. Dhillon, A.E. Melchinger, H.-P. Piepho, A.P. Sørensen, and **M. Frisch**. 2009. Molecular marker-based prediction of hybrid performance in maize using unbalanced data from multiple experiments with factorial crosses. *Theoretical and Applied Genetics* 118:741–751.

- (40) Longin, F., A.E. Melchinger, and **M. Frisch**. 2009. Optimum allocation of test resources and relative efficiency of alternative procedures of within-family selection in hybrid breeding. *Plant Breeding* 128:213–216.
- (39) Warburton, M.L., J.C. Reif, **M. Frisch**, M. Bohn, C. Bedoya, X.C. Xia, J. Crossa, J. Franco, D. Hoisington, K. Pixley, S. Taba, and A.E. Melchinger. 2008. Genetic diversity in CIMMYT nontemperate maize germplasm: Landraces, open pollinated varieties, and inbred lines. *Crop Science* 48:617–624.
- (38) Heckenberger, M., H.P. Maurer, A.E. Melchinger, and **M. Frisch**. 2008. The Plabsoft database: a comprehensive database management system for integrating phenotypic and genomic data in academic and commercial plant breeding programs. *Euphytica* 161:173–179.
- (37) Maurer, H.P., A.E. Melchinger, and **M. Frisch**. 2008. Population genetic simulation and data analysis with Plabsoft. *Euphytica* 161:133–139.
- (36) Prigge V., H.P. Maurer, D.J. Mackill, A.E. Melchinger, and **M. Frisch**. 2008. Comparison of the observed with the simulated distributions of the parental genome contribution in two marker-assisted backcross programs in rice. *Theoretical and Applied Genetics* 116:739–744.
- (35) **Frisch, M.** and A.E. Melchinger. 2008. Precision of recombination frequency estimates after random intermating with finite population sizes. *Genetics* 178:597–600.
- (34) Maurer, H.P., A.E. Melchinger, and **M. Frisch**. 2007. A new incomplete enumeration algorithm for an exact test of Hardy-Weinberg proportions with multiple alleles. *Theoretical and Applied Genetics* 115:393–398.
- (33) Schrag, T.A., H.P. Maurer, A.E. Melchinger, H.-P. Piepho, J. Peleman, and **M. Frisch**. 2007. Prediction of single-cross hybrid performance in maize using haplotype blocks associated with QTL for grain yield. *Theoretical and Applied Genetics* 114:1345–1355.
- (32) **Frisch, M.** and A.E. Melchinger. 2007. Variance of the parental genome contribution to inbred lines derived from biparental crosses. *Genetics* 176:477–488.
- (31) Falke K.C., H.P. Maurer, A.E. Melchinger, H.-P. Piepho, C. Flachenecker, and **M. Frisch**. 2007. Linkage disequilibrium in two European F₂ flint maize population under modified recurrent full-sib selection. *Theoretical and Applied Genetics* 115:289–297.
- (30) Falke, K.C., C. Flachenecker, A.E. Melchinger, H.-P. Piepho, H. P. Maurer, and **M. Frisch**. 2007. Temporal changes in allele frequencies in two European F₂ flint maize populations under modified recurrent full-sib selection. *Theoretical and Applied Genetics* 114:765–776.
- (29) Flachenecker C., **M. Frisch**, K.C. Falke, and A.E. Melchinger. 2006. Genetic drift and selection effects of modified recurrent full-sib selection programs in two F₂ populations of European flint maize. *Theoretical and Applied Genetics* 113:1113–1120.

