# MEMORANDUM

**TO:** APCOM members

**FROM:** Joanne Chory, Wolfgang Busch, Joe Ecker, Julie Law, Todd Michael, Lena Mueller and Joe Noel

**RE:** Request to Continue Adjunct Professor Appointment for Detlef Weigel

**DATE:** June 19, 2024

---

Dear Members of APCOM,

This is a request for the re-appointment of our colleague and friend, Detlef Weigel, as Adjunct Professor. As you may be aware, Detlef was a faculty member in PBIO for 10 years (1993-2002). In 2002, he was recruited by the Max Planck Society to Tübingen and was appointed as Director at the Max Planck Institute of Developmental Biology. When he left Salk in 2003, Detlef was approved as an Adjunct Professor for a 3-year period, and he has remained in that status ever since having been reappointed seven times. As such, he is very familiar with the activities of all the labs in PBIO, as well as HPI, and Joanne-Director of PBIO, personally consults with Detlef on a regular basis.

Detlef Weigel's unique blend of biology and technology has been instrumental to the development of the field of modern developmental biology of plants. During his >30-year career as an independent investigator, Detlef has made contributions in three major areas related to flowering. The first major finding from his lab was that an *Arabidopsis thaliana* gene could dramatically accelerate flowering of trees; this established a proof of concept for Arabidopsis genetics as a platform for biotechnological discoveries. His group later discovered the first plant microRNA mutant and identified the factor that we now know to be the long sought-after mobile flower-inducing signal. Together with Joanne, Detlef was one of the first to exploit natural genetic variation for understanding how the environment affects plant development. In recent years, his work in evolutionary genetics and genomics has focused on plant immunity and epigenetics. As you will note on his CV, Detlef's laboratory has published a large number of high impact papers, making him one of the most highly cited plant geneticists in the world.

In addition to hypothesis-driven research, his group has a long history of providing new technologies and resources to the community. This has culminated with a collaboration with Joe Ecker, Magnus Nordborg and Todd Michael in generating the sequences of the genomes of over 1000 natural *A. thaliana* strains (The 1001 Genomes Project). This study has thus provided a blueprint for the study of genetic diversity in many different plant species, Wolfgang Busch in particular benefitted from having this sequenced data for his GWAS studies.

Weigel has an extensive record of service to the scientific community, having served on many editorial and scientific advisory boards (including the MAB of HHMI). He is a forceful advocate of open access publishing and founding deputy editor of e-LIFE. In addition, his service to the European scientific community, makes him a very influential liaison for Salk scientists in Europe.

Finally, we have been approved for a new senior faculty position in Plant Biology Laboratory. During the coming months, we are planning to use Detlef's familiarity with his field and knowledge of European scientists to identify the best available candidates.

PBIO certainly wants to maintain strong ties with him and have him frequently visit us. This will likely happen as Detlef's wife's family lives in San Diego and they visit often. Having him visit our labs to speak with our students is a big plus for our program. As such, we respectfully request your consideration for this reappointment.

Sincerely,

Joanne Chory

Joanne Chory, PhD

Julie Law

Julie Law, PhD

Joseph R. Ecker, PhD

Wolfgang Busch, PhD

Joseph P. Noel, PhD

Todd Michael, PhD

Lena Mueller, PhD

# CURRICULUM VITAE

## Detlef Weigel

Director, Department of Molecular Biology
Max Planck Institute for Biology Tübingen
Max-Planck-Ring 5
D-72076 Tübingen
GERMANY

Ph +49.7071.601.1411
Em weigel@tue.mpg.de
URL http://weigelworld.org

| | |
|---|---|
| DOB | December 15, 1961 |
| Nationality | German and USA (naturalized on May 24, 2001) |

## Education

| | |
|---|---|
| 1989-1993 | Research Fellow, Division of Biology, California Institute of Technology, Pasadena, CA l Advisor: Dr. E. M. Meyerowitz |
| 1988-1989 | Research Associate, Institute of Genetics, University of Munich, Germany l Advisor: Dr. H. Jäckle |
| 1988 | Ph.D. in Genetics, Max Planck Institute of Developmental Biology and Eberhard Karls University, Tübingen, Germany l Advisor: Dr. H. Jäckle |
| 1986 | Diploma (M.S.) in Biology, University of Cologne, Germany l Advisor: Dr. J. A. Campos-Ortega |

## Professional Experience

| | |
|---|---|
| 2020- | Member, Institute for Bioinformatics and Medical Informatics (IBMI), University of Tübingen, Tübingen, Germany |
| 2019-2021 | Executive Director, Max Planck Institute for Developmental Biology, Tübingen, Germany |
| 2007-2009 | Executive Director, Max Planck Institute for Developmental Biology, Tübingen, Germany |
| 2004- | Adjunct Professor, Department of Biology, Eberhard Karls University, Tübingen, Germany |
| 2003- | Adjunct Professor, Plant Biology Laboratory, The Salk Institute for Biological Studies, La Jolla, CA |
| 2001- | Director, Department of Molecular Biology, Max Planck Institute for Biology Tübingen (until 2021: Max Planck Institute for Developmental Biology), Tübingen, Germany |
| 2001-2003 | Associate Adjunct Professor, Department of Biology, University of California, San Diego, La Jolla, CA |
| 1999-2002 | Associate Professor, Plant Biology Laboratory, The Salk Institute for Biological Studies, La Jolla, CA |
| 1997-2001 | Assistant Adjunct Professor, Department of Biology, University of California, San Diego, La Jolla, CA |
| 1993-1999 | Assistant Professor, Plant Biology Laboratory, The Salk Institute for Biological Studies, La Jolla, CA |

## Honors

| | |
|---|---|
| 2023 | Doctor honoris causa, University of Helsinki |

| | |
|---|---|
| 2021 | Stephen Hales Prize of the American Society of Plant Biologists |
| 2020 | Novozymes Prize of the Novo Nordisk Foundation |
| 2019 | Fellow, American Academy of Arts and Sciences |
| 2019 | Barbara McClintock Prize for Plant Genetics and Genome Studies |
| 2016 | Doctor honoris causa, Swedish Agricultural University |
| 2016 | GSA Medal of the Genetics Society of America |
| 2015 | Mendel Medal of the German National Academy of Sciences Leopoldina |
| 2011 | Fellow, American Association for the Advancement of Science |
| 2011 | State Research Prize of Baden-Württemberg |
| 2010 | Corresponding Member, Heidelberg Academy of Sciences and Humanities |
| 2010 | Foreign Member, Royal Society of London |
| 2010 | Otto Bayer Award of the Bayer Foundation |
| 2009 | Member, US National Academy of Sciences |
| 2008 | Member, German National Academy of Sciences Leopoldina |
| 2007 | Gottfried Wilhelm Leibniz Award of the German Research Council (DFG) |
| 2003 | Member, European Molecular Biology Organisation (EMBO) |
| 2001 | Charles Albert Shull Award of the American Society of Plant Biologists |
| 1994 | National Science Foundation Young Investigator Award |
| 1991 | Senior Fellowship, American Cancer Society, California Division |
| 1991 | HFSPO Long Term Fellowship (declined) |
| 1989 | EMBO Long Term Fellowship |
| 1989 | Dieter Rampacher Award (youngest PhD graduate of the Max Planck Society 1988) |
| 1988 | Ph.D., "summa cum laude" |
| 1987 | Boehringer Ingelheim Fonds Graduate Fellowship |
| 1986 | Diploma (M.S.), "summa cum laude" |
| 1981 | Studienstiftung des Deutschen Volkes (German Academic Scholarship Foundation) Undergraduate Fellowship |

## Professional Activities

### *Advisory Boards*

| | |
|---|---|
| 2023- | Scientific Commission of the State of Lower Saxony |
| 2021- | Award Committee for the Novozymes Prize, Novo Nordisk Foundation (2023-, Chair) |
| 2021- | ARC Centre of Excellence for Plant Success in Nature and Agriculture |
| 2020- | Medical Advisory Board, Howard Hughes Medical Institute |
| 2017- | KWS Saat SE |
| 2017- | Helsinki Institute of Life Science (HiLIFE) |
| 2017- | Institute of Molecular Biology, Academia Sinica |
| 2017- | Grow More Foundation |
| 2016-2018 | Gemeinschaft zur Förderung von Pflanzeninnovation e. V. (GFPi) |
| 2014-2018 | CeMeT (Co-founder) |
| 2014-2017 | ARC Centre of Excellence in Plant Energy Biology, Perth |
| 2012- | Computomics, (Co-founder) |
| 2012-2025 | Max Planck Digital Library |
| 2010- | Sainsbury Laboratory Cambridge University |
| 2010-2012 | Bayer Crop Science |
| 2009-2013 | GrassRoots Biotechnology |

| | |
|---|---|
| 2009-2012 | The Arabidopsis Information Resource (TAIR) |
| 2007- | Flanders Institute for Biotechnology (VIB) (2012-2019, Vice-/Co-Chair; 2020-, Chair) |
| 2007-2012 | Temasek Life Sciences Laboratory, (2010-2012, Deputy Chair) |
| 2005-2011 | The Sainsbury Laboratory |
| 2002-2007 | Program in Developmental Biology of Plants, Umeå Plant Science Center |
| 1999-2001 | Arabidopsis Biological Resource Center |

### *Community and Institutional Service*

| | |
|---|---|
| 2024- | Presidential Committee on Scientific Freedom and Export Control & Foreign Trade, Max Planck Society |
| 2024-2026 | Sectional Committee 9, Royal Society |
| 2022- | Athena Ambassador, Max Planck Society |
| 2021- | Member, Cyber Security Committee, Max Planck Society |
| 2021 | Medals and Awards Review Group, Royal Society |
| 2021 | Member-at-Large, Class II Membership Committee, National Academy of Sciences |
| 2021-2022 | Committee for Data Science, Novo Nordisk Foundation |
| 2019-2025 | GSA Awards Committee, Genetics Society of America |
| 2018-2020 | Sectional Committee 7, Royal Society |
| 2017-2019 | EMBO/EMBL Symposia Committee, EMBO |
| 2016-2020 | Vice Chair, Open Access 2020 Steering Committee, Max Planck Society |
| 2014-2020 | Scientific Commission for the Review of Management Functions of Scientific Members, Max Planck Society |
| 2013-2015 | Chair, Council, European Molecular Biology Organisation (EMBO) |
| 2012- | Board, Quantitative Biology Center (QBiC), University of Tübingen |
| 2012- | Committee for Research Strategy and Coordination, University of Tübingen |
| 2011 | EMBO Ambassador to China |
| 2010-2015 | Council, European Molecular Biology Organisation (EMBO) |
| 2005-2008 | Courses, Workshops and Conferences Committee, EMBO |
| 2003-2005 | Committee on Future Research Directions, Biomedical Section of the Max Planck Society |
| 2002-2010 | Steering Committee, German Ministry of Education and Research (BMBF) Project "Genome Analysis in the Biological System Plant (GABI)" |
| 2002- 2010 | Steering Committee, The Arabidopsis Functional Genomics Network (AFGN) of the DFG, Germany |
| 2001-2008 | Board of Directors, International Society for Plant Molecular Biology |
| 2000-2002 | Academic Council, The Salk Institute for Biological Studies |
| 1999-2000 | Co-chair, North American Arabidopsis Steering Committee |
| 1997-2000 | North American Arabidopsis Steering Committee |

### *Meeting Organization*

| | |
|---|---|
| 2025 | Co-organizer, Novozymes Symposium: Elevating Africa's Participation in Plant Genomics, by Africans, for Africans |
| 2024 | Co-organizer, EMBO \| EMBL Symposium "Diversity of Plants: From Genomes to Metabolism", Heidelberg, Germany |
| 2023 | Co-organizer, EMBO \| EMBL Symposium "The Organism and Its Environment", Heidelberg, Germany |
| 2022 | Co-organizer, Max Planck Frontier Symposium "Rapid Polygenic Adaptation", Berlin, Germany |

| | |
|---|---|
| 2017 | Co-organizer, German Conference on Bioinformatics, Tübingen, Germany |
| 2015 | Co-organizer, EMBO Workshop on Mechanisms of Plant Speciation, Åkersberga, Sweden |
| 2013-2016 | Co-organizer, EMBO \| EMBL Symposium, New Model Systems for Linking Evolution and Ecology, Heidelberg, Germany |
| 2013 | Co-chair, International Program Committee, XXI International Congress of Genetics, Singapore |
| 2012 | Co-organizer, VIB-Nature Conference on Plant Biology, Gent, Belgium |
| 2010 | Co-organizer, Wenner-Gren Foundation Symposium on Adaptive Responses During Plant Development, Kristineberg, Sweden |
| 2009-2013 | Co-organizer, CSHL Meeting on Plant Genomes, Cold Spring Harbor, NY |
| 2007 | Co-organizer, National Evolutionary Synthesis Center (NESCent) Meeting on Developing New Model Systems for Evolutionary Genomics Using Poeciliid Fishes, Durham, NC |
| 2006 | Co-organizer, 3rd Trinational Arabidopsis Meeting, Tübingen, Germany |
| 2005 | Co-organizer, Juan March/EMBO Meeting on Plant Stem Cells, Madrid, Spain |
| 2004 | Co-organizer, Banbury Conference on RNAi-Related Processes in Plants: Chromatin, Development and Defense, Cold Spring Harbor, NY |
| 2004 | Co-organizer, 15th International Arabidopsis Conference, Berlin, Germany |
| 2004 | Co-organizer, Keystone Conference on Natural Variation and Quantitative Genetics in Model Organisms, Breckenridge, CO |
| 2003 | Co-organizer, EMBO Practical Course in Developmental Genetics, Tübingen, Germany |
| 2000 | Co-organizer, 11th International Arabidopsis Conference, Madison, WI |

### *Editorial Boards*

| | |
|---|---|
| 2023-2024 | eLife (Co-Editor-in-Chief, with Tim Behrens) |
| 2011-2023 | eLife (Deputy Editor) |
| 2011-2015 | Annual Review of Cell and Developmental Biology |
| 2010-2023 | Genome Biology |
| 2009-2011 | Cell |
| 2007-2021 | Faculty of 1000/Faculty Opinions, Plant-Environment Interaction Section |
| 2007-2011 | Science (Board of Reviewing Editors) |
| 2005-2012 | EMBO Journal & EMBO Reports |
| 2005-2009 | Current Opinion in Plant Biology (Co-Editor-in-Chief, with Jeff Dangl) |
| 2003-2008 | Public Library of Science Biology |
| 2003-2006 | Genetics (Associate Editor) |
| 2002-2011 | Nature Reviews Genetics (Highlights Advisor) |
| 2001-2011 | Developmental Cell |
| 2000-2009 | Genes and Development |
| 2000-2006 | Genesis |
| 2000-2007 | Faculty of 1000, Plant Growth and Development Section |
| 1997-2005 | Current Opinion in Plant Biology |
| 1996-2005 | Plant Cell (Coeditor) |
| 1996-1997 | Genes and Function |
| 1995-2012 | Mechanisms of Development |

