


# Martin Mascher

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## Education

- 2014 Ph. D. in Bioinformatics, IPK Gatersleben and Bielefeld University, Germany, Advisors: U. Scholz at IPK and J. Stoye in Bielefeld
- 2011 Diploma in Mathematics, University of Magdeburg, Germany, Advisor: W. Willems

## Professional experience

- 2015– Independent group leader at IPK Gatersleben and member of the German Center for Integrative Biodiversity Research (iDiv)
- 2011–2014 Research assistant, IPK Gatersleben

## Fellowships and awards

- 2017 Leadership award of the International Wheat Genome Sequencing Consortium
- 2015 Nominated for the Young Scientists Award of the Leibniz Association
- 2014 Research fellowship of the German Research Foundation (DFG) (declined)
- 2014 Ph. D. degree awarded *summa cum laude*, University of Bielefeld
- 2011 Best Diploma Thesis 2010/2011, Faculty of Mathematics, University of Magdeburg
- 2008–2011 Undergraduate Fellowship of the German National Academic Foundation (Studienstiftung des deutschen Volkes)

## Professional memberships

2016– German Society for Plant Breeding (GPZ)

## Professional service

2017– Editorial board member of Functional and Integrative Genomics

Journal peer review (last two years): *Annals of Botany*, *Bioinformatics*, *BMC Bioinformatics*, *BMC Genetics*, *BMC Genomics*, *BMC Plant Biology*, *Crop Science*, *Current Opinion in Plant Biology*, *Frontiers in Genetics*, *Frontiers in Plant Science*, *G3*, *Genome Research*, *GigaScience*, *Journal of Experimental Botany*, *Molecular Biology and Evolution*, *Molecular Plant*, *Nature Communications*, *Nature Genetics*, *Nucleic Acids Research*, *PeerJ*, *Plant Journal*, *Plant Genome*, *Plant Methods*, *PNAS*, *Scientific Reports*, *Theoretical and Applied Genetics*

Ad-hoc grant reviewer for US National Science Foundation, Genome Canada, Genoscope, Israeli Ministry of Agriculture, Swiss National Science Foundation, UK Natural Environment Research Council (NERC)

## Funding

German Research Foundation (DFG), Regulatory architecture and variation of gene expression in wild and domesticated barley (PI), since 2016

German Federal Ministry of Research and Education (BMBF), Genomics-based exploitation of wheat genetic resources for plant breeding (co-PI), since 2016

German Federal Ministry of Research and Education (BMBF), Structural genome variation, haplotype diversity and the barley pan-genome - Exploring structural genome diversity for barley breeding (co-PI), since 2016

Bayer Crop Science, Mapping and validating genes underlying yield components by an integrated population genomics and quantitative genetics approach in a wheat population reflecting different decades of breeding (PI), since 2017

German Research Foundation (DFG), Three-dimensional organization of chromatin across the plant cell cycle (PI), since 2018

## Invited talks

11. *Barley diversity now and 6000 years ago*. Botanikertagung, Kiel, Germany, Sep 2017.
10. *Barley diversity now and 6000 years ago: archaeogenetics and genebank genomics*. Institute of Experimental Botany, Olomouc, Czech Republic, Jun 2017.
9. *Allele mining wild barley exomes: how many genes does it take to make you six-rowed?* Whealbi Workshop Allele Mining / Genetic Analysis, Wageningen, Netherlands, Jun 2017.
8. *Twenty thousand genebank accessions under analysis: from cold room to GWAS*. 14th Systems Biology Workshop, AgriBio Victoria, Melbourne, Australia, May 2017.
7. *Barley diversity now and 6000 years ago*. 14th Systems Biology Workshop, AgriBio Victoria, Melbourne, Australia, May 2017.
6. *Barley diversity now and 6000 years ago*. 28th Colloquium of the Research Center of Biotechnology and Plant Breeding, University of Hohenheim, Stuttgart, Germany, Nov 2016.
5. *De novo genome assembly: what every biologist should know*. Eduard Strasburger Workshop, Munich, Germany, Sep 2016.
4. *Genetic diversity in the genome era: a fine-scale map of sequence variation in the barley genome*. 12th International Barley Genetics Symposium, Minneapolis, USA, Jun 2016.
3. *Conservation and rearrangement: gene order in peri-centromeric regions of Triticeae genomes*. Wheat wild relatives conference, Tel Aviv, Israel, Apr 2016.
2. *Plant variation data - what's available, which new projects are expected*. 4th trans-PLANT Workshop, Hinxton, UK, Jul 2015.
1. *Sequence-based genetic mapping in barley: applications to genome assembly and gene isolation*. Department of Plant Sciences, Weizmann Institute of Science, Israel, Jun 2014.