- (28) **Frisch, M.** and A.E. Melchinger. 2006. Marker-based prediction of the parental genome contribution to inbred lines derived from biparental crosses. *Genetics* 174:795–803.
- (27) Schrag, T.A., A.E. Melchinger, A.P. Sørensen, and **M. Frisch**. 2006. Prediction of single-cross hybrid performance for grain yield and grain dry matter content in maize using AFLP markers associated with QTL. *Theoretical and Applied Genetics* 113:1037–1047.
- (26) Falke, K.C., A.E. Melchinger, C. Flachenecker, B. Kusterer, and **M. Frisch**. 2006. Comparison of linkage maps from F₂ and three times intermated generations in two populations of European flint maize (*Zea mays L.*). *Theoretical and Applied Genetics* 113:857–866.
- (25) Maurer H.P., C. Knaak, A.E. Melchinger, M. Ouzunova, and **M. Frisch**. 2006. Linkage disequilibrium between SSR markers in six pools of elite lines of an European breeding program for hybrid maize. *Maydica* 51:269–279.
- (24) Flachenecker, C., **M. Frisch**, J. Muminović, K.C. Falke, and A.E. Melchinger. 2006. Modified full-sib selection and best linear unbiased prediction of progeny performance in a European F₂ maize population. *Plant Breeding* 125:248–253.
- (23) Reif, J.C., M.L. Warburton, X.C. Xia, D.A. Hoisington, J. Crossa, S. Taba, J. Muminović, M. Bohn, **M. Frisch**, and A.E. Melchinger. 2006. Grouping of accessions of Mexican races of maize revisited with SSR markers. *Theoretical and Applied Genetics* 113:177–185.
- (22) Stich, B., H.P. Maurer, A.E. Melchinger, **M. Frisch**, M. Heckenberger, J. Rouppe van der Voort, J. Peleman, A.P. Sørensen, and J.C. Reif. 2006. Comparison of linkage disequilibrium in elite European maize inbred lines using AFLP and SSR markers. *Molecular Breeding* 17:217–226.
- (21) Flachenecker, C., **M. Frisch**, K.C. Falke, and A.E. Melchinger. 2006. Trends in population parameters and best linear unbiased prediction of progeny performance in a European F₂ maize population under modified recurrent full-sib selection. *Theoretical and Applied Genetics* 112:483–491.
- (20) Xia, X.C., J.C. Reif, A.E. Melchinger, **M. Frisch**, D.A. Hoisington, D. Beck, K. Pixley, and M.L. Warburton. 2005. Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers: II. Subtropical, tropical mid-altitude and highland maize inbred lines and their relationships with elite U.S. and European maize. *Crop Science* 45:2573–2582.
- (19) Heckenberger M., M. Bohn, **M. Frisch**, H.P. Maurer, and A.E. Melchinger. 2005. Identification of essentially derived varieties with molecular markers: An approach based on statistical test theory and computer simulations. *Theoretical and Applied Genetics* 111:598–608.
- (18) Stich, B., A.E. Melchinger, **M. Frisch**, H.P. Maurer, M. Heckenberger, and J.C. Reif. 2005. Linkage disequilibrium in European elite maize germplasm investigated with SSRs. *Theoretical and Applied Genetics* 111:723–730.
- (17) **Frisch, M.** and A.E. Melchinger. 2005. Selection theory for marker-assisted backcrossing. *Genetics* 170:909–917.

- (16) Reif, J.C., A.E. Melchinger, and **M. Frisch**. 2005. Genetical and mathematical properties of similarity and dissimilarity coefficients applied in plant breeding and seed bank management. *Crop Science* 45:1–7.
- (15) **Frisch, M.** 2005. Optimum design of marker-assisted backcross programs. In: *Biotechnology in Agriculture and Forestry* Vol. 55, Eds. H. Loerz, G. Wenzel. Springer Verlag Heidelberg. p. 319–334.
- (14) Xia, X.C., J.C. Reif, D.A. Hoisington, A.E. Melchinger, **M. Frisch**, and M.L. Warburton. 2004. Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers: I. Lowland tropical maize. *Crop Science* 44:2230–2237.
- (13) **Frisch, M.**, M. Quint, T. Lübberstedt, and A.E. Melchinger. 2004. Duplicate marker loci can result in incorrect locus orders on linkage maps. *Theoretical and Applied Genetics* 109:305–316.
- (12) Reif, J.C., X.C. Xia, A.E. Melchinger, M.L. Warburton, D.A. Hoisington, D. Beck, M. Bohn, and **M. Frisch**. 2004. Genetic diversity determined within and among CIMMYT maize populations of tropical, subtropical, and temperate germplasm by SSR markers. *Crop Science* 44:326–334.
- (11) Reif, J.C., A.E. Melchinger, X.C. Xia, M.L. Warburton, D.A. Hoisington, S.K. Vasal, D. Beck, M. Bohn, and **M. Frisch**. 2003. Use of SSRs for establishing heterotic groups in subtropical maize. *Theoretical and Applied Genetics* 107:947–957.
- (10) Reif, J.C., A.E. Melchinger, X.C. Xia, M.L. Warburton, D.A. Hoisington, S.K. Vasal, G. Srinivasan, M. Bohn, and **M. Frisch**. 2003. Genetic distance based on simple sequence repeats and heterosis in tropical maize populations. *Crop Science* 43:1275–1282.
- (9) Hagdorn, S., K.R. Lamkey, **M. Frisch**, P.E.O. Guimaraes, and A.E. Melchinger. 2003. Molecular genetic diversity among progenitors and derived elite lines of BSSS and BSCB1 maize populations. *Crop Science* 43:474–482.
- (8) Warburton, M., X. Xianchun, J. Crossa, J. Franco, A.E. Melchinger, **M. Frisch**, M. Bohn, and D.A. Hoisington. 2002. Genetic characterization of CIMMYT inbred maize lines and open pollinated populations using large scale fingerprinting methods. *Crop Science* 42:1832–1840.
- (7) **Frisch, M.**, K.R. Lamkey, and A.E. Melchinger. 2002. Storage of molecular marker data in databases for efficient use in plant breeding programs. *Zeitschrift für Agrarinformatik* 10:23–27.
- (6) **Frisch, M.** and A.E. Melchinger. 2001. Marker-assisted backcrossing for simultaneous introgression of two genes. *Crop Science* 41:1716–1725.
- (5) **Frisch, M.** and A.E. Melchinger. 2001. Marker-assisted backcrossing for introgression of a recessive gene. *Crop Science* 41:1485–1494.
- (4) **Frisch, M.** and A.E. Melchinger. 2001. The length of the intact chromosome segment around a target gene in marker-assisted backcrossing. *Genetics* 157: 1343–1356.