### *Grant Advisory Panels*

| | |
|---|---|
| 2022 | Swiss National Science Foundation, Advanced Grants, Life Sciences III (International Chair) |
| 2018-2020 | Howard Hughes Medical Institute, Scientific Review Board |
| 2017 | Howard Hughes Medical Institute, Investigator review panel (ad hoc member) |
| 2011-2012 | Bavarian Research Network for Molecular Biosystems (BioSysNet) |
| 2009-2011 | ERC, Life Sciences 8: Evolutionary, Population and Environmental Biology |
| 2004-2005 | NIH Genetic Variation and Evolution |
| 2001-2004 | GEN-AU, Austrian Genome Project |
| 2001-2004 | NIH Genetics |
| 2001 | DFG (German Research Council) Arabidopsis Proteome Project |
| 1998-2000 | NSF Eukaryotic Genetics |
| 1998 | NIH Molecular Biology (ad hoc member) |
| 1996 | USDA Plant Growth & Development |

## Keynotes and Named Lectures

| | |
|---|---|
| 2023 | XXIII International Congress of Genetics, Melbourne, Australia (Keynote) |
| 2022 | German Conference on Bioinformatics, Halle, Germany (Keynote) |
| | Stephen Hales Award Lecture, Plant Biology 2022, Portland, OR |
| | Darwin Day Lecture, Centre for Ecological and Evolutionary Synthesis, University of Oslo, Norway |
| 2021 | Wiley Weinheim Online Symposium: 'Plant Biology in the 21st Century: Scientific milestones and real-world challenges' (Keynote) |
| | 31st International Conference on Arabidopsis Research, Seattle, WA (Keynote) |
| | Annual Meeting Experimental Plant Sciences, Wageningen, Netherlands (Keynote) |
| 2020 | Prof. J. C. Bose Memorial Lecture, National Institute of Plant Genome Research, New Delhi, India |
| | EMBO l EMBL Symposium: The Organism and Its Environment, Heidelberg, Germany (Keynote) |
| | Israel Plant Ecology Meeting, Rehovot, Israel (Keynote) |
| 2019 | CSHL Meeting on Plant Genomes, Cold Spring Harbor, NY (Keynote) |
| | Delbrück Lecture, German Society for Genetics Annual Meeting, Berlin, Germany |
| | Genetics 2019: Old Questions and New Frontiers, Heidelberg, Germany (Keynote) |
| | Noble Gespräche Lecture, Beutenberg Campus, Jena, Germany |
| 2018 | International Plant Molecular Biology 2018, Montpellier, France (Keynote) |
| 2017 | Saclay Plant Sciences Meeting, Versailles, France (Keynote) |
| | VIB Conference "At the Forefront of Plant Biology", Gent, Belgium (Keynote) |
| 2016 | Jenkinson Memorial Lecture, Oxford University, UK |
| | Symposium in Honor of Joanne Chory's 60th Birthday (Keynote) |
| | Lorne Genome Conference, Lorne, Australia (EMBO Lecture) |
| 2015 | Australasian Genome Technology Association Conference 2015, Hunter Valley, Australia (Keynote) |
| | Darlington Lecture, John Innes Centre, Norwich, UK |
| 2014 | Trinational Arabidopsis Meeting, Heidelberg, Germany (Keynote) |
| 2013 | Fritz Lipmann Lecture, German Society for Biochemistry and Molecular Biology, Frankfurt, Germany |

| | |
|---|---|
| | 24th International Conference on Arabidopsis Research, Sydney, Australia (Keynote) |
| | Hilgendorf Lecture, University of Tübingen, Germany |
| 2012 | EMBO Conference on Plant Development and Environmental Interactions, Matera, Italy (Keynote) |
| | "Major Issues in Modern Biology" Lecture, UC Davis, CA |
| 2011 | Bernhard Rensch Lecture, University of Münster, Germany |
| | EMBL Distinguished Visitor Lecture, Heidelberg, Germany |
| | Helmholtz Lecture, Humboldt University, Berlin, Germany |
| 2010 | Annual Meeting, Genome Analysis in the Biological System Plant (GABI) Program, Potsdam, Germany (Keynote) |
| 2009 | Distinguished Lecturer, Boyce Thompson Institute, Ithaca, NY |
| 2007 | Annual Meeting of the Dutch Molecular Genetics Society, Luchteren, Netherlands (Keynote) |
| 2006 | Public Lecture, Annual Meeting of the Max Planck Society, Frankfurt, Germany |
| | 15th Congress of the Federation of European Societies of Plant Biology, Lyon, France (EMBO Lecture) |
| 2005 | Trinational Arabidopsis Meeting, Neuchatel, Switzerland (Keynote) |
| | 47th Maize Conference, Lake Geneva, Wisconsin (Keynote) |
| 2003 | First Douglas Falconer Lecture in Quantitative Genetics, Edinburgh University, UK |
| 2002 | EMBO Lecture Course, Genetics after the Genome, Brno, Czech Republic (Mendel Lecture) |

## Publications

ORCID 0000-0002-2114-7963 • ResearcherID C-1418-2008

### *Research articles*

1. Knust, E., Dietrich, U., Tepass, U., Bremer, K. A., **Weigel, D.**, Vässin, H., and Campos-Ortega, J. A. (1987) EGF homologous sequences encoded in the genome of *Drosophila melanogaster*, and their relation to neurogenic genes. EMBO J. *6*, 761-766.
2. **Weigel, D.**, Knust, E., and Campos-Ortega, J. A. (1987) Molecular organization of *master mind*, a neurogenic gene of *Drosophila melanogaster*. Mol. Gen. Genet. *207*, 374-384.
3. Rijsewijk, F., Schuermann, M., Wagenaar, E., Parren, P., **Weigel, D.**, and Nusse, R. (1987) The *Drosophila* homolog of the mouse mammary oncogene *int-1* is identical to the segment polarity gene *wingless*. Cell *50*, 649-657.
4. De la Concha, A., Dietrich, U., **Weigel, D.**, and Campos-Ortega, J. A. (1988) Functional interactions between neurogenic genes of *Drosophila melanogaster*. Genetics *118*, 499-508.
5. Jürgens, G., and **Weigel, D.** (1988) Terminal versus segmental development in the *Drosophila* embryo: the role of the homeotic gene *fork head*. Roux´s Arch. Dev. Biol. *197*, 345-354.
6. **Weigel, D.**, Jürgens, G., Küttner, F., Seifert, E., and Jäckle, H. (1989) The homeotic gene *fork head* encodes a nuclear protein and is expressed in the terminal regions of the *Drosophila* embryo. Cell *57*, 645-658.

7. **Weigel, D.**, Bellen, H. J., Jürgens, G., and Jäckle, H. (1989) Primordium specific requirement of the homeotic gene *fork head* in the developing gut of the *Drosophila* embryo. Roux´s Arch. Dev. Biol. *198*, 201-210.
8. **Weigel, D.**, Seifert, E., Reuter, D., and Jäckle, H. (1990) Regulatory elements controlling expression of the *Drosophila* homeotic gene *fork head*. EMBO J. *9*, 1199-1207.
9. **Weigel, D.**, Jürgens, G., Klingler, M., and Jäckle, H. (1990) Two gap genes mediate maternal terminal pattern information in *Drosophila*. Science *248*, 495-498.
10. Gaul, U., and **Weigel, D.** (1991) Regulation of *Krüppel* expression in the anlage of the Malpighian tubules in the *Drosophila* embryo. Mech. Dev. *33*, 57-68.
11. Panzer, S., **Weigel, D.**, and Beckendorf, S. K. (1992) Organogenesis in *Drosophila melanogaster*: Control of embryonic salivary gland determination by homeotic and dorsoventral patterning genes. Development *114*, 49-57.
12. Bowman, J. L., Sakai, H., Jack, T., **Weigel, D.**, Mayer, U., and Meyerowitz, E. M. (1992) *SUPERMAN*, a regulator of floral homeotic genes in *Arabidopsis*. Development *114*, 599-615.
13. **Weigel, D.**, Alvarez, J., Smyth, D. R., Yanofsky, M. F., and Meyerowitz, E. M. (1992) *LEAFY* controls floral meristem identity in *Arabidopsis*. Cell *69*, 843-859.
14. **Weigel, D.**, and Meyerowitz, E. M. (1993) Activation of floral homeotic genes in *Arabidopsis*. Science *261*, 1723-1726.
15. Bowman, J. L., Alvarez, J., **Weigel, D.**, Meyerowitz, E. M., and Smyth, D. R. (1993) Control of flower development in *Arabidopsis thaliana* by *APETALA1* and interacting genes. Development *119*, 721-743.
16. Brönner, G., Chu-LaGraff, Q., Doe, C. Q., Cohen, B., **Weigel, D.**, Taubert, H., and Jäckle, H. (1994) Sp1/egr-like zinc-finger protein required for endoderm specification and germ layer morphogenesis in *Drosophila*. Nature *369*, 664-668.
17. **Weigel, D.**, and Nilsson, O. (1995) A developmental switch sufficient for flower initiation in diverse plants. Nature *377*, 495-500.
18. Lee, I., Wolfe, D. S., Nilsson, O., and **Weigel, D.** (1997) A *LEAFY* co-regulator encoded by *UNUSUAL FLORAL ORGANS*. Curr. Biol. *7*, 95-104.
19. Blázquez, M. A., Soowal, L. N. S., Lee, I., and **Weigel, D.** (1997) *LEAFY* expression and flower initiation in *Arabidopsis*. Development *124*, 3835-3844.
20. Hempel, F. D., **Weigel, D.**, Ditta, G., Mandel, M. A., Zambryski, P., Feldman, L. J., and Yanofsky, M. F. (1997) Photoinduction of flowering-gene expression and floral determination in *Arabidopsis*. Development *124*, 3845-3853.
21. Blázquez, M. A., Green, R., Nilsson, O., Sussman, M. R., and **Weigel, D.** (1998) Gibberellins promote flowering of Arabidopsis by activating the *LEAFY* promoter. Plant Cell *10*, 791-800
22. Nilsson, O., Lee, I., Blázquez, M. A., and **Weigel, D.** (1998) Flowering-time genes modulate the response to *LEAFY* activity. Genetics *150*, 403-410.
23. Parcy, F., Nilsson, O., Lee, I., Busch, M. A., and **Weigel, D.** (1998) A genetic framework for floral patterning. Nature *395*, 561-566.
24. Nilsson, O., Wu, E., Wolfe, D. S., and **Weigel, D.** (1998) Ablation of flowers in transgenic *Arabidopsis*. Plant J. *15*, 799-804.

25. Aukerman, N. J., Lee, I., **Weigel, D.,** and Amasino, R. M. (1999) The Arabidopsis flowering-time gene *LUMINIDEPENDENS* is expressed primarily in regions of cell proliferation and encodes a nuclear protein that regulates *LEAFY* expression. Plant J. *18*, 195-203.
26. Busch, M. A., Bomblies, K., and **Weigel, D.** (1999) Activation of a floral homeotic gene in *Arabidopsis*. Science *285*, 585-587.
27. Blázquez, M. A., and **Weigel, D.** (1999) Regulation of flowering by phytochrome B and gibberellins in Arabidopsis. Plant Physiol. *120*, 1025-1032.
28. Sessions, A., **Weigel, D.**, and Yanofsky, M. F. (1999) The *Arabidopsis thaliana MERISTEM LAYER 1* promoter specifies epidermal expression in meristems and young primordia. Plant J. *20*, 259-263.
29. Bomblies, K., Dagenais, N., and **Weigel, D.** (1999) Redundant enhancers mediate transcriptional repression of *AGAMOUS* by *APETALA2*. Dev. Biol. *216*, 260–264.
30. Kardailsky, I., Shukla, V., Ahn, J. H., Dagenais, N., Christensen, S. K., Nguyen, J. T., Chory, J., Harrison, M. J., and **Weigel, D.** (1999) Activation tagging of the floral inducer *FT*. Science *286*, 1962-1965.
31. Christensen, S. K., Dagenais, N., Chory, J., and **Weigel, D.** (2000) Regulation of auxin response by the protein kinase PINOID. Cell *100*, 469-478.
32. **Weigel, D.**, Ahn, J. H., Blázquez, M. A., Borevitz, J., Christensen, S. K., Fankhauser, C., Ferrándiz, C., Kardailsky, I., Malancharuvil, E. J., Neff, M. M., Nguyen, J. T., Sato, S., Wang, Z., Xia, Y., Dixon, R. A., Harrison, M. J., Lamb, C. J., Yanofsky, M. F., and Chory, J. (2000) Activation tagging in Arabidopsis. Plant Physiol. *122*, 1003-1014.
33. Blázquez, M. A., and **Weigel, D.** (2000) Integration of floral inductive signals in *Arabidopsis*. Nature *404*, 889-892.
34. Trieu, A. T., Burleigh, S. H., Kardailsky, I. V., Maldonado-Mendoza, I. E., Versaw, W. K., Blaylock, L. A., Shin, H., Chiou, T. J., Katagi, H., Dewbre, G. R., **Weigel, D.**, and Harrison, M. J. (2000) Transformation of *Medicago truncatula* via infiltration of seedlings or flowering plants with *Agrobacterium*. Plant J. *22*, 532-541.
35. Sessions, A., Yanofsky, M. F., and **Weigel, D.** (2000) Cell-cell signaling and movement by the floral transcription factors LEAFY and APETALA1. Science *289*, 779-781.
36. He, Z., Zhu, Q., Dabi, T., Li, D., **Weigel, D.**, and Lamb, C. J. (2000) Transformation of rice with the *Arabidopsis* floral regulator *LEAFY* confers early heading. Transgenic Res. *9*, 223-227.
37. Zhao, Y., Christensen, S. K., Fankhauser, C., Cashman, J. R., Cohen, J. D., **Weigel, D.**, and Chory, J. (2001) A role for flavin-containing monooxygenases in auxin biosynthesis. Science *291*, 306-309.
38. Gocal, G. F. W., King, R. W., Blundell, C. A., Schwartz, O. M., Andersen, C. H., and **Weigel, D.** (2001) Evolution of floral meristem identity genes: analysis of *Lolium* genes related to *APETALA1* and *LEAFY* of Arabidopsis. Plant Physiol. *125*, 1788-1801.
39. Mimida, N., Goto, K., Kobayashi, Y., Araki, T., Ahn, J. H., **Weigel, D.**, Murata, M., Motoyoshi, F., and Sakamoto, W. (2001) Functional divergence of the *TFL1*-like gene family in *Arabidopsis* revealed by characterization of a novel homologue. Genes Cells *6*, 327-336.