## Peer reviewed publications

\*equal contributor, §corresponding author, group members are underlined

Google Scholar: <https://tinyurl.com/scholar-mascher>

44. Rajaraman J, Douchkov D, Lueck L, Hensel G, Nowara D, Pogoda M, Rutten T, Meitzel T, Hoefle C, Hueckelhoven R, Klinkenberg J, Trujillo M, Bauer E, Schmutzer T, Himmelbach A, **Mascher M**, Lazzari B, Stein N, Kumlehn J,

- Schweizer P (2017). The partial duplication of an E3-ligase gene in Triticeae species mediates resistance to powdery mildew fungi. *BioRxiv* doi:10.1101/190728.
43. Wicker T, Schulman AH, Tanskanen J, Spannagl M, Twardziok S, **Mascher M**, Springer NM, Li Q, Waugh R, Li C, Zhang G, Stein N, Mayer KFX, Gundlach H (2017). The repetitive landscape of the 5,100 Mbp barley genome. *MOBILE DNA* 8:22.
  42. Meier AK, Worch S, Böer E, Hartmann A, **Mascher M**, Marzec M, Scholz U, Riechen J, Baronian K, Schauer F, Bode R, Kunze G (2017). Agdc1p — a Gallic Acid Decarboxylase Involved in the Degradation of Tannic Acid in the Yeast *Blastobotrys (Arxula) adenivorans*. *FRONTIERS IN MICROBIOLOGY* 8:1777.
  41. Dreissig S, Fuchs J, Himmelbach A, **Mascher M**<sup>§</sup>, Houben A<sup>§</sup> (2017). Sequencing of single pollen nuclei reveals meiotic recombination events at megabase resolution and circumvents segregation distortion caused by postmeiotic processes. *FRONTIERS IN PLANT SCIENCE* 8:1620.
  40. Wendler N, **Mascher M**, Himmelbach A, Bini F, Kumlehn J, Stein N (2017). A high-density, sequence enriched genetic map of *Hordeum bulbosum* and its collinearity to *H. vulgare*. *PLANT GENOME* 10.
  39. Avni R, Nave M, Barad O, Baruch K, Twardziok SO, Gundlach H, Hale I, **Mascher M**, Spannagl M, Wiebe K, Jordan KW, Golan G, Deek J, Ben-Zvi B, Ben-Zvi G, Himmelbach A, MacLachlan RP, Sharpe AG, Fritz A, Ben-David R, Budak H, T, Korol A, Faris JD, Hernandez A, Mikel MA, Levy AA, Steffenson B, Maccaferri M, Tuberosa R, Cattivelli L, Faccioli P, Ceriotti A, Kashkush K, Pourkheirandish M, Komatsuda T, Eilam T, Sela H, Sharon A, Ohad N, Mayer KFX, Chamovitz DA, Stein N, Ronen G, Peleg Z, Pozniak CJ, Akhunov ED, Distelfeld A (2017). Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. *SCIENCE* 357:93–97.
  38. Beier S, Thiel T, Münch T, Scholz U, **Mascher M** (2017). MISA-web: a web server for microsatellite prediction. *BIOINFORMATICS* 33:2583–2585.
  37. Braatz J, Harloff HJ, **Mascher M**, Stein N, Himmelbach A, Jung C (2017). CRISPR-Cas9 targeted mutagenesis leads to simultaneous modification of different homoeologous gene copies in polyploid oilseed rape (*Brassica napus*) *PLANT PHYSIOLOGY* 174:935–942.
  36. **Mascher M**<sup>\*</sup>, Gundlach H<sup>\*</sup>, Himmelbach A, Beier S, Twardziok SO, Wicker T, Radchuk V, Dockter C, Hedley PE, Russell J, Bayer M, Ramsay L, Liu H, Haberer G, Zhang X-Q, Zhang Q, Barrero RA, Li L, Taudien S, Groth M, Felder M, Hastie A, Šimková H, Staňková H, Vrána J, Chan S, Muñoz-Amatriaín M, Ounit R, Wanamaker S, Bolser D, Colmsee C, Schmutzer T, Aliyeva-Schnorr L, Grasso S, Tanskanen J, Chailyan A, Sampath D, Heavens D, Clissold L, Cao S, Chapman B,