- (3) **Frisch, M.**, M. Bohn, and A.E. Melchinger. 2000. Plabsoft: Software for simulation of marker-assisted backcrossing. *Journal of Heredity* 91:86–87.
- (2) **Frisch, M.**, M. Bohn, and A.E. Melchinger. 1999. Comparison of selection strategies for marker-assisted backcrossing of a gene. *Crop Science* 39:1295–1301.
- (1) **Frisch, M.**, M. Bohn, and A.E. Melchinger. 1999. Minimum sample size and optimal positioning of flanking markers in marker-assisted backcrossing for transfer of a target gene. *Crop Science* 39:967–975.

2.) Conference contributions

- (c22) Falke K.C., **Frisch, M.**, and T. Miedaner. 2010. Optimum design of rye introgression libraries and their use for hybrid breeding. International Symposium on Rye Breeding & Genetics, 29 June–2 July 2010, Minsk, Belarus.
- (c21) Thiemann, A., J. Fu, T.A. Schrag, A.E. Melchinger, S. Scholten, and **M. Frisch**. 2010. Prediction of maize hybrid performance with transcription profiles of parental inbred lines. In: Abstracts of the 10. GPZ-Haupttagung, 15–17 Mar. 2010, Freising-Weihenstephan, p. 63.
- (c20) Herzog, E., and **M. Frisch**. 2010. Using high-throughput marker systems for efficient marker-assisted backcrossing. In: Abstracts of the 10. GPZ-Haupttagung, 15–17 Mar. 2010, Freising-Weihenstephan, p. 30.
- (c19) **Frisch, M.**, A. Thiemann, J. Fu, T.A. Schrag, S. Scholten, A.E. Melchinger. 2009. Transcriptome-based prediction of heterosis in experimental hybrids of maize. In: Proceedings of the International Conference on Heterosis in Plants, University of Hohenheim, Stuttgart, 7–9 Sept. 2009, p. 44.
- (c18) Schrag T.A., A.E. Melchinger, and **M. Frisch**. 2009. Prediction of heterosis and hybrid performance in maize by marker-based approaches. In: Proceedings of the International Conference on Heterosis in Plants, University of Hohenheim, Stuttgart, 7–9 Sept. 2009, p. 43.
- (c17) Heckenberger M., A.E. Melchinger, H.P. Maurer, and **M. Frisch**. 2006. A comprehensive database management system for integrating phenotypic and genomic data in scientific and applied plant breeding programs. *Agriculturae conspectus scientificus* Volume 71 (2006) Supplement 1. XIII EUCARPIA Biometrics in Plant Breeding Section Meeting, p. 25.
- (c16) Maurer H.P, A.E. Melchinger, and **M. Frisch**. 2006. Population genetical simulation and data analysis with Plabsoft. *Agriculturae conspectus scientificus*, Volume 71 (2006) Supplement 1. XIII EUCARPIA Biometrics in Plant Breeding Section Meeting, p. 18.
- (c15) Falke K.C., A.E. Melchinger, C. Flachenecker, B. Kusterer, and **M. Frisch**. 2006. Comparison of genetic maps constructed from an F₂ and an F₂SYN₃ population in maize (in German). *Vorträge für Pflanzenzüchtung* 68, p. 91.
- (c14) Falke K.C., C. Flachenecker, **M. Frisch**, and A.E. Melchinger. 2006. Allele frequency changes in full-sib recurrent selection of maize. In: Proceeding of

the XXth Meeting of the Eucarpia Maize and Sorghum Section, June 20-24, 2006, Budapest, Hungary. p. 84.