40. Lohmann, J. U., Hong, R. L., Hobe, M., Busch, M. A., Parcy, F., Simon, R., and **Weigel, D.** (2001) A molecular link between stem cell regulation and floral patterning in *Arabidopsis*. Cell *105*, 793-803.
41. Ahearn, K. P., Johnson, H. A., **Weigel, D.**, and Wagner, D. R. (2001) *NFL1*, a *Nicotiana tabacum LEAFY*-like gene, controls meristem and floral structure. Plant Cell Physiol. *42*, 1130-1139.
42. Gocal, G. F. W., Sheldon, C. C., Gubler, F., Moritz, T., Bagnall, B., Li, S. F., Parish, R. W., Dennis, E. S., **Weigel, D.**, and King, R. W. (2001) *GAMYB-like* genes, flowering and gibberellin signaling in Arabidopsis. Plant Physiol. *127*, 1682-1693.
43. Maloof, J. N., Borevitz, J. O., Dabi, T., Lutes, J., Nehring, R. B., Redfern, J. L., Trainer, G. T., Wilson, J. M., Asami, T., Berry, C. C., **Weigel, D.**, and Chory, J. (2001) Natural variation of light sensitivity in *Arabidopsis*. Nat. Genet. *29*, 441-446.
44. Nordborg, M., Borevitz, J. O., Bergelson, J., Berry, C. C., Chory, J., Hagenblad, J., Kreitman, M., Maloof, J. N., Noyes, T., Oefner, P. J., Stahl, E., and **Weigel, D.** (2002) The extent of linkage disequilibrium in *Arabidopsis thaliana*. Nat. Genet. *30*, 190-193.
45. Yun, J. Y., **Weigel, D.**, and Lee, I. (2002) Ectopic expression of *SUPERMAN* suppresses development of petals and stamens. Plant Cell Physiol. *43*, 52-57.
46. Borevitz, J. O., Maloof J. N., Lutes, J., Dabi, T., Redfern, J. L., Trainer, G. T., Werner, J. D., Asami, T., Berry, C. C., **Weigel, D.**, and Chory, J. (2002) Quantitative trait loci controlling light and hormone response in two accessions of *Arabidopsis thaliana*. Genetics *160*, 683-696.
47. Parcy, F., Bomblies, K., and **Weigel, D.** (2002) Interaction of *LEAFY*, *AGAMOUS*, and *TERMINAL FLOWER1* in maintaining floral identity in *Arabidopsis*. Development *129*, 2519-2527.
48. Blázquez, M. A., Trénor, M., and **Weigel, D.** (2002) Independent control of gibberellins and flowering time by the circadian clock in *Arabidopsis*. Plant Physiol. *130*, 1770-1775.
49. Blázquez, M. A., Ahn, J. H., and **Weigel, D.** (2003) A thermosensory pathway controlling flowering time in *Arabidopsis*. Nat. Genet. *33*, 168-171.
50. Borevitz, J. O., Liang, D., Plouffe, D., Chang, H.-S., Zhu, T., **Weigel, D.**, Berry, C. C., Winzeler, E., and, Chory, J. (2003) Large scale identification of single feature polymorphisms in complex genomes. Genome Res. *13*, 513-523.
51. Hong, R. L., Hamaguchi, L., Busch, M. A., and **Weigel, D.** (2003) Regulatory elements of the floral homeotic gene *AGAMOUS* identified by phylogenetic footprinting and shadowing. Plant Cell *15*, 1296-1309.
52. Durfee, T., Roe, J. L., Sessions R. A., Inouye, C., Serikawa, K., Feldmann, K. A., **Weigel, D.**, and Zambryski, P. C. (2003) The F-box containing protein UFO and *AGAMOUS* participate in antagonistic pathways governing early petal development in *Arabidopsis*. Proc. Natl. Acad. Sci. USA *100*, 8571-8576.
53. Wu, X., Dinneny, J., Crawford, K., Zambryski, P., Citovsky, V., and **Weigel, D.** (2003) Modes of intercellular transcription factor movement in the *Arabidopsis* apex. Development *130*, 3735-3745.
54. Alonso, J. M., Stepanova, A. N., Leisse, T. J., Kim, C. J., Chen, H., Shinn, P., Stevenson, D. K., Zimmerman, J., Barajas, P., Cheuk, R., Gadrinab, C., Heller, C., Jeske, A., Koesema, E., Meyers, C. C., Parker, H. Prednis, L., Ansari, Y., Choy, N., Deen, H., Geralt, M., Hazari, N.,

Hom, E., Karnes, M., Mulholland, C., Ndubaku, R., Schmidt, I., Guzman, P., Aguilar-Henonin, L., Schmid, M., **Weigel, D.**, Carter, D. E., Marchand, T., Risseeuw, E., Brogden, D., Zeko, A., Crosby, W. L., Berry, C. C., and Ecker, J. R. (2003) Global gene functional analysis in Arabidopsis using T-DNA insertional mutagenesis. Science *301*, 653-657.

55. Palatnik, J. F., Allen, E., Wu, X., Schommer, C., Schwab, R., Carrington, J. C., and **Weigel, D.** (2003) Control of leaf morphogenesis by microRNAs. Nature *425*, 257-263.
56. Schmid, M., Uhlenhaut, N. H., Godard, F., Demar, M., Bressan, R., **Weigel, D.**, and Lohmann, J. U. (2003) Dissection of floral induction pathways using global expression analysis. Development *130*, 6001-6012.
57. Dinneny, J. R., Yadegari, R., Fischer, R. L.,Yanofsky, M. F., and **Weigel, D.** (2004) The role of *JAGGED* in shaping lateral organs. Development *131*, 1101-1110.
58. Yoo, S. Y., Kardailsky, I., Lee, J. S., **Weigel, D.**, Ahn, J. H. (2004) Acceleration of flowering by overexpression of *MFT* (*MOTHER OF FT AND TFL1*). Mol. Cells *17*, 95-101.
59. Maizel, A., and **Weigel, D.** (2004) Temporally and spatially controlled induction of gene expression in *Arabidopsis thaliana*. Plant J. *38*, 164-171.
60. Hagenblad, J., Tang, C., Molitor, J., Werner, J., Zhao, K., Zheng, H., Marjoram, P., **Weigel, D.**, and Nordborg, M. (2004) Haplotype structure and phenotypic associations in the chromosomal regions surrounding two *Arabidopsis thaliana* flowering time loci. Genetics *168*, 1627-1638.
61. Werner, J. D., Borevitz, J. O., Warthmann, N., Trainer, G. T., Ecker, J. R., Chory, J., and **Weigel, D.** (2005) Quantitative trait locus mapping and DNA array hybridization identify an *FLM* deletion as a cause for natural flowering-time variation. Proc. Natl. Acad. Sci. USA *102*, 2460-2465.
62. Yoo, S. Y., Bomblies, K., Yoo, S. K., Yang. J. W., Choi, M. S., Lee, J. S., **Weigel, D.**, and Ahn, J. H. (2005) The 35S promoter used in a selectable marker gene of a plant transformation vector affects the expression of the transgene. Planta *221*, 523-530.
63. Wu, X., Dabi, T., and **Weigel, D.** (2005) Requirement of homeobox gene *STIMPY/WOX9* for Arabidopsis meristem growth and maintenance. Curr. Biol. *15*, 436-440.
64. de Folter, S., Immink, R. G. H., Kieffer, Pařenicová, M. L., Henz, S. R., **Weigel, D.**, Busscher, M., Kooiker, M., Colombo, L., Kater, M. M., Davies, Angenent, G. C. (2005) Comprehensive interaction map of the Arabidopsis MADS box transcription factors. Plant Cell *17*, 1424-1433.
65. Schmid, M., Davison, T. S., Henz, S. R., Pape, U. J., Demar, M., Vingron, M. Schölkopf, B., **Weigel, D.**, and Lohmann, J. (2005) A gene expression map of *Arabidopsis* development. Nat. Genet. *37*, 501-506.
66. Schwab, R., Palatnik, J. F., Riester, M., Schommer, C., Schmid, M., and **Weigel, D.** (2005) Specific effects of microRNAs on the plant transcriptome. Dev. Cell *8*, 517-527.
67. Maizel, A., Busch, M. A., Tanahashi, T., Perkovic, J., Kato, M., Hasebe, M., and **Weigel, D.** (2005) The floral regulator LEAFY evolves by substitutions in the DNA binding domain. Science *308*, 260-263. (Correction published on October 12, 2018)
68. Werner, J. D., Borevitz, J. O., Uhlenhaut, N. H., Ecker, J. R., Chory, J., and **Weigel, D.** (2005) *FRIGIDA*-independent variation in flowering time of natural *A. thaliana* accessions. Genetics *170*, 1197-1207.

69. Lempe, J., Balasubramanian, S., Sureshkumar, S., Singh, S., Schmid, M., and **Weigel, D.** (2005) Diversity of flowering responses in wild *Arabidopsis thaliana* strains. PLoS Genet. *1*, e6.
70. Wigge, P. A., Kim, M. C., Jaeger, K. E., Busch, W., Schmid, M., Lohmann, J. U., and **Weigel, D.** (2005) Integration of spatial and temporal information during floral induction in *Arabidopsis*. Science *309*, 1056-1059.
71. Lee, J. H., Cho, Y. S., Yoon, H. S., Suh, M. C., Moon, J., Lee, I., **Weigel. D.**, Yun, C. H., and Kim, J. K. (2005) Conservation and divergence of FCA function between *Arabidopsis* and rice. Plant Mol. Biol. *58*, 823-838.
72. Dinneny, J. R., **Weigel, D.**, and Yanofsky, M. F. (2005) A genetic framework for fruit patterning in *Arabidopsis*. Development *132*, 4687-4696.
73. Dezulian, T., Remmert, M., Palatnik, J., **Weigel, D.**, and Huson, D. (2006) Identification of plant microRNA homologs. Bioinformatics *22*, 359-360.
74. Ahn, J. A., Miller, D., Winter, V. J., Banfield, M. J., Lee, J. H., Yoo, S. Y., Henz, S. R., Brady, R. L., and **Weigel, D.** (2006) A divergent external loop confers antagonistic activity on floral regulators FT and TFL1. EMBO J. *25*, 605-614.
75. Martyn, U., **Weigel, D.**, and Dreyer, C. (2006) *In vitro* culture of the guppy, *Poecilia reticulata*. Dev. Dyn. *235*, 617-622.
76. Dinneny, J. R., **Weigel, D.**, and Yanofsky, M. F. (2006) *NUBBIN* and *JAGGED* define stamen and carpel shape in *Arabidopsis*. Development *133,* 1645-1655.
77. Schwab, R., Ossowski, S., Riester, M., Warthmann, N., and **Weigel, D.** (2006) Highly specific gene silencing by artificial microRNAs in *Arabidopsis*. Plant Cell *18*, 1121-1133.
78. Balasubramanian, S., Sureshkumar, S., Agrawal, M., Michael, T. P., Wessinger, C., Maloof, J., Clark, R., Warthmann, N., Chory, J., and **Weigel, D.** (2006) The PHYTOCHROME C photoreceptor gene mediates natural variation in flowering and growth responses of *Arabidopsis thaliana*. Nat. Genet. *38*, 711-715.
79. Balasubramanian, S., Sureshkumar, S., Lempe J., and **Weigel, D.** (2006) Potent induction of *Arabidopsis thaliana* flowering by elevated growth temperature. PLoS Genet. *2*, e106.
80. Dezulian, T., Schaefer, M., Wiese, R., **Weigel, D.**, and Huson, D. (2006) CrossLink: visualization and exploration of sequence relationships between (micro) RNAs. Nucleic Acids Res. *34 (Web Server Issue),* W400-W404.
81. Sliwinski, M. K., White, M. A., Maizel, A., **Weigel, D.**, and Baum, D. A. (2006) Evolutionary divergence of *LFY* function in the mustards *Arabidopsis thaliana* and *Leavenworthia crassa*. Plant Mol. Biol. *62*, 27-289.
82. Hoffmann, M., Tripathi, N., Henz, S. R., Lindholm, A. K., **Weigel, D.**, Breden, F., Dreyer, C. (2007) Opsin gene duplication and diversification in the guppy, a model for sexual selection. Proc. R. Soc. Lond. B *274,* 33-42.
83. Henz, S. R., Cumbie, J. S., Kasschau, K. D., Lohmann, J. U., Carrington, J. C., **Weigel, D.**, and Schmid, M. (2007) Distinct expression patterns of natural antisense transcripts in *Arabidopsis*. Plant Physiol. *144*, 1247-1255.
84. Palatnik, J. F., Wollmann, H., Schommer, C., Schwab, R., Boisbouvier, J., Rodriguez, R., Allen, E., Dezulian, T., Huson, D., Carrington, J. C., and **Weigel, D.** (2007) Sequence and expression differences underlie functional specialization of *Arabidopsis* microRNAs miR159

and miR319. Dev. Cell *13*, 115-125. (Editorial Note and Correction published on October 7, 2019; Dev. Cell *51*, 129; see also *bioRxiv* article #24 below)

85. Borevitz, J., Hazen, S. P., Michael, T. P., Morris, G. P., Baxter, I. R., Hu, T. T., Chen, H.-M., Werner, J., Nordborg, M., Salt, D. E., Kay, S. A., Chory, J., **Weigel, D.**, Jones, J. D. G., and Ecker, J. R. (2007) Genome wide patterns of single feature polymorphism diversity in *Arabidopsis thaliana*. Proc. Natl. Acad. Sci. USA *104*, 12057-12062.
86. Clark, R. M., Schweikert, G., Toomajian, C., Ossowski, S., Zeller, G., Shinn, P., Warthmann, N., Hu, T. T., Fu, G., Hinds, D., Chen, H.-M., Frazer, K. A., Huson, D. H., Schölkopf, B., Nordborg, M., Rätsch, G., Ecker, J. R., and **Weigel, D.** (2007) Common sequence polymorphisms shaping genetic diversity in *Arabidopsis thaliana*. Science *317*, 338-342.
87. Franco-Zorrilla, J. M., Valli, A., Todesco, M., Mateos, I., Puga, M. I., Rubio-Somoza, I., Leyva, A., **Weigel, D.**, García, J. A., and Paz-Ares, J. (2007) Target mimicry provides a new mechanism for regulation of microRNA activity. Nat. Genet. *39*, 1033-1037.
88. Tang, C., Toomajian, C., Sherman-Broyles, S., Plagnol, V., Guo, Y.-L., Hu, T. T., Clark, R. M., Nasrallah, J. B., **Weigel, D.**, and Nordborg, M. (2007) The evolution of selfing in *Arabidopsis thaliana*. Science *317*, 1070-1072.
89. Wu, X., Chory, J., and **Weigel, D.** (2007) Combinations of *WOX* activities regulate tissue proliferation during *Arabidopsis* embryonic development. Dev. Biol. *309*, 306-316.
90. Kim, S., Plagnol, V., Hu, T. T., Toomajian, C., Clark, R. M., Ossowski, S., Warthmann, N., Ecker, J. R., **Weigel, D.**, and Nordborg, M. (2007) Recombination and linkage disequilibrium in *Arabidopsis thaliana*. Nat. Genet. *39*, 1151-1155.
91. Dreyer, C., Hoffmann, M., Lanz, C., Willing, E.-M., Riester, M., Warthmann, N., Sprecher, A., Tripathi, N., Henz, S. R., and **Weigel, D.** (2007) ESTs and EST-linked polymorphisms for genetic mapping and phylogenetic reconstruction in the guppy, *Poecilia reticulata*. BMC Genomics *8*, 269.
92. Bomblies, K., Lempe, J., Epple, P., Warthmann, N., Lanz, C., Dangl, J. L., and **Weigel, D.** (2007) Autoimmune response as a mechanism for a Dobzhansky-Muller-type incompatibility syndrome in plants. PLoS Biol. *5*, e236.
93. Wang, Q., Sajja, U., Rosloski, S., Humphrey, T., Kim, M. C., Bomblies, K., **Weigel, D.**, Grbic, V. (2007) *HUA2* caused natural variation in shoot morphology of *A. thaliana*. Curr. Biol. *17*, 1513-1519.
94. Warthmann, N., Fitz, J., and **Weigel, D.** (2007) MSQT for choosing SNP assays from multiple DNA alignments. Bioinformatics *23*, 2784-2787.
95. Michniewicz, M., Zago, M. K., Abas, L., Weijers, D., Schweighofer, A., Meskiene, I., Heisler, M. G., Ohno, C., Zhang, J., Huang, F., Schwab, R., **Weigel, D.**, Meyerowitz, E. M., Luschnig, C., Offringa, R., and Friml, J. (2007) Antagonistic regulation of PIN phosphorylation by PP2A and PINOID directs auxin flux. Cell *130*, 1044-1056.
96. Zeller, G., Henz, S. R., Laubinger, S., **Weigel, D.**, and Rätsch, G. (2008) Transcript normalization and segmentation of tiling array data. Pac. Symp. Biocomput. *12*, 527-538.
97. Ossowski, S., Schwab, R., and **Weigel, D.** (2008) Gene silencing in plants using artificial microRNAs and other small RNAs. Plant J. *53*, 674-690.
98. Nolte, V., **Weigel, D.**, and Schlötterer, C. (2008) The impact of shared ancestral variation on hybrid male lethality - a 16 codon insertion-deletion in the *D. simulans Lhr* gene. J. Evol. Biol. *21*, 551-555.