- Dai F, Han Y, Li H, Li X, Lin C, McCooke JK, Tan C, Wang P, Wang S, Yin S, Zhou G, Poland JA, Bellgard MI, Borisjuk L, Houben A, Doležel J, Ayling S, Lonardi S, Kersey P, Langridge P, Muehlbauer GJ, Clark MD, Caccamo M, Schulman AH, Mayer KFX, Platzer M, Close TJ, Scholz U, Hansson M, Zhang G, Braumann I, Spannagl M, Li C, Waugh R, Stein N (2017). A chromosome conformation capture ordered sequence of the barley genome. *NATURE* 544:427–433.
35. Beier S, Himmelbach A, Colmsee C, Zhang X-Q, Barrero RA, Zhang Q, Li L, Bayer M, Bolser D, Taudien S, Groth M, Felder M, Hastie A, Šimková H, Staňková H, Vrána J, Chan S, Muñoz-Amatriáin M, Ounit R, Wanamaker S, Schmutzer T, Aliyeva-Schnorr L, Grasso S, Tanskanen J, Sampath D, Heavens D, Cao S, Chapman B, Dai F, Han Y, Li H, Li X, Lin C, McCooke JK, Tan C, Wang S, Yin S, Zhou G, Poland JA, Bellgard MI, Houben A, Doležel J, Ayling S, Lonardi S, Langridge P, Muehlbauer GJ, Kersey P, Clark MD, Caccamo M, Schulman AH, Platzer M, Close TJ, Hansson M, Zhang G, Braumann I, Li C, Waugh R, Scholz U, Stein N, **Mascher M**<sup>§</sup> (2017). Construction of a map-based reference genome sequence for barley, *Hordeum vulgare* L. *SCIENTIFIC DATA* 4:170044.
34. Youssef HM\*, **Mascher M**\*, Ayoub MA, Stein N, Kilian B, Schnurbusch T (2017). Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (*Hordeum vulgare* L.). *GENETIC RESOURCES AND CROP EVOLUTION* 64:843.
33. Bauer E, Schmutzer T, Barilar I, **Mascher M**, Gundlach H, Martis MM, Twardziok SO, Hackauf B, Gordillo A, Wilde P, Schmidt M, Korzun V, Mayer KFX, Schmid K, Schön CC, Scholz U (2017). Towards a whole-genome sequence for rye (*Secale cereale* L.). *PLANT JOURNAL* 89:853–869.
32. Rauter M, Kasprzak J, Becker K, Riechen J, Worch S, Hartmann A, **Mascher M**, Scholz U, Baronian K, Bode R, Schauer F, Vorbrodt M, Kunze G (2016). Aadh2p – an *Arxula adenivorans* alcohol dehydrogenase involved in the first step of the 1-butanol degradation pathway. *MICROBIAL CELL FACTORIES* 15:175.
31. **Mascher M**\*, Schuenemann VJ\*, Davidovich U, Marom N, Himmelbach A, Hübner S, Korol A, David M, Reiter E, Riehl S, Schreiber M, Vohr SH, Green RE, Dawson IK, Russell J, Kilian B, Muehlbauer GJ, Waugh R, Fahima T, Krause J, Weiss E, Stein N (2016). Genomic analysis of 6000-year-old cultivated grain illuminates the domestication history of barley. *NATURE GENETICS* 48:1089–1093.
30. Russell J\*, **Mascher M**\*, Dawson IK, Kyriakidis S, Calixto C, Freund F, Bayer M, Milne I, Marshall-Griffiths T, Heinen S, Hofstad A, Sharma R, Himmelbach A, Knauff M, van Zonneveld M, Brown JWS, Schmid K, Kilian B, Muehlbauer GJ, Stein N, Waugh R (2016). Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. *NATURE GENETICS* 48:1024–1030.