- (c13) Schrag T., H.P. Maurer, A.E. Melchinger, and **M. Frisch**. 2005. Linkage disequilibrium of 80 European elite maize inbred lines analysed with SSR and AFLP. In: Abstracts of the Plant & Animal Genomes XIII Conference, January 15-19, 2005, San Diego, CA, p. 169.
- (c12) Buntjer J., A. Sørensen, D. Lensink, T. Schrag, **M. Frisch**, A.E. Melchinger, and J. Peleman. 2005. AFLP Marker haplotypes for whole genome association mapping in maize. In: Abstracts of the Plant & Animal Genomes XIII Conference, January 15-19, 2005, San Diego, CA, p. 118.
- (c11) Falke, K.C., C. Flachenecker, **M. Frisch**, and A.E. Melchinger. 2004. Analysis of recurrent full-sib selection in maize with quantitative genetic methods (in German). *Vorträge für Pflanzenzüchtung* 64, pp. 70–72
- (c10) Flachenecker, C., K.C. Falke, **M. Frisch**, and A.E. Melchinger. 2004. Quantitative genetic analysis of full-sib family recurrent selection in an F2 maize population. In: Proceedings of the 17th Eucarpia General Congress, 8–11 September 2004, Tulln, Austria. pp. 403–406.
- (c9) Reif, J.C., A.E. Melchinger, and **M. Frisch**. 2003. Establishing heterotic groups in CYMMIT maize breeding material with molecular markers (in German). In: Bericht über die 54. Tagung der Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs 2003, Gumpenstein. pp. 31–36.
- (c8) **Frisch, M.** and A.E. Melchinger. 2002. Experimental design of marker-assisted backcross programs. In: Proceedings of the XXIst International Biometric Conference. July 21–26, 2002 Freiburg, Germany. Ed. International Biometric Society. p. 53.
- (c7) **Frisch, M.** and A.E. Melchinger. 2002. Optimal design of marker-assisted backcross programs (in German). *Vorträge für Pflanzenzüchtung* 54:29–34.
- (c6) Heckenberger, M., A.E. Melchinger, and **M. Frisch**. 2002. Application of databases in plant breeding programs at the example of MS Access (in German). In: Bericht über die 53. Tagung der Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs 2002, Gumpenstein. pp. 47–53.
- (c5) Xia, X.C.M.L. Warburton, D.A. Hoisington, M. Bohn, **M. Frisch**, and A.E. Melchinger. 2000. Optimizing fingerprinting of maize germplasm using SSR Markers. Poster presented at the 3rd International Crop Science Congress, Hamburg, Germany, August, 17–22, 2000.
- (c4) **Frisch, M.** and A.E. Melchinger. 2000. Theoretical basics of molecular-marker aided gene introgression. In: Proceedings of the XXth International Biometric Conference. July 1–7, 2000 University of California at Berkeley, CA, USA. Ed. International Biometric Society. pp. 173–174.
- (c3) **Frisch, M.**, M. Bohn, and A.E. Melchinger. 1998. Marker density and required number of marker data points in marker-assisted backcross programs (in German). *Vorträge für Pflanzenzüchtung* 42:1–3.

- (c2) **Frisch, M.** and E. Schumacher. 1998. SAS-Macros for permutation tests (in German). In: Konferenzbeiträge zur 2. Konferenz der SAS-Benutzer in Forschung und Entwicklung, 26.–27.2.1998 Jena. Ed. Rechenzentrum der Friedrich-Schiller-Universität Jena. pp. 41–49.
- (c1) **Frisch, M.** and E. Schumacher. 1997. A SAS-Macro for calculating generalized Kendall's Tau (in German). In: Konferenzbeiträge zur 1. Konferenz der SAS-Benutzer in Forschung und Entwicklung, 20.–21.2.1997 Berlin. Ed. Rechenzentrum der Humboldt-Universität zu Berlin. pp. 202–207.