99. Filiault, D., Wessinger, C., Dinneny, J. R., Lutes, J., Borevitz, J., **Weigel, D.**, Chory, J., and Maloof, J. N. (2008) Amino acid polymorphisms in *Arabidopsis* phytochrome B causes differential response to light. Proc. Natl. Acad. Sci. USA *105*, 3157-3162.
100. Warthmann, N., Das, S., Lanz, C., and **Weigel, D.** (2008) Comparative analysis of the *MIR319A* microRNA locus in *Arabidopsis* and related Brassicaceae. Mol. Biol. Evol. *25*, 892-902.
101. Zeller, G., Clark, R. M., Schneeberger, K., Bohlen, A., **Weigel, D.**, and Rätsch, G. (2008) Detecting polymorphic regions in the *Arabidopsis thaliana* genome with resequencing microarrays. Genome Res. *18*, 918-929.
102. Warthmann, N., Chen, H., Ossowski, S., **Weigel, D.**, and Hervé, P. (2008) Highly specific gene silencing by artificial miRNAs in rice. PLoS ONE *3*, e1829.
103. Hanikenne, M., Talke, I. N., Haydon, M. J., Lanz, C., Nolte, A., Motte, P., Kroymann, J., **Weigel, D.**, Krämer, U. (2008) Metal hyperaccumulation evolved through *cis*-regulatory changes and triplication of *HMA4*. Nature *453*, 391-395.
104. Wang, J.W., Schwab, R., Czech, B., Mica, E., and **Weigel, D.** (2008) Dual effects of miR156-targeted *SPL* genes and *CYP78A5/KLUH* on plastochron length and organ size in *Arabidopsis thaliana*. Plant Cell *20*, 1231-1243.
105. Laubinger, S., Sachsenberg, T., Zeller, G., Busch, W., Lohmann, J. U., Rätsch, G., and **Weigel, D.** (2008) Dual roles of the nuclear cap binding complex and SERRATE in pre-mRNA splicing and microRNA processing in *Arabidopsis thaliana*. Proc. Natl. Acad. Sci. USA *105*, 8795-8800.
106. Laubinger, S., Zeller, G., Henz, S. R., Sachsenberg, T., Widmer, C. K., Naouar, N., Vuylsteke, M., Schölkopf, B., Rätsch G., and **Weigel, D.** (2008) At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in *Arabidopsis thaliana*. Genome Biol. *9*, R112.
107. Khraiwesh, B., Ossowski, S., **Weigel, D.**, Reski R., and Frank, W. (2008) Specific gene silencing by artificial microRNAs in *Physcomitrella patens*: An alternative to targeted gene knockouts. Plant Physiol. *148*, 684-693.
108. Schommer, C., Palatnik, J. F., Aggarwal, P., Chételat, A., Cubas, P., Farmer, E. E., Nath, U., and **Weigel, D.** (2008) Control of jasmonate biosynthesis and senescence by miR319 targets. PLoS Biol. *9*, e230.
109. Ossowski, S., Schneeberger, K., Clark, R. M., Lanz, C., and **Weigel, D.** (2008) Sequencing of natural strains of *Arabidopsis thaliana* with short reads. Genome Res. *18*, 2024-2033.
110. Loudet, O., Michael, T. P., Burger, B. T., Le Metté, C., Mockler, T. C., **Weigel, D.**, and Chory, J. (2008) A zinc knuckle protein that negatively controls morning-specific growth in *Arabidopsis thaliana*. Proc. Natl. Acad. Sci. USA *105*, 17193-17198.
111. de Felippes, F. F., Schneeberger, K., Dezulian, T., Schröder, M., Huson, D. H., and **Weigel, D.** (2008) Evolution of *Arabidopsis thaliana* microRNAs from random sequences. RNA *14*, 2455-2459.
112. Naouar, N., Vandepoele, K. Lammens, T., Casneuf, T., Zeller, G., van Hummelen, P., **Weigel, D.**, Rätsch, G., Inzé, D., Kuiper, M., De Veylder, L., and Vuylsteke, M. (2009) Quantitative RNA expression analysis with Affymetrix Tiling 1.0R Arrays identifies new E2F target genes. Plant J. *57*, 184-194.

113. Molnar, A., Thuenemann, E., Bassett, A., Schwach, F., Karkare, S., Ossowski, S., **Weigel, D.**, and Baulcombe, D. (2009) Highly specific gene silencing by artificial microRNAs in the unicellular alga *Chlamydomonas reinhardtii*. Plant J. *58*, 165-174.
114. Sureshkumar, S., Todesco, M., Schneeberger, K., Harilal, R., Balasubramanian, S., and **Weigel, D.** (2009) A genetic defect caused by a triplet repeat expansion in *Arabidopsis thaliana*. Science *323*, 1060-1063.
115. Felippes, F. F. d., and **Weigel, D.** (2009) Triggering tasiRNA formation in *Arabidopsis thaliana*: the role of microRNA miR173. EMBO Rep. *10*, 264-270.
116. Balasubramanian, S., Schwartz, C., Singh, A., Warthmann, N., Kim, M. C., Maloof, J. N., Loudet, O., Trainer, G. T., Dabi, T., Borevitz, J. O., Chory, J., and **Weigel, D.** (2009) QTL mapping in new *Arabidopsis thaliana* advanced intercross-recombinant inbred lines. PLoS ONE *4*, e4318.
117. Plantegenet, S., Weber, J., Goldstein, D. R., Zeller, G., Nussbaumer, C., Thomas, J., **Weigel, D.**, Harshman, K., and Hardtke, C. S. (2009) Comprehensive analysis of *Arabidopsis* expression level polymorphisms with simple inheritance. Mol. Systems Biol. *5*, 242.
118. Guo, Y.-L., Bechsgaard, J. S., Slotte, T., Neuffer, B., Lascoux, M., **Weigel, D.**, and Schierup, M. H. (2009) Recent speciation of *Capsella rubella* from *C. grandiflora*, associated with loss of self-incompatibility and an extreme bottleneck. Proc. Natl. Acad. Sci. USA *106*, 5246-5251.
119. Zeller, G., Henz, S., Widmer, C. K., Sachsenberg, T., Rätsch. R., **Weigel, D.**, and Laubinger, S. (2009) Stress-induced changes in the *Arabidopsis thaliana* transcriptome analyzed using whole genome tiling arrays. Plant J. *58*, 1068-1082.
120. Tripathi, N., Hoffmann, M., Willing, E.-M., Lanz, C., **Weigel, D.**, and Dreyer, C. (2009) Genetic linkage map of the guppy, *Poecilia reticulata*, and QTL analysis of male color and size variation. Proc. R. Soc. London B *276*, 2195-2208.
121. Tripathi, N., Hoffmann, M., Willing, E.-M., Lanz, C., **Weigel, D.**, and Dreyer, C. (2009) Linkage analysis reveals independent origin of Poeciliid sex chromosomes and a case of atypical sex inheritance in the guppy (*Poecilia reticulata*). Genetics *182*, 365-374.
122. Maier, A. T., Stehling-Sun, S., Wollmann, H., Demar, M., Hong, R. L., Haubeiß, S., **Weigel, D.,** and Lohmann, J. U. (2009) Dual roles of the bZIP transcription factor PERIANTHIA in the control of floral architecture and homeotic gene expression. Development *136*, 1613-1620.
123. Trigueros, M., Navarrete-Gómez, M., Sato, S., Christensen, S. K., Pelaz, S., **Weigel, D.**, Yanofsky, M. F., and Ferrandiz, C. (2009) The *NGATHA* genes direct style development in the *Arabidopsis* gynoecium. Plant Cell *21*, 1394-1409.
124. McNally, K. L., Childs, K. L., Bohnert, R., Davidson, R. M., Zhao, K., Ulat, V. J., Zeller, G., Clark, R. M., Hoeng, D. R., Bureau. T. E., Stokowski, R., Ballinger, D. G., Frazer, K. A., Cox, D. R., Padhukasahasram, B., Bustamante, C. D., **Weigel, D.,** Mackill, D. J., Bruskiewich, R. M., Rätsch, G., Buell, C. R., Leung, H., and Leach, J. E. (2009) Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. Proc. Natl. Acad. Sci. USA *106*, 12273-12278.
125. Schneeberger, K., Ossowski, S., Lanz, C., Juul, T., Petersen, A. H., Nielsen, K. H., Jørgensen, J.-H., **Weigel, D.***, and Andersen, S. U.* (2009) SHOREmap: mapping and

mutation identification in one step by deep sequencing. Nat. Methods *6*, 550-551. *corresponding authors.

126. Schwartz, C., Balasubramanian, S., Warthmann, N., Michael, T. P., Lempe, J., Sureshkumar, S., Maloof, J. N., Borevitz, J. O., Chory, J., and **Weigel, D.** (2009) Cis-regulatory changes at *FLOWERING LOCUS T* mediate natural variation in flowering responses of *Arabidopsis thaliana*. Genetics *183*, 723-732.
127. Wang, J.-W., Czech, B., and **Weigel, D.** (2009) miR156-regulated SPL transcription factors define an endogenous flowering pathway in *Arabidopsis thaliana*. Cell *138*, 738-749.
128. Wu, G., Park, M. Y., Conway, S. R., Wang, J.-W., **Weigel, D.**, and Poethig, R. S. (2009) The sequential action of miR156 and miR172 regulates developmental timing in *Arabidopsis*. Cell *138*, 750-759.
129. Mirouze, M., Reinders, J., Bucher, E., Nishimura, T., Schneeberger, K., Ossowski, S., Cao, J., **Weigel, D.**, Paszkowski, J., and Mathieu, O. (2009) Selective epigenetic control of retrotransposition in *Arabidopsis*. Nature *416*, 427-430.
130. Schneeberger, K., Hagmann, J., Ossowski, S., Warthmann, N., Gesing, S., Kohlbacher, O., and **Weigel, D.** (2009) Simultaneous alignment of short reads against multiple genomes. Genome Biol. *10*, R98.
131. Out, A. A., van Minderhout, I. J. H. M., Goeman, J. J., Ariyurek, Y., Ossowski, S., Schneeberger, K., **Weigel, D.**, van Galen, M., Taschner, P. E. M., Tops, C. C. M., Breuning, M. H., van Ommen, G.-J. B., den Dunnen, J. T., Devilee, P., and Hes, F. J. (2009) Estimation of *MUTYH* gene variant frequencies in pooled DNA with massive parallel sequencing. Hum. Mutat. *30*, 1703-1712.
132. Rodriguez, R. E., Mecchia, M. A., Debernardi, J. M., Schommer, C., **Weigel, D.**, and Palatnik, J. F. (2010) Coordination of cell proliferation in *Arabidopsis thaliana* by microRNA miR396. Development *137*, 103-112.
133. Rehrauer, H., Aquino, C., Gruissem, W., Henz, S., Hilson, P., Laubinger, S., Naouar, N., Patrignani, A., Rombauts, S., Shu, H., Van de Peer, Y., Vuylsteke, M., **Weigel, D.**, Zeller, G., and Hennig, L. (2010) AGRONOMICS1 – A new resource for *Arabidopsis* transcriptome profiling. Plant Physiol. *152*, 487-499.
134. Werner, S., Wollmann, H., Schneeberger, K., and **Weigel, D.** (2010) Structure determinants for accurate processing of miR172a in *Arabidopsis thaliana*. Curr. Biol. *20*, 42-48.
135. Ossowski, S., Schneeberger, K., Lucas-Lledó, J. I., Warthmann, N., Clark, R. M., Shaw, R. G., **Weigel, D.**, and Lynch, M. (2010) The rate and molecular spectrum of spontaneous mutations in *Arabidopsis thaliana*. Science *327*, 92-94.
136. Khraiwesh, B., Arif, M. A., Seumel, G. I., Ossowski, S., **Weigel, D.**, Reski, R., and Frank, W. (2010) Epigenetic silencing of microRNA targets by stable microRNA:target RNA duplexes. Cell *140*, 111-122.
137. Skylar, A., Hong, F.-X., Chory, J., **Weigel, D.**, and Wu, X. (2010) *STIMPY* mediates cytokinin signaling during shoot meristem establishment in *Arabidopsis* seedlings. Development *137*, 541-549.
138. Platt, A., Horton, M., Huang, Y. S., Li, Y., Anastasio, A. E., Mulyati, N. W., Ågren, J., Bossdorf, O., Byers, D., Donohue, K., Dunning, M., Holub, E. B., Hudson, A., Le Corre, V., Loudet, O., Roux, F., Warthmann, N., **Weigel, D.**, Rivero, L., Scholl, R., Nordborg, M.,

Bergelson, J., and Borevitz, J. O. (2010) The scale of population structure in *Arabidopsis thaliana*. PLoS Genet. *6*, e1000843.