29. Jost M, Taketa S, **Mascher M**, Himmelbach A, Yuo T, Shahinnia F, Rutten T, Druka A, Schmutzer T, Steuernagel B, Beier S, Taudien S, Scholz U, Morgante M, Waugh R, Stein N (2016). A homolog of Blade-On-Petiole 1 and 2 (BOP1/2) controls internode length and homeotic changes of the barley inflorescence. *PLANT PHYSIOLOGY* 171:1113–1127.
28. Nagel M, Kodde J, Pistrick S, **Mascher M**, Börner A, Groot SPC (2016). Barley seed ageing: genetics behind the dry elevated pressure of oxygen ageing and moist controlled deterioration. *FRONTIERS IN PLANT SCIENCES* 7:388.
27. Beier S, Himmelbach A, Schmutzer T, Felder M, Taudien S, Mayer KFX, Platzer M, Stein N, Scholz U, **Mascher M**<sup>S</sup> (2016). Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. *PLANT BIOTECHNOLOGY JOURNAL* 14:1511–1522.
26. Spannagl M, Alaux M, Lange M, Bolser DM, Bader KC, Letellier T, Kimmel E, Flores R, Pommier C, Kerhornou A, Walts B, Nussbaumer T, Grabmuller C, Chen J, Colmsee C, Beier S, **Mascher M**, Schmutzer T, Arend D, Thanki A, Ramirez-Gonzalez R, Ayling M, Ayling S, Caccamo M, Mayer KFX, Scholz U, Steinbach D, Quesneville H, Kersey PJ (2016). transPLANT resources for Triticeae genomic data. *PLANT GENOME* 9.
25. Livaja M, Unterseer S, Erath W, Lehermeier C, Wieseke R, Plieske J, Polley A, Luerßen H, Wieckhorst S, **Mascher M**, Hahn V, Ouzonova M, Schön CC, Ganai MW (2016). Diversity analysis and genomic prediction of Sclerotinia resistance in sunflower using a new 25K SNP genotyping array. *THEORETICAL AND APPLIED GENETICS* 129:317–329.
24. Zakhrabekova S, Dockter C, Ahmann K, Braumann I, Gough SP, Wendt T, Lundqvist U, **Mascher M**, Stein N, Hansson M (2015). Genetic linkage facilitates cloning of *Ert-m* regulating plant architecture in barley and identified a strong candidate of *Ant1* involved in anthocyanin biosynthesis. *PLANT MOLECULAR BIOLOGY* 88:609–626.
23. Pourkheirandish M, Hensel G, Kilian B, Senthil N, Chen G, Sameri M, Azhaguvel P, Sakuma S, Dhanagond S, Sharma R, **Mascher M**, Himmelbach A, Gottwald S, Nair SK, Tagiri A, Yukuhiro F, Nagamura Y, Kanamori H, Matsumoto T, Willcox G, Middleton CP, Wicker T, Walther A, Waugh R, Fincher GB, Stein N, Kumlehn J, Sato K, Komatsuda T (2015). Evolution of the grain dispersal system in barley. *CELL* 162:527–539.
22. Wendler N, **Mascher M**, Himmelbach A, Johnston P, Pickering R, Stein N (2015). *Bulbosum* to go: a toolbox to utilize *Hordeum vulgare* / *bulbosum* introgressions for breeding and beyond. *MOLECULAR PLANT* 8:1507–1519.
21. Lermontova I, Sandmann M, **Mascher M**, Schmit AC, Chabouté ME (2015). Centromeric chromatin and its dynamics in plants. *PLANT JOURNAL* 83:4–17.