139. Willing, E. M., Bentzen, P., van Oosterhout, C., Hoffmann, M., Cable, J., Breden, F., **Weigel, D.**, and Dreyer, C. (2010) Genome-wide single nucleotide polymorphisms reveal population history and adaptive divergence in wild guppies. Mol. Ecol. *19*, 968-984.
140. Koo, S. C., Bracko, O., Park, M. S., Schwab, R., Chun, H. J., Park, K. M., Seo, J. S., Grbic, V., Balasubramanian, S., Schmid, M., Godard, F., **Weigel, D.**, and Kim, M. C. (2010) Control of flowering time and lateral organ development by the *Arabidopsis thaliana* MADS-box gene *AGAMOUS-LIKE6*. Plant J. *62*, 807-816.
141. Massonnet, C., Vile, D., Fabre, J., Hannah, M. A., Caldana, C., Lisec, J., Beemster, G. T. S., Meyer, R. C., Messerli, G., Gronlund, J., Perkovic, J., Wigmore, E., May, S., Bevan, M., Meyer C., Rubio-Díaz, S., **Weigel, D.**, Micol, J. L., Buchanan-Wollaston, V., Fiorani, F., Walsh, S., Rinn, B., Gruissem, W., Hilson, P., Hennig, L., Willmitzer, L., and Granier, C. (2010) Probing the reproducibility of leaf growth and molecular phenotypes: a comparison of three *Arabidopsis* accessions cultivated in ten laboratories. Plant Physiol. *152*, 2142-2157.
142. Atwell, S., Huang, Y., Vilhjálmsson, B., Willems, G., Horton, M., Li, Y., Meng, D., Platt, A., Tarone, A., Jiang, R., Hu, T. T., Muliati, W., Zhang, X., Amer, M. A., Baxter, I., Brachi, B., Chory, J., Dean, C., Debieu, M., de Meaux, J., Ecker, J. R., Faure, N., Kniskern, J., Jones, J. D. G., Michael, T., Nemri, A., Roux, F., Salt, D. E., Tang, C., Todesco, M., Traw, M. B., **Weigel, D.**, Marjoram, P., Borevitz, J. O., Bergelson, J., and Nordborg, M. (2010) Genome-wide association study of 107 phenotypes in a common set of *Arabidopsis thaliana* inbred lines. Nature *465*, 627-631.
143. Bomblies, K., Yant, L., Laitinen, R., Kim, S.-T., Hollister, J. D., Warthmann, N., Fitz, J., and **Weigel, D.** (2010) Local-scale patterns of genetic variability, outcrossing and spatial structure in natural stands of *Arabidopsis thaliana*. PLoS Genet. *6*, e1000890.
144. Laitinen, R. A. E., Schneeberger, K., Jelly, N. S., Ossowski, S., and **Weigel, D.** (2010) Identification of a spontaneous frame shift mutation in a non-reference *Arabidopsis thaliana* accession using whole genome sequencing. Plant Physiol. *153*, 652-654.
145. Fahlgren, N., Jogdeo, S., Kasschau, K. D., Sullivan, C. M., Chapman, E. J., Laubinger, S., Smith, L. M., Dasenko, M., Givan, S. A., **Weigel, D.**, and Carrington, J. C. (2010) MicroRNA evolution in *Arabidopsis lyrata* and *Arabidopsis thaliana*. Plant Cell *22*, 1074-1089.
146. Gonzalez, N., De Bodt, S., Sulpice, R., Jikumaru, Y., Chae, E., Van Daele, T., De Milde, L., **Weigel, D.**, Kamiya, Y., Stitt, M., Beemster, G. T. S., and Inzé, D. (2010) Multiple pathways regulate leaf size in *Arabidopsis thaliana*. Plant Physiol. *153*, 1261-1279.
147. Todesco, M., Balasubramanian, S., Hu, T. T., Traw, B. M., Horton, M., Epple, P., Kuhns, C., Sureshkumar, S., Schwartz, C., Lanz, C., Laitinen, R. A. E., Chory, J., Lipka, V., Borevitz, J. O., Dangl, J. L., Bergelson, J., Nordborg, M., and **Weigel, D.** (2010) Natural allelic variation underlying a major fitness tradeoff in *Arabidopsis thaliana*. Nature *465*, 632-636.
148. Rosloski, S. M., Balasubramanian, S., **Weigel, D.**, and Grbic, V. (2010) Natural diversity in flowering responses of *Arabidopsis thaliana* caused by variation in a tandem gene array. Genetics *186*, 263-276.
149. Todesco, M., Rubio-Somoza, I., Paz-Ares, J., and **Weigel, D.** (2010) A collection of target mimics for comprehensive analysis of miRNA function in *Arabidopsis thaliana*. PLoS Genet. *6*, e1001031.

150. Laubinger, S., Zeller, S., Henz, S. R., Buechel, S., Sachsenberg, T., Wang, J.-W., Rätsch, G., and **Weigel, D.** (2010) Global effects of the small RNA biogenesis machinery on the *Arabidopsis* transcriptome. Proc. Natl. Acad. Sci. USA *107*, 17466-17473.
151. Wollmann, H. Mica, E., Todesco, M., Long, J. A., and **Weigel, D.** (2010) On reconciling the interactions of *APETALA2*, miR172 and *AGAMOUS* with the ABC model of flower development. Development *137*, 3633-3642.
152. Salomé, P. A., **Weigel, D.**, and McClung, D. R. (2010) The role of the *Arabidopsis* morning loop components CCA1, LHY, PRR7 and PRR9 in temperature compensation. Plant Cell *22*, 3650-3611.
153. Felippes, F. F., Ott, F., and **Weigel, D.** (2011) Comparative analysis of non-autonomous effects of tasiRNAs and miRNAs in *Arabidopsis thaliana*. Nucleic Acids Res. *39*, 2880-2889.
154. Watson, C. T., Gray, S. M., Hoffmann, M., Lubieniecki, K. P., Joy, J. B., Sandkam, B. A., **Weigel, D.**, Loew, E., Dreyer, C., Davidson, W. S., and Breden, F. (2011) Gene duplication and divergence of long wavelength-sensitive opsin genes in the guppy, *Poecilia reticulata*. J. Mol. Evol. *72*, 240-252.
155. Hollister, J., Smith, L. M., Guo, Y.-L., Ott, F., **Weigel, D.**, and Gaut, B. S. (2011) On the role of transposable elements and small RNAs in driving gene expression divergence between *Arabidopsis thaliana* and *Arabidopsis lyrata*. Proc. Natl. Acad. Sci. USA *108*, 2322-2327.
156. Gorman, K. F., Christians, J. K., Parent, J., Ahmadi, R., **Weigel, D.**, Dreyer, C., and Breden, F. (2011) A major QTL controls susceptibility to spinal curvature in the curveback guppy. BMC Genomics *12*, 16.
157. Wang, J.-W., Park, M. Y., Wang, L.-J., Koo, Y., Chen, X.-Y., **Weigel, D.**, and Poethig, R. S. (2011) MiRNA control of vegetative phase change in trees. PLoS Genet. *7*, e1002012.
158. Salomé, P. A., Bomblies, K., Laitinen, R. A. E., Yant, L., and **Weigel, D**. (2011) Genetic architecture of flowering time variation in *Arabidopsis thaliana*. Genetics *188*, 421-433.
159. Hu, T. T., Pattyn, P., Bakker, E. G., Cao, J., Cheng, J.-F., Clark, R. M., Fahlgren, N., Fawcett, J. A., Grimwood, J., Gundlach, H., Haberer, G., Hollister, J. D., Ossowski, S., Ottilar, R. O., Salamov, A. A., Spannagl, M., Wang, X., Yang, L., Nasrallah, M. E., Bergelson, J., Carrington, J. C., Gaut, B. S., Schmutz, J., Mayer, K. F. X., Van de Peer, Y., Grigoriev, I. V., Nordborg, M., **Weigel, D.**, and Guo, Y.-L. (2011) The *Arabidopsis lyrata* genome and the basis of rapid genome size change. Nat. Genet. *43*, 476-481.
160. Gou, J.-Y., Felippes, F. F., Liu, C.-J., **Weigel. D.**, and Wang, J.-W. (2011) Negative control of anthocyanin biosynthesis by a miR156-targeted SPL transcription factor. Plant Cell *23*, 1512-1522.
161. Moyroud, E., Gómez Minguet, E., Ott, F., Yant, L., Posé, D., Blanchet, S., Monniaux, M., Bastien, O., Thévenon, E., **Weigel, D.**, Schmid, M., and Parcy, F. (2011) A biophysical DNA binding model for the LEAFY transcription factor reveals the evolutionary fluidity of its binding sites. Plant Cell *23*, 1293-1306.
162. Sonmez, C., Bäurle, I., Magusin, A., Dreos, R., Laubinger, S., **Weigel, D.**, and Dean, C. (2011) RNA 3' processing functions of *Arabidopsis* FCA and FPA limit intergenic transcription. Proc. Natl. Acad. Sci. USA *108*, 8508-8513.
163. Schneeberger, K., Ossowski, S., Ott, F., Klein, J. D., Wang, X., Lanz, C., Smith, L. M., Cao, J., Fitz, J., Warthmann, N., Henz, S. R., Huson, D. H., and **Weigel, D.** (2011) Reference-

guided assembly of four diverse *Arabidopsis thaliana* genomes. Proc. Natl. Acad. Sci. USA *108*, 10249-10254.

164. Willing, E.-M., Hoffmann, M., Klein, J. D., **Weigel, D.**, and Dreyer, C. (2011) Paired-end RAD-seq for de-novo assembly and marker design without available reference. Bioinformatics *27*, 2187-2193.
165. Smith, L. M., Bomblies, K., and **Weigel, D.** (2011) Complex evolutionary events at a tandem cluster of *Arabidopsis thaliana* genes resulting in a single-locus genetic incompatibility. PLoS Genet. *7*, e1002164.
166. Klein, J. D., Ossowski, S., Schneeberger, K., **Weigel, D.**, and Huson, D. H. (2011) LOCAS – A low coverage assembly tool for resequencing projects. PLoS ONE *6*, e23455.
167. Guo, Y.-L., Fitz, J., Schneeberger, K., Ossowski, S., Cao, J., and **Weigel, D.** (2011) Genome-wide comparison of nucleotide-binding site-leucine-rich repeat-encoding genes in *Arabidopsis*. Plant Physiol. *157*, 757-769.
168. Guo, Y.-L., Zhao, X., Lanz, C., and **Weigel, D.** (2011) Evolution of the *S*-locus region in *Arabidopsis thaliana* relatives. Plant Physiol. *157*, 937-946.
169. Cao, J., Schneeberger, K., Ossowski, S., Günther, T., Bender, S., Fitz, J., Koenig, D., Lanz, C., Stegle, O., Lippert, C., Wang, X., Ott, F., Müller, J., Alonso-Blanco, C., Borgwardt, K., Schmid, K. J., and **Weigel, D.** (2011) Whole-genome sequencing of multiple *Arabidopsis thaliana* populations. Nat. Genet. *43*, 956-963.
170. Becker, C., Hagmann, J., Müller, J., Koenig, D., Stegle, O., Borgwardt, K., and **Weigel, D.** (2011) Spontaneous epigenetic variation in the methylome of *Arabidopsis thaliana*. Nature *480*, 245-249.
171. Davila, J. I., Arrieta-Montiel, M. P., Wamboldt, Y., Cao, J., Hagmann, J., Shedge, V., Xu, Y.-Z., **Weigel, D.**, and Mackenzie, S. A. (2011) Double-strand break repair processes drive evolution of the mitochondrial genome in Arabidopsis. BMC Biology *9*, 64.
172. Breakfield, N. W., Corcoran, D. L., Petricka, J. J., Shen, J., Sae-Seaw, J., Rubio-Somoza, I., **Weigel, D.**, Ohler, U., and Benfey, P. N. (2012) High-resolution experimental and computational profiling of tissue-specific known and novel miRNAs in *Arabidopsis*. Genome Res. *22*, 163-176.
173. Todesco, M., Balasubramanian, S., Ott, F., Cao, J., Sureshkumar, S., Schneeberger, K., Meyer, R., Altmann, T., and **Weigel, D.** (2012) Natural variation in biogenesis efficiency of individual *Arabidopsis thaliana* microRNAs. Curr. Biol. *22*, 1-5.
174. Salomé, P. A., Bomblies, K., Fitz, J., Laitinen, R. A. E., Warthmann, N., Yant, L., and **Weigel, D.** (2012) The recombination landscape in *Arabidopsis thaliana* $F_2$ populations. Heredity *108*, 447-455.
175. Felippes, F. F., Wang, J.-W., and **Weigel, D.** (2012) MIGS: miRNA induced gene silencing. Plant J. *70*, 541-547.
176. Manavella, P. A., Koenig, D., and **Weigel, D.** (2012) Plant secondary siRNA production determined by microRNA-duplex structure. Proc. Natl. Acad. Sci. USA *109*, 2461-2466.
177. Rutter, M., Roles, A., Conner, J. K., Shaw, R., Shaw, F., Schneeberger, K., Ossowski, S., **Weigel, D.,** and Fenster, C. B. (2012) Fitness of *Arabidopsis thaliana* mutation accumulation lines whose spontaneous mutations are known. Evolution *66*, 2335-2339.

178. Galvão, V., Nordström, K., Lanz, C., Sulz, P., Mathieu, J., Posé, D., Schmid, M., **Weigel, D.**, and Schneeberger, K. (2012) Synteny-based mapping-by-sequencing enabled by targeted enrichment. Plant J. *71*, 517-526.
179. Joshi, H. J., Christiansen, K. M., Fitz, J., Cao, J., Schackwitz, W. S., Smith-Moritz, A. M., Lister, R., Pennacchio, C., Pennacchio, L., Nordborg, M., Ecker, J. R., **Weigel, D.**, and Heazlewood, J. L. (2012) 1001 Proteomes: A functional proteomics portal for the analysis of natural variants of *Arabidopsis thaliana*. Bioinformatics *28*, 1303-1306.
180. Giacomelli, J., **Weigel, D.**, Chan, R., and Manavella, P. (2012) Role of recently evolved miRNA regulation of sunflower *HaWRKY6* in response to temperature damage. New Phytol. *195*, 766-773.
181. Guo, Y-L., Todesco, M., Hagmann, J., Das, S., and **Weigel, D.** (2012) Independent *FLC* mutations as causes of flowering time variation in *Arabidopsis thaliana* and *Capsella rubella*. Genetics *192*, 729-739.
182. Manavella, P. A., Hagmann, J., Ott, F., Laubinger, S., Franz, M., Macek, B., and **Weigel, D.** (2012) Fast-forward genetics identifies CPL phosphatases as regulators of plant miRNA-processing. Cell *151*, 859-870.
183. Rosloski, S. M., Singh, A., Jali, S. S., Balasubramanian, S., **Weigel, D.**, and Grbic, V. (2013) Functional analysis of splice variant expression of *MADS AFFECTING FLOWERING 2* of *Arabidopsis thaliana*. Plant Mol. Biol. *81*, 57-69.
184. Kopischke, M., Westphal, L., Schneeberger, K., Clark, R., Ossowski, S., Wewer, V., Fuchs, R., Landtag, J., Doermann, P., Lipka, V., **Weigel, D.**, Schulze-Lefert, P., Scheel, D., and Rosahl, S. (2013) Impaired sterol ester synthesis alters the response of *Arabidopsis thaliana* to *Phytophthora infestans*. Plant J. *73*, 456-568.
185. Manavella, P. A., Koenig, D., Rubio-Somoza, I., Burbano, H. A., Becker, C., and **Weigel, D.** (2013) Tissue-specific silencing of *Arabidopsis thaliana SU(VAR)3-9 HOMOLOG8* by miR171a*. Plant Physiol. *161*, 805-812.
186. Salomé, P. A., Oliva, M., **Weigel, D.**, and Krämer, U. (2013) Circadian clock adjustment to plant iron status depends on chloroplast and phytochrome function. EMBO J. *32*, 511-23.
187. Wang, X., **Weigel, D.**, and Smith, L. M. (2013) Transposon variation and its effects on gene expression in *Arabidopsis*. PLoS Genet. *9*, e1003255.
188. Grimm, D., Hagmann. J., Koenig, D., **Weigel, D.**, and Borgwardt, K. (2013) Accurate indel prediction using paired-end short reads. BMC Genomics *14*, 132.
189. Rubio-Somoza, I., and **Weigel, D.** (2013) Coordination of flower maturation by a regulatory circuit of three microRNAs. PLoS Genet. *9*, e1003374.
190. Slotte, T., Hazzouri, K. M., Ågren, J. A., Koenig, D., Maumus, F., Guo, Y.-L., Steige, K., Platts, A. E., Escobar, J. S., Newman, L., Wang, W., Mandáková, T., Vello, E., Smith, L. M., Henz, S. R., Steffen, J., Takuno, S., Brandvain, Y., Coop, G., Andolfatto, P., Hu, T. T., Blanchette, M., Clark, R. M., Quesneville, H., Nordborg, M., Gaut, B. S., Lysak, M. A., Jenkins, J., Grimwood, J., Chapman, J., Prochnick, S., Shu, S., Rokhsar, D., Schmutz, J., **Weigel, D.**, and Wright, S. I. (2013) The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution. Nat. Genet. *45*, 831-835.
191. Velikkakam James, G., Patel, V., Nordström, K. J. V., Klasen, J. R., Salomé, P. A., **Weigel, D.**, and Schneeberger, K. (2013) User guide for mapping-by-sequencing in Arabidopsis. Genome Biol. *14*, R61.

192. Kottler, V. A., Fadeev, A., **Weigel, D.**, and Dreyer, C. (2013) Pigment pattern formation in the guppy, *Poecilia reticulata*, involves the Kita and Csf1ra receptor tyrosine kinases. Genetics *194*, 631-646.
193. Yoshida, K., Schuenemann, V. J., Cano, L. M., Pais, M., Mishra, B., Sharma, R., Lanz, C., Martin, F., Kamoun, S., Krause, J., Thines, M., **Weigel, D.**, and Burbano, H. A. (2013) The rise and fall of the *Phytophthora infestans* lineage that triggered the Irish potato famine. eLife *2013*, e00731.
194. Koenig, D., Jiménez-Gómez, J. M., Kimura, S., Fulop, D., Chitwood, D. H., Headland, L. R., Kumar, R., Covington, M. F., Devisetty, U. K., Tat, A. V., Tohge, T., Bolger, A., Schneeberger, K., Ossowski, S., Lanz, C., Xiong, G., Taylor-Teeples, M., Brady, S. M., Pauly, M., **Weigel, D.***, Usadel, B., Fernie, A. R., Peng, J., Sinha, N. R., and Maloof, J. N.* (2013) Comparative transcriptomics reveals patterns of selection in wild and domesticated tomato. Proc. Natl. Acad. Sci. USA *110*, E2655-E2662. *corresponding authors.
195. Rugnone, M., Faigón, A., Sanchez, S. E., Schlaen, R. G., Hernando, C. E., Seymour, D. K., Mancini, E., Chernomoretz, A., **Weigel, D.**, Más, P., and Yanovsky, M. J. (2013) *LNK* genes integrate light and clock signaling networks at the core of the *Arabidopsis* oscillator. Proc. Natl. Acad. Sci. USA *110*, 12120-12125.
196. Nekrasov, V., Staskawicz, B., **Weigel, D.**, Jones, J. D. G., and Kamoun, S. (2013) Targeted mutagenesis in plants using the Cas9 RNA-guided endonuclease. Nat. Biotech. *31*, 691-693.
197. Merelo, M., Xie, Y., Brand, K., Ott, F., **Weigel, D.**, Bowman, J., Heisler, M., Wenkel, S. (2013) Genome-wide identification of KANADI1 target genes. PLoS ONE *8*, e77341.
198. Wijnker, E., Velikkakam James, G., Ding, J., Becker, F., Klasen, J. R., Rawat, V., Rowan, B. A., de Jong, D. F., de Snoo, C. B., Zapata Ortiz, L., Huettel, B., de Jong, H., Ossowski, S., **Weigel, D.,** Koornneef, M., Keurentjes, J. J. B., and Schneeberger, K. (2013) The genomic landscape of meiotic crossovers and gene conversions in *Arabidopsis thaliana*. eLife *2*, e01426.
199. Kottler, V. A., Koch, I., Flötenmeyer, M., Hashimoto, H., **Weigel, D.**, and Dreyer, C. (2014) Multiple pigment cell types contribute to the black, blue, and orange ornaments of male guppies (*Poecilia reticulata*). PLoS ONE *9*, e85647.
200. Sayou, C., Monniaux, M., Nanao, M., Moyroud, E.,. Brockington, S. F., Thévenon, E., Chahtane, H., Warthmann, N., Melkonian, M., Zhang, Y., Ka-Shu Wong, G., **Weigel, D.**, Parcy, F., and Dumas, R. (2014) A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity. Science *343*, 645-648.
201. Ho, W. H. H., and **Weigel, D.** (2014) Structural features determining flower-promoting activity of FLOWERING LOCUS T. Plant Cell *26*, 552-564.
202. Fitz Gerald, J. N., Carlson, A. L., Smith, E., Maloof, J., **Weigel, D.**, Chory, J., Borevitz, J. O., and Swanson, R. J. (2014) New *Arabidopsis* advanced intercross recombinant inbred lines (Van-0 X Col-0) reveal female control of nonrandom mating. Plant Physiol. *165*, 175-185.
203. Muralidharan, S., Box, M. S., Sedivy, E. L., Wigge, P. A., **Weigel, D.**, and Rowan, B. A. (2014) Different mechanisms for *Arabidopsis thaliana* hybrid necrosis cases inferred from temperature responses. Plant Biol. *16*, 1033-1041.

204. Sharma, E., Künstner, A., Fraser, B. A., Zipprich, G., Kottler, V. A., Henz, S. R., **Weigel, D.**, and Dreyer, C. (2014) Transcriptome assemblies for studying sex-biased gene expression in the guppy, *Poecilia reticulata*. BMC Genomics *15*, 400.
205. Dinh, T. T., Gao, L., Liu, X., Li, D., Li, S., Zhao, Y., O'Leary, M., Le, B., Schmitz, R. J., Manavella, P., Li, S., **Weigel, D.**, Pontes, O., Ecker, J. R., and Chen, X. (2014) DNA topoisomerase 1alpha promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in *Arabidopsis*. PLoS Genet. *10*, e1004446.
206. Todesco, M., Kim, S.-T., Chae, E., Bomblies, K., Smith, L. M., **Weigel, D.***, and Laitinen, R. A. E. (2014) Activation of the *Arabidopsis thaliana* immune system by combinations of common *ACD6* alleles. PLoS Genet. *10*, e1004459. *corresponding author.
207. Dettmer, J., Ursache, R., Campilho, A., Miyashima, S., Belevich, I., O'Regan, S., Mullendore, D. L., Yadav, S. R., Lanz, C., Schneeberger, K., **Weigel, D.**, Stierhof, Y.-D., Moritz, T., Knoblauch, M., Jokitalo, E., and Helariutta, Y. (2014) CHOLINE TRANSPORTER LIKE1 (CHER1) is required for sieve plate development to mediate long distance cell-to-cell communication. Nat. Commun. *10*,4276.
208. Bolger A., Scossa, F., Bolger, M., Lanz, C., Maumus, F., Tohge, T., Quesneville, H., Alseekh, S., Sørensen, I., Lichtenstein, G., Fich, E. A., Conte, M., Keller, K., Schneeberger, K., Schwacke, R. Osorio, S., Alves Aflitos, S., Schijlen, E., Jiménez-Gomez, J., Kimura, S. Kumar, R., Koenig, D., Headland, L., Maloof. J. N., Sinha, N., Van Ham, R., Klein Lankhorst, R., Mao, L., Arsova, B., Fei, Z., Rose, J. K. C., Zamir, D., Carrari, F., Giovannoni, J. J., **Weigel, D.**, Usadel, B., and Fernie, A. R. (2014) The genome of the highly stress tolerant wild species tomato *Solanum pennellii*. Nat. Genet. *46*, 1034-1038.
209. Ågren, J. A., Wang, W., Koenig, D., Neuffer, B., **Weigel, D.**, and Wright, S. I. (2014) Mating system shifts and transposable element evolution in the plant genus *Capsella*. BMC Genomics *15*, 602.
210. Weßling, R., Epple, P. M., Altmann, S., He, Y., Yang, L., Henz, S. R., McDonald, M., Wiley, K., Bader, K. C., Gläßer, C., Mukhtar, M. S., Haigis, S., Ghamsari, L., Stephens, A. E., Ecker, J. R., Vidal, V., Jones, J. D. G., Mayer, K. F. X., Ver Loren van Themaat, E., **Weigel, D.**, Schulze-Lefert, P., Dangl, J. L., Panstruga, R., and Braun, P. (2014) Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. Cell Host Microbe *16*, 364–375.
211. Köster, T., Meyer, K., Weinholdt, C., Smith, L. M., Lummer, M., Speth, C., Grosse, I., **Weigel, D.,** and Staiger, D. (2014) Regulation of pri-miRNA processing by the hnRNP-like protein AtGRP7 in *Arabidopsis*. Nucleic Acids Res. *42*, 9925-9936.
212. Lim, E.-C., Müller, J., Hagmann, J., Henz, S. R., Kim, S.-T., and **Weigel, D.** (2014) Trowel: a fast and accurate error correction module for Illumina sequencing reads. Bioinformatics *15*, 3264-3265.
213. Heyndrickx, K. S., Van de Velde, J., Wang, C., **Weigel, D.**, and Vandepoele, K. (2014) A functional and evolutionary perspective on transcription factor binding in *Arabidopsis thaliana*. Plant Cell, *26*, 3894-3910.
214. Rubio-Somoza, I., Zhou, C.-M., Confraria, A., Martinho, C., von Born, P., Baena-Gonzalez, E., Wang, J.-W., and **Weigel, D.** (2014) Temporal control of leaf complexity by miRNA-regulated licensing of protein complexes. Curr. Biol. *24*, 2714–2719.

215. Seymour, D. K., Koenig, D., Hagmann, J., Becker, C., and **Weigel, D.** (2014) Evolution of DNA methylation patterns in the Brassicaceae is driven by differences in genome organization. PLoS Genet. *10*, e1004785.
216. Chae, E., Bomblies, K., Kim, S.-T., Karelina, D., Zaidem, M., Ossowski, S., Martin Pizarro, C., Laitinen, R. A. E., Rowan, B. A., Tenenboim, H., Lechner, S., Demar, M., Habring-Müller, A., Lanz, C., Rätsch, G., and **Weigel, D.** (2014) Species-wide genetic incompatibility analysis identifies immune genes as hotspots of deleterious epistasis. Cell *159*, 1341-1351.
217. Alcázar, R., von Reth, M., Bautor, J., Chae, E., **Weigel, D.**, Koornneef, M., and Parker, J. E. (2014) A complex resistance gene locus underlying immune-related hybrid incompatibility and its occurrence in natural *Arabidopsis thaliana* populations. PLoS Genet. *10*, e1004848.
218. Wang, C., Liu, C., Schwab, R., Becker, C., Lanz, C., and **Weigel, D.** (2015) Genome-wide analysis of local chromatin packing in *Arabidopsis thaliana*. Genome Res. *25*, 246-256.
219. Martinho, C., Confraria, A., Elias, C., Crozet, P., Rubio-Somoza, I., **Weigel, D.**, and Baena-Gonzalez, E. (2015) Dissection of miRNA pathways using *Arabidopsis* mesophyll protoplasts. Mol. Plant *8*, 261-275.
220. Geißler, K., Eschen-Lippold, L., Naumann, K., Schneeberger, K., **Weigel, D.**, Scheel, D., Rosahl, S., and Westphal, L. (2015) Mutations in *Enhanced Disease Resistance1* (*EDR1*) alter the response of *Arabidopsis thaliana* to *Phytophthora infestans* and the bacterial PAMPs flg22 and elf18. Mol. Plant Microbe Interact *28*, 122-133.
221. Fraser, B. A., Künstner, A., Reznick, D. N., Dreyer, C., and **Weigel, D.** (2015) Population genomics of natural and experimental populations of guppies (*Poecilia reticulata*). Mol. Ecol. *24*, 389-408.
222. Salomé, P. A. & **Weigel, D.** (2015) Plant genomic archaeology: whole-genome sequencing reveals the pedigree of a classical trisomic line. G3 *5*, 253-259.
223. Smith, L. M., Burbano, H. A., Wang, X., Fitz, J., Wang, G., Ural-Blimke, Y., & **Weigel, D.** (2015) Diversity and divergence of miRNAs and miRNA targets in the Camelineae. Plant J. *81*, 597-610.
224. Hagmann, J., Becker, C., Müller, J., Stegle, O., Meyer, R., Wang, G., Schneeberger, K., Fitz, J., Altmann, T., Bergelson, J., Borgwardt, K., and **Weigel, D.** (2015) Century-scale methylome stability in a recently diverged *Arabidopsis thaliana* lineage. PLoS Genet. *11*, e1004920.
225. Rowan, B. A., Patel, V., **Weigel, D.**, and Schneeberger, K. (2015) Rapid and inexpensive whole-genome genotyping-by-sequencing for crossover localization and fine-scale genetic mapping. G3 *5*, 385-398.
226. Schneeberger, K., Willing, E.-M., Rawat, V., Mandáková, T., Maumus, F., Velikkakam James, G., Nordström, K., Becker, C., Warthmann, N., Chica, C., Szarzynska, B., Zytnicki, M., Albani, M., Kiefer, C., Bergonzi, S., Castaings, L., Mateos, J., Berns, M., Bujdoso, N., Piofczyk, T., de Lorenzo, L., Barrero-Sicilia, C., Mateos, I., Piednoël, M., Hagmann, J., Chen-Min-Tao, R., Iglesias-Fernández, R., Schuster, S., Alonso-Blanco, C., Roudier, F., Carbonero, P., Paz-Ares, J., Davis, S., Pecinka, A., Quesneville, H., Colot, V., Lysak, M., **Weigel, D.**, and Coupland, G. (2015) Lack of symmetric CG methylation and long-lasting retrotransposon activity have shaped the genome of *Arabis alpina*. Nat. Plants *1*, 14023.
227. Lu, X., Dittgen, J., Piślewska-Bednarek, M., Molina, A., Schneider, B., Svatoš, A., Schneeberger, K., **Weigel, D.**, Bednarek, P., and Schulze-Lefert, P. (2015) Mutant allele-

specific uncoupling of PENETRATION3 functions reveals engagement of the ATP-binding cassette transporter in distinct tryptophan metabolic pathways. Plant Physiol. *168*, 814-827.