20. Colmsee C, Beier S, Himmelbach A, Schmutzer T, Stein N, Scholz U, **Mascher M<sup>S</sup>** (2015). BARLEX – the barley draft genome explorer. *MOLECULAR PLANT* 8:964–966.
19. Brown RH, Singh J, Singh S, Dahleen LS, Lemaux PG, Stein N, **Mascher M**, Breigitz P (2015). Behavior of a modified *Dissociation* element in barley: a novel tool for genetic studies and for breeding transgenic barley. *MOLECULAR BREEDING* 35:85.
18. Chapman JA\*, **Mascher M\***, Buluc AN, Barry K, Georganas E, Session A, Strnadova V, Jenkins J, Sehgal S, Olikar L, Schmutz J, Yelick KA, Scholz U, Waugh R, Poland JA, Muehlbauer GJ, Stein N, Rokhsar DS (2015). A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. *GENOME BIOLOGY* 16:R26.
17. Kuhlmann M, Finke A, **Mascher M**, Mette MF (2014). DNA methylation maintenance consolidates RNA-directed DNA methylation and transcriptional gene silencing over generations in *Arabidopsis thaliana*. *PLANT JOURNAL* 80:269–281.
16. The International Wheat Genome Sequencing Consortium (2014). A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *SCIENCE* 345:1251788 (as part of IWGSC).
15. Wendler N, **Mascher M**, Nöh C, Himmelbach A, Scholz U, Ruge-Wehling B, Stein N (2014). Unlocking the secondary gene-pool of barley with next-generation sequencing. *PLANT BIOTECHNOLOGY JOURNAL* 12:1122–1131.
14. **Mascher M<sup>S</sup>**, Stein N (2014). Genetic anchoring of whole-genome shotgun assemblies. *FRONTIERS IN GENETICS* 5:208.
13. **Mascher M\***, Jost M\*, Kuon JE, Himmelbach A, Aßfalg A, Scholz U, Graner A, Stein N (2014). Mapping-by-sequencing accelerates forward genetics in barley. *GENOME BIOLOGY* 15:R78.
12. **Mascher M\***, Gerlach N\*, Gahrtz M, Bucher M, Scholz U, Dresselhaus T (2014). Sequence and ionomic analysis of divergent strains of maize inbred line B73 with an altered growth phenotype. *PLOS ONE* 9:e96782.
11. Kunze G, Gaillardin C, Czernicka M, Durrens P, Martin T, Böer E, Gabaldón T, Cruz JA, Talla E, Marck C, Goffeau A, Barbe V, Baret P, Baronian K, Beier S, Bleykasten C, Bode R, Casaregola S, Despons L, Fairhead C, Giersberg M, Gierski PP, Hähnel U, Hartmann A, Jankowska D, Jubin C, Jung P, Lafontaine I, Leh-Louis V, Lemaire M, Marcet-Houben M, **Mascher M**, Morel G, Richard GF, Riechen J, Sacerdot C, Sarkar A, Savel G, Schacherer J, Sherman DJ, Stein N, Straub ML, Thierry A, Trautwein-Schult A, Vacherie B, Westhof E, Worch S, Dujon B, Souciet JL, Wincker P, Scholz U, Neuvéglise C (2014). The complete