228. Warren, R. L., Keeling, C. I., Yuen, M. M. S., Raymond, A., Taylor, G. A., Vandervalk, B. P., Paulino, D., Robertson, G., Yang, C., Hoffmann, M., **Weigel, D.**, Ritland, C., Isabel, N., Jaquish, B., Yanchuk, A., Bousquet, J., Jone, S. J. M., MacKay, J., Birol, I., and Bohlmann, J. (2015) Improved white spruce (*Picea glauca*) genome assemblies and annotation of large gene families of conifer defense metabolism. Plant J. *83*, 189-212.
229. Busoms, S., Teres, J., Huang, X.-Y., Bomblies, K., Danku, J., Douglas, A., **Weigel, D.**, Poschenrieder, C., and Salt, D. E. (2015) Salinity is an agent of divergent selection driving local adaptation of *Arabidopsis thaliana* to coastal habitats. Plant Physiol. *168*, 915-929.
230. Kottler, V. A., Künstner, A., Koch, I., Flötenmeyer, M., Langenecker, T., Hoffmann, M., Sharma, E., **Weigel, D.**, and Dreyer, C. (2015) Adenylate cyclase 5 is required for melanophore and male pattern development in the guppy (*Poecilia reticulata*). Pigment Cell Melanoma Res. *28*, 545-558.
231. Rawat, V., Abdelsamad, A., Pietzenuk, B., Seymour, D., Koenig, D., **Weigel, D.**, Pecinka, A., and Schneeberger, K. (2015) Improving the annotation of *Arabidopsis lyrata* using RNA-seq data. PLoS ONE *10*, e0137391.
232. Lutz, U., Posé, D., Pfeifer, M., Gundlach, H., Hagmann, J., Wang, C., **Weigel, D.**, Mayer, K. F. X., Schmid, M., and Schwechheimer, C. (2015) Modulation of ambient temperature-dependent flowering in *Arabidopsis thaliana* by natural variation of *FLOWERING LOCUS M*. PLoS Genet. *11*, e1005588.
233. Woodson, J. D., Joens, M. S., Sinson, A. S., Gilkerson, J., Salomé, P. A., **Weigel, D.,** Fitzpatrick, J. A., and Chory, J. (2015) Ubiquitin facilitates a quality control pathway that removes damaged chloroplasts. Science *350*, 450-454.
234. Venturelli, S., Belz, R. G., Kämper, A., Berger, A., von Horn, K., Wegner, A., Böcker, A., Zabulon, G., Langenecker, T., Kohlbacher, O., Barneche, F., **Weigel, D.**, Lauer, U. M., Bitzer, M., Becker, C. (2015) Plants release precursors of potent histone deacetylase inhibitors to suppress growth of competitors. Plant Cell *11*, 3175-3189.
235. Agler, M. T., Ruhe, J., Morhenn, C., Kim, S.-T., **Weigel, D.**, and Kemen, E. M. (2016) Microbial hub taxa link host and abiotic factors to plant microbiome variation. PLoS Biol. *14*, e1002352.
236. Rigal, M. Becker, C., Pélissier, T., Pogorelcnik, R., Devos, J., Ikeda, Z., **Weigel, D.**, and Mathieu, O. (2016) Epigenome confrontation triggers immediate reprogramming of DNA methylation and transposon silencing in *Arabidopsis thaliana* F1 epihybrids. Proc. Natl. Acad. Sci. USA *113*, E2083-E2092.
237. Venturelli, S., Petersen, S., Langenecker, T., **Weigel. D.**, Lauer, U. M., and Becker, C. (2016) Allelochemicals of the phenoxazinone class act at physiologically relevant concentrations. Plant Signal Behav. *11*, e1176818.
238. Liu, C., Wang, C., Wang, G., Becker, C., Zaidem, M., and **Weigel, D**. (2016) Genome-wide analysis of chromatin packing in *Arabidopsis thaliana* at single-gene resolution. Genome Res. *26*, 1057-1068.
239. Wibowo, A.*, Becker, C.*, Marconi, G., Dürr, J., Price, J., Hagmann, J., Papareddy, R., Putra, H., Kageyama, J., Becker, J., **Weigel, D.**, and Gutierrez-Marcos, J. (2016) Hyperosmotic stress memory in *Arabidopsis* is mediated by distinct epigenetically labile

sites in the genome and is restricted in the male germline by DNA glycosylase activity. eLife *5*, e13546. *co-first authors; C.B. Weigel lab member.

240. The 1001 Genomes Consortium (2016) 1,135 genomes reveal the global pattern of polymorphism in *Arabidopsis thaliana*. Cell *166*, 481-491. (D. Weigel & M. Nordborg, corresponding authors).
241. Kawakatsu, K., Huang, S.-s. C., Jupe, F., Sasaki, E., Schmitz, R. J., Urich, M. A., Castanon, R., Nery, J. R., Barragan, C., He, Y., Chen, H., Dubin, M., Lee, C.-R., Wang, C., Bemm, F., Becker, C., O'Neil, R., O'Malley, R. C., Quarless, D. X., The 1001 Genomes Consortium, Schork, N. J., **Weigel, D.**, Nordborg, M., and Ecker, J. R. (2016) Epigenomic diversity in a global collection of *Arabidopsis thaliana* accessions. Cell *166*, 492-505.
242. Iakovidis, M., Teixeira, P. J. P. L., Exposito-Alonso, M., Cowper, M. G., Law, T. F., Liu, Q., Vu, M. C., Dang, T. M., Corwin, J. A., **Weigel, D.**, Dangl, J. L., and Grant, S. R. (2016) Effector triggered immunity in *Arabidopsis thaliana* is a quantitative trait. Genetics *204*, 337-353.
243. Novikova, P. Y., Hohmann, N., Nizhynska, V., Tsuchimatsu, T., Ali, J., Muir, G., Guggisberg, A., Paape, T., Schmid, K. J., Fedorenko, O. M., Holm, S., Säl, T., Schlötterer, C., Marhold, K., Widmer, A., Sese, J., Shimizu, K. K., **Weigel, D.**, Krämer, U., Koch, M. A., and Nordborg, M. (2016) Sequencing of the genus *Arabidopsis* reveals a complex history of non-bifurcating speciation and abundant trans-specific polymorphism. Nat. Genet. *48*, 1077-1082.
244. Seymour, D. K., Chae, E. Grimm, D. G., Martín Pizarro, C., Habring-Müller, A., Vasseur, F., Rakitsch, B., Borgwardt, K. M., Koenig, D., and **Weigel, D.** (2016) The genetic architecture of non-additive inheritance in *Arabidopsis thaliana* hybrids. Proc. Natl. Acad. Sci. USA *113*, E7317-E7326.
245. Dueck, A., Evers, M., Henz, S. R., Unger, K., Eichner, N., Merkl, R., Berezikov, E., Engelmann, J. C., **Weigel, D.**, Wenzl, S., and Meister, G. (2016) Gene silencing pathways found in the green alga *Volvox carteri* reveal insights into evolution and origins of small RNA systems in plants. BMC Genomics *17*, 853.
246. Świadek, M., Proost, S., Sieh, D., Yu, J., Todesco, M., Rodriguez Cubillos, A. E., Plötner, B., Nikoloski, Z., Chae, E., Jorzig, C., Giavalisco, P., Fischer, A., Schröder, F., Kim, S.-T., **Weigel, D.**, and Laitinen, R. A. E. (2017) Novel allelic variants in *ACD6* cause hybrid necrosis in a local collection of *Arabidopsis thaliana*. New Phytol. *213*, 900-915.
247. Nam, Y. J., Herman, D., Blomme, J., Chae, E, Kojima, M., Coppens, F., Storme, V., Van Daele, T., Dhondt, S., Sakakibara, H., **Weigel, D.**, Inzé, D., and Gonzalez, N. (2017) Natural variation of molecular and morphological gibberellin responses. Plant Physiol. *173*, 703-714.
248. Seren, Ü., Grimm, D. G., Fitz, J., **Weigel, D.**, Nordborg, M., Borgwardt, K. M., and Korte, A. (2017) AraPheno: A public database for *Arabidopsis thaliana* phenotypes. Nucleic Acids. Res. *45*, D1054-D1059.
249. Mable, B., Hagmann, J., Kim, S.-T., Adam, A., Kilbride, E., **Weigel, D.**, and Stift, M. (2017) What causes mating system shifts in plants? *Arabidopsis lyrata* as a case study. Heredity *118*, 52-63.
250. Künstner, A., Hoffmann, M., Fraser, B. A., Kottler, V. A., Sharma, E., **Weigel, D.**, and Dreyer, C. (2017) The genome of the Trinidadian guppy, *Poecilia reticulata*, and variation in the Guanapo population. PLoS ONE *11*, e0169087.

251. Grimm, D. G., Roqueiro, D., Salomé, P. A., Kleeberger, S., Greshake, B., Zhu, W., Liu, C., Lippert, C., Stegle, O., Schölkopf, B., **Weigel, D.**, and Borgwardt, K. M. (2017) easyGWAS: A cloud-based platform for comparing the results of genome-wide association studies. Plant Cell *29*, 5-19.
252. Vanhaeren, H., Nam, Y.-J., De Milde, L., Chae, E., Storme, V., **Weigel, D.**, Gonzalez, N., and Inzé, D. (2017) Forever Young: the role of ubiquitin receptor DA1 and E3 Ligase BIG BROTHER in controlling leaf growth and development. Plant Physiol. *173*, 1269-1282.
253. Catoni, M., Griffiths, J., Dapp, M., Zabet, N. R., Lieberman-Lazarovich, M., Becker, C., **Weigel, D.**, and Paszkowski, J. (2017) DNA sequence properties that predict susceptibility to epiallelic switching. EMBO J. *36*, 617-628.
254. Lee, C.-R., Svardal, H., Farlow, A., Exposito-Alonso, M., Ding, W., Novikova, P., Alonso-Blanco, C., **Weigel, D.**, and Nordborg, M. (2017) On the post-glacial spread of human commensal *Arabidopsis thaliana*. Nat. Commun. *8*, 14458.
255. Kasulin, L., Rowan, B., León, R. J., Schuenemann, V. J., **Weigel, D.**, and Botto J. F. (2017) A single haplotype hyposensitive to light and requiring strong vernalization dominates *Arabidopsis thalian*a populations in Patagonia, Argentina. Mol. Ecol. *26*, 3389-3404.
256. Soto-Suárez, M., Baldrich, P., **Weigel, D.**, Rubio-Somoza, I., and San Segundo, B. (2017) The Arabidopsis miR396 mediates pathogen-associated molecular pattern-triggered immune responses against fungal pathogens. Sci Rep. *7*, 44898.
257. Nekrasov, V., Wang, C., Win, J., Lanz, C., **Weigel, D.**, and Kamoun, S. (2017) Rapid generation of a transgene-free powdery mildew resistant tomato by genome deletion. Sci Rep. *7*, 482.
258. Plötner, B., Nurmi, M., Fischer, A., Watanabe, M., Schneeberger, K., Holm, S., Vaid, N., Walther, D., Schöttler, M. A., Hoefgen, R., **Weigel, D.**, and Laitinen, R. A. E. (2017) Chlorosis caused by two recessively interacting genes reveals a role of RNA helicase in hybrid breakdown in *Arabidopsis thaliana*. Plant J. *91*, 251-262.
259. Tran, D. T. N., Chung, E. H., Habring-Müller, A., Demar, M., Schwab, R., Dangl, J. L., **Weigel, D.***, and Chae, E.* (2017) Activation of a plant NLR complex through heteromeric association with an autoimmune risk variant of another NLR. Curr. Biol. *27*, 1148-1160. *corresponding authors.
260. Daccord, N., Celton, J.-M., Linsmith, G., Becker, C., Choisne, N., Schijlen, E., van de Geest, H., Bianco, L., Micheletti, D., Velasco, R., Di Pierro, E. A., Gouzy, J., Rees, D. J. G., Muranty, H., Durel, C.-E., Laurens, F., Lespinasse, Y., Gaillard, S., Aubourg, S., Quesneville, H., **Weigel, D.**, van de Weg, E., Troggio, M., and Bucher, E. (2017) High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. Nat. Genet. *49*, 1099-1106.
261. Ikeda, Y., Pélissier, T., Bourguet, P., Becker, C., Pouch-Pélissier, M. N., Pogorelcnik, R., Weingartner, M., **Weigel, D.**, Deragon, J. M., and Mathieu, O. (2017) *Arabidopsis* proteins with a transposon-related domain act in gene silencing. Nat. Commun. *8*, 15122.
262. Swarts, K., Gutaker, R. M., Benz, B., Blake, M., Bukowski, R., Holland, J., Kruse-Peeples, M., Lepak, N., Prim, L., Romay, M. C., Ross-Ibarra, J., Sanchez-Gonzalez, J. d. J., Schmidt, C., Schuenemann, V. J., Krause, J., Matson, R. G., **Weigel, D.**, Buckler, E. S., and Burbano, H. A. (2017) Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. Science *357*, 512-515.