- genome of *Blastobotrys (Arxula) adenivorans* LS3 - a yeast of biotechnological interest. *BIOTECHNOLOGY FOR BIOFUELS* 7:66.
10. Ariyadasa R\*, **Mascher M\***, Nussbaumer T\*, Schulte D, Frenkel Z, Poursarebani N, Zhou R, Steuernagel B, Gundlach H, Taudien S, Felder M, Platzer M, Himmelbach A, Schmutzer T, Hedley PE, Muehlbauer GJ, Scholz U, Korol A, Mayer KFX, Waugh R, Langridge P, Graner A, Stein N (2014). A sequence-ready physical map of barley anchored genetically by two million single-nucleotide polymorphisms. *PLANT PHYSIOLOGY* 164:412–423.
  9. **Mascher M\***, Muehlbauer GJ\*, Rokhsar DS, Chapman J, Schmutz J, Barry K, Muñoz-Amatriaín M, Close TJ, Wise RP, Schulman AH, Himmelbach A, Mayer KFX, Scholz U, Poland JA, Stein N, Waugh R (2013). Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). *PLANT JOURNAL* 76:718–727.
  8. **Mascher M**, Richmond TA, Gerhardt DJ, Himmelbach A, Clissold L, Sampath D, Ayling S, Steuernagel B, Pfeifer M, D’Ascenzo M, Akhunov ED, Hedley PE, Gonzales AM, Morrell PL, Kilian B, Blattner FR, Scholz U, Mayer KFX, Flavell AJ, Muehlbauer GJ, Waugh R, Jeddelloh JA, Stein N (2013). Barley whole exome capture: a tool for genomic research in the genus *Hordeum* and beyond. *PLANT JOURNAL* 76:494–505.
  7. **Mascher M**, Wu S, Amand PS, Stein N, Poland J (2013). Application of genotyping-by-sequencing on semiconductor sequencing platforms: a comparison of genetic and reference-based marker ordering in barley. *PLOS ONE* 8:e76925.
  6. Muñoz-Amatriaín M, Eichten SR, Wicker T, Richmond TA, **Mascher M**, Steuernagel B, Scholz U, Ariyadasa R, Spannagl M, Nussbaumer T, Mayer KFX, Taudien S, Platzer M, Jeddelloh JA, Springer NM, Muehlbauer GJ, Stein N (2013). Distribution functional impact and origin mechanisms of copy number variation in the barley genome. *GENOME BIOLOGY* 14:R58.
  5. **Mascher M<sup>S</sup>**, Schubert I, Scholz U, Friedel S (2013). Patterns of nucleotide asymmetries in plant and animal genomes. *BIOSYSTEMS* 111:181–189.
  4. Colmsee C, **Mascher M**, Czauderna T, Hartmann A, Schlüter U, Zellerhoff N, Schmitz J, Bräutigam A, Pick TR, Alter P, Gahrtz M, Witt S, Fernie AR, Börnke F, Fahnenstich H, Bucher M, Dresselhaus T, Weber AP, Schreiber F, Scholz U, Sonnewald U (2012). OPTIMAS-DW: a comprehensive transcriptomics, metabolomics, ionomics, proteomics and phenomics data resource for maize. *BMC PLANT BIOLOGY* 12:245.
  3. The International Barley Genome Sequencing Consortium (2012). A physical, genetic and functional sequence assembly of the barley genome. *NATURE* 491:711–716 (as part of IBSC).



2. Schlüter U, **Mascher M**, Colmsee C, Scholz U, Bräutigam A, Fahnenstich H, Sonnnewald U (2012). Maize source leaf adaptation to nitrogen deficiency affects not only nitrogen and carbon metabolism but also control of phosphate homeostasis. *PLANT PHYSIOLOGY* 160:1384–1406.
1. Haseneyer G, Schmutzer T, Seidel M, Zhou R, **Mascher M**, Schön CC, Taudien S, Scholz U, Stein N, Mayer KFX, Bauer E (2011). From RNA-seq to large-scale genotyping – genomics resources for rye (*Secale cereale* L.). *BMC PLANT BIOLOGY* 11:131.