263. Xin, R., Zhu, L., Salomé, P. A., Mancini, E., Marshall, C., Harmon, F. G., Yanovsky, M. J., **Weigel, D.**, and Huq, E. (2017) SPLICING FACTOR FOR PHYTOCHROME SIGNALING promotes photomorphogenesis by regulating pre-mRNA splicing in Arabidopsis. Proc. Natl. Acad. Sci. USA *114*, E7018-E7027.
264. Zhu, W., Hu, B., Becker, C., Doğan, E. S., Berendzen, K. W., **Weigel, D.***, and Liu, C.* (2017) Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific *Arabidopsis* hybrid. Genome Biol. *18*, 157. *corresponding authors.
265. Liu, C.*, Cheng, Y.-J., Wang, J.-W., and **Weigel, D.*** (2017) Prominent topologically associated domains differentiate global chromatin packing in rice from *Arabidopsis*. Nat. Plants *3*, 742-748. *corresponding authors.
266. Alhajturki, D., Muralidharan, S., Nurmi, M., Rowan, B. A., Lunn, J., Boldt, H., Salem, M., Alseekh, S., Jorzig, C., Feil, R., Giavalisco, P., Fernie, A., **Weigel, D.**, and Laitinen, R. A. E. (2018) Dose-dependent interactions between two loci trigger altered shoot growth in BG-5 x Krotzenburg-0 (Kro-0) hybrids of *Arabidopsis thaliana*. New Phytol. *217*, 392-406.
267. Salvador-Guirao, R., Baldrich, P., **Weigel, D.**, Rubio-Somoza, I., and San Segundo, B. (2018) The microRNA miR773 is involved in the Arabidopsis immune response to fungal pathogens. Mol. Plant Microbe Inter. *31*, 249-259.
268. Togninalli, M., Seren, Ü., Meng, D., Fitz, J., Nordborg, M., **Weigel, D.**, Borgwardt, K., Korte, A., and Grimm, D. (2018) The AraGWAS Catalog: A curated and standardized *Arabidopsis thaliana* GWAS catalog. Nucleic Acids Res. *46*, D1150-D1156.
269. Lang, P. L. M., Christie, M. D., Dogan, E. S., Schwab, R., Hagmann, J., Van de Weyer, A.-L., Scacchi, E., and **Weigel, D.** (2018) A role for the F-box protein HAWAIIAN SKIRT in plant microRNA function. Plant Physiol. *176*, 730-741.
270. Exposito-Alonso, M. A., Vasseur, F., Ding, W., Wang, G., Burbano, H. A., and **Weigel, D.** (2018) Genomic basis and evolutionary potential for extreme drought adaptation in *Arabidopsis thaliana*. Nat. Ecol. Evol. *2*, 352-358.
271. Alexandre, C. M., Urton, J. R., Jean-Baptiste, K., Huddleston, J. L., Dorrity, M. W., Cuperus, J. C., Sullivan, A. M., Bemm, F., Jolic, D., Arsovski, A. A., Thompson, A., Nemhauser, J. L., Fields, S., **Weigel, D.**, Bubb, K. L., and Queitsch, C. (2018) Complex relationships between chromatin accessibility, sequence divergence, and gene expression in *A. thaliana*. Mol. Biol. Evol. *35*, 837-854.
272. Stein, J. C., Yu, Y., Copetti, D., Zwickl, D. J., Zhang, L., Zhang, C., Chougule, K., Gao, D., Iwata, A., Goicoechea, J. L., Wei, S., Wang, J., Liao, Y., Wang, M., Jacquemin, J., Becker, C., Kudrna, D., Zhang, J., Londono, C. E. M., Song, X., Lee, S., Sanchez, P., Zuccolo, A., Ammiraju, J. S. S., Talag, J., Danowitz, A., Rivera, L. F., Gschwend, A. R., Noutsos, C., Wu, C. C., Kao, S. M., Zeng, J. W., Wei, F. J., Zhao, Q., Feng, Q., El Baidouri, M., Carpentier, M. C., Lasserre, E., Cooke, R., Rosa Farias, D. D., da Maia, L. C., Dos Santos, R. S., Nyberg, K. G., McNally, K. L., Mauleon, R.Alexandrov, N., Schmutz, J., Flowers, D., Fan, C., **Weigel, D.**, Jena, K., K., Wicker, T., Chen, M., Han, B., Henry, R., Hsing, Y. C., Kurata, N., de Oliveira, A. C., Panaud, O., Jackson, S. A., Machado, C. A., Sanderson, M. J., Long, M., Ware, D., and Wing, R. A. (2018) Genomes of 13 domesticated and wild rice relatives unveil genetic conservation, turnover and innovation across the genus *Oryza*. Nat. Genet. *50*, 285-296.

273. Michael, T. P., Jupe, F., Bemm, F., Motley, S. T., Sandoval, J. P., Lanz. C., Loudet, O., **Weigel, D.,** and Ecker, J. R. (2018) High contiguity *Arabidopsis thaliana* genome assembly with a single nanopore flow cell. Nat. Commun. 9, *541*.
274. Exposito-Alonso, M., Becker, C., Schuenemann, V. J., Reitter, E., Setzer, C., Slovak, R., Brachi, B., Hagmann, J., Grimm, D. G., Jiahui, C., Busch, W., Bergelson, J., Ness, R. W., Krause, J., Burbano, H. A., and **Weigel, D.** (2018) The rate and potential relevance of new mutations in a colonizing plant lineage. PLoS Genet. *14*, e1007155.
275. Tabas-Madrid, D., Méndez-Vigo, B., Arteaga, N., Marcer, A., Pascual-Montano, A., **Weigel, D.**, Picó, X. F., and Alonso-Blanco, C. (2018) Genome-wide signatures of flowering adaptation to climate temperature: regional analyses in a highly diverse native range of *Arabidopsis thaliana*. Plant Cell Environ. *41*, 1806-1820.
276. Vasseur, F., Exposito-Alonso, M., Ayala-Garay, O., Wang, G., Enquist, B. J., Vile, D., Violle, C., and **Weigel, D.** (2018) Adaptive diversification of growth allometry in the plant *Arabidopsis thaliana*. Proc. Natl. Acad. Sci. USA *115*, 3416–3421.
277. Karasov, T. L., Almario, J., Friedemann, C., Ding, W., Giolai, M., Heavens, D., Kersten, S., Lundberg, D. S., Neumann, M., Regalado, J., Neher, R. A., Kemen, E., and **Weigel, D.** (2018) *Arabidopsis thaliana* and *Pseudomonas* pathogens exhibit stable associations over evolutionary time scales. Cell Host Microbe *24*, 168-179.
278. Vasseur, F., Wang, G., Bresson, J., Schwab, R., and **Weigel, D.** (2018) Image-based methods for phenotyping growth dynamics and fitness components in *Arabidopsis thaliana*. Plant Methods *14*, 65.
279. Wu, R., Lucke, M., Jang, Y.-t., Zhu, W., Symeonidi, E., Wang, C., Fitz, J., Xi, W., Schwab, R., and **Weigel, D.** (2018) An efficient CRISPR vector toolbox for engineering large deletions in *Arabidopsis thaliana*. Plant Methods *14*, 63.
280. Wibowo, A., Becker, C., Durr, J., Price, J., Staepen, S., Hilton, S., Putra, H., Papareddy, R., Saintain, Q., Harvey, S., Bending, G. D., Schulze-Lefert, P., **Weigel, D.***, and Gutierrez-Marcos, J.* (2018) Partial maintenance of organ-specific epigenetic marks during plant asexual reproduction leads to heritable phenotypic variation. Proc. Natl. Acad. Sci. USA *115*, E9145-E9152. *corresponding authors.
281. Zhu, W., Zaidem, M., Van de Weyer, A.-L., Gutaker, R. M., Chae, E., Kim, S.-T., Bemm, F., Li, L., Schwab, R., Unger, F., Beha, M. J., Demar, M., and **Weigel, D.** (2018) Modulation of ACD6 dependent hyperimmunity by natural alleles of an *Arabidopsis thaliana* NLR resistance gene. PLoS Genet. *14*, e1007628.
282. Tedeschi, F., Rizzo, P., Huong, B., Czihal, A., Rutten, T., Altschmied, L., Scharfenberg, S., Grosse, I., Becker, C., **Weigel, D.**, Bäumlein, H., and Kuhlmann, M. (2019) EFFECTOR OF TRANSCRIPTION factors are novel plant-specific regulators of genomic DNA methylation in *Arabidopsis*. New Phytol. *221*, 261-278.
283. Wan, W.-L., Zhang, L., Pruitt, R., Zaidem, M., Brugman, R., Ma, X., Krolf, E., Grossmann, G., Kilian, J., Stahl, M., Shan, L., Zipfel, C., van Kan, J. A. L., Hedrich, R., **Weigel, D.**, Gust, A. A., and Nürnberger, T. (2019) Comparing *Arabidopsis* receptor kinase and receptor protein-mediated immune signaling reveals BIK1-dependent differences. New Phytol. *221*, 2080-2095.
284. Weng, M.-L., Becker, C., Hildebrandt, J., Rutter, M. T., Shaw, R. G., **Weigel, D.,** and Fenster, C. B. (2019) Fine-grained analysis of spontaneous mutation spectrum and frequency in *Arabidopsis thaliana*. Genetics *211*, 2703-2714.

285. Seymour, D. K., Chae, E., Ariöz, B. I., Koenig, K., and **Weigel, D.** (2019) Transmission ratio distortion is frequent in *Arabidopsis thaliana* controlled crosses. Heredity *122*, 294-304.
286. Koenig, D., Hagmann, J., Li, R., Bemm, F., Slotte, T., Neuffer, B., Wright, S. I., and **Weigel, D.** (2019) Long-term balancing selection drives evolution of immunity genes in *Capsella*. eLife *8*, e43606.
287. Vasseur, F., Fouqueau, L., de Vienne, D., Nidelet, T., Violle, C., and **Weigel, D.** (2019) Non-linear phenotypic variation uncovers the emergence of heterosis in *Arabidopsis thaliana*. PLoS Biol. *17*, e3000214.
288. Fang, X., Ishikawa, R., Wang, L., Li, Y., Liu, F., Rowan, B. A., **Weigel, D.**, Li, P., and Dean, C. (2019) *Arabidopsis* FLL2 promotes liquid-liquid phase separation of polyadenylation complexes. Nature *569*, 265-226.
289. Yoo, C. Y., Pasoreck, E. K., Wang, H., Cao, J., Decker, P., **Weigel, D.**, and Chen, M. (2019) Phytochrome activates the plastid-encoded RNA polymerase for chloroplast biogenesis via nucleus-to-plastid signaling. Nat. Commun. *10*, 2629.
290. Yang, E. J., Yoo1, C. Y., Liu, J., Wang, H., Cao, J., Li, F.-W., Pryer, K. M., Sun, T.-P., **Weigel, D.**, Zhou, P., and Chen, M. (2019) NCP activates chloroplast transcription by controlling light-dependent dual nuclear and plastidial switches. Nat. Commun. *10*, 2630.
291. Barragan, C. A., Wu, R., Kim, S.-T., Xi, W., Habring, A., Hagmann, J., Van de Weyer, A.-L., Zaidem, M., Ho, W. W. H., Wang, G., Bezrukov, I., **Weigel, D.***, and Chae, E.* (2019) RPW8/HR repeats control NLR activation in *A. thaliana*. PLoS Genet. *15*, e1008313. *corresponding authors.
292. Van de Weyer, A.-L., Monteiro, F., Furzer, O. J., Nishimura, M. T., Cevik, V., Witek, K., Jones, J. D. G., Dangl, J. L., **Weigel, D.***, and Bemm, F. (2019) A species-wide inventory of NLR genes and alleles in *Arabidopsis thaliana*. Cell *178*, 1260-1272.e14. *Lead contact.
293. Lange, H., Ndecky, S. Y. A., Gomez-Diaz, C., Pflieger, D., Butel, N., Zumsteg, J., Kuhn, L., Piermaria, C., Chicher, J., Christie, M., Karaaslan, E. S., Lang, P. L. M., **Weigel, D.**, Vaucheret, H., Hammann, P., and Gagliardi, D. (2019) RST1 and RIPR connect the cytosolic RNA exosome to the SKI complex in *Arabidopsis*. Nat. Commun. *10*, 3871.
294. Exposito-Alonso, M. A., 500 Genomes Field Experiment Team, Burbano, H. A., Bossdorf, O., Nielsen, R., and **Weigel, D.** (2019) Natural selection on the *Arabidopsis thaliana* genome in present and future climates. Nature *573*, 126-129.
295. Rowan, R. A., Heavens, D., Feuerborn, T. R., Tock, A. J., Henderson, I. R., and **Weigel, D.** (2019) An ultra high-density *Arabidopsis thaliana* crossover map that refines the influences of structural variation and epigenetic features. Genetics 213, *771-787*.
296. Kreiner, J. M., Giacomini, D., Bemm, F., Waithaka, B., Regalado, J., Lanz, C., Hildebrandt, J., Sikkema, P. H., Tranel, P. J., **Weigel, D.**,* Stinchcombe, J. R., Wright, S. I. (2019) Multiple modes of convergent adaptation in the spread of glyphosate-resistant *Amaranthus tuberculatus*. Proc. Natl. Acad. Sci. USA *15*, 21076-21084. *corresponding author.
297. Togninalli, M., Seren, Ü., Freudenthal, J., Monroe, J., Dazhe, M., Nordborg, M., **Weigel, D.**, Borgwardt, K., Korte, A., and Grimm, D. (2020) AraPheno and the AraGWAS Catalog 2020: A major database update including RNA-Seq and knockout mutation data for *Arabidopsis thaliana*. Nucleic Acids Res. *48*, D1063-D1068.

298. Li, L., Habring, A., Wang, K., and **Weigel, D.** (2020) Atypical resistance protein RPW8/HR triggers oligomerization of the NLR immune receptor RPP7 and autoimmunity. Cell Host Microbe *27*, 405-417.
299. Na Ayutthaya, P. P., Lundberg, D., **Weigel. D.**, and Li, L. (2020) Blue Native Polyacrylamide Gel Electrophoresis (BN-PAGE) for the analysis of protein oligomers in plants. Curr. Protoc. Plant Biol. *5*, e20107.
300. Voichek, Y., and **Weigel, D.** (2020) Finding genetic variants underlying phenotypic variation in plants without complete genomes. Nat. Genet. *52*, 534-540.
301. Regalado, J., Lundberg, D. S., Deusch, O., Kersten, S., Karasov, T. L., Poersch, K., Shirsekar, G., and **Weigel, D.** (2020) Combining whole genome shotgun sequencing and rRNA gene amplicon analyses to improve detection of microbe-microbe interaction networks in plant leaves. ISME J. *14*, 2116-2130.
302. Fraser, B. A., Whiting, J. R., Paris, J. R., Weadick, C. J., Parsons, P. J., Charlesworth, D., Bergero, R., Bemm, F., Hoffmann, M., Verena A Kottler, Liu, C., Dreyer, C., and **Weigel, D.** (2020) Improved reference genome uncovers novel sex-linked regions in the guppy (*Poecilia reticulata*). Genome Biol. Evol. *12*, 1789-1805.
303. Montgomery, J. S., Giacomini, D., Waithaka, B., Murphy, B. P., Lanz, C., Campe, R., Lerchl, J., Landes, A., Gatzmann, F., Janssen, A., Antonise, R., Patterson, E., **Weigel, D.**, and Tranel, P. J. (2020) Draft genomes of *Amaranthus tuberculatus*, *Amaranthus hybridus* and *Amaranthus palmeri*. Genome Biol. Evol. *12*, 1988-1993.
304. Antunez-Sanchez, J., Naish, M., Ramirez-Prado. J. S., Ohno, S., Huang, Y., Dawson, A., Opassathian, K., Manza-Mianza, D., Ariel, F., Raynaud, C., Wibowo, A., Daron, J., Ueda, M., Latrasse, D., Slotkin, K., **Weigel, D.**, Benhamed, M., and Gutierrez-Marcos, J. (2020) A new role for histone demethylases in the maintenance of plant genome integrity. eLife *9*, e58533.
305. Barragan, A. C., Collenberg, M., Wang, J., Lee, R. R. Q., Yuan Cher, W., Rabanal, F. A., Ashkenazy, H., **Weigel, D.***, and Chae, E.* (2021) A truncated singleton NLR causes hybrid necrosis in *Arabidopsis thaliana*. Mol. Biol. Evol. *38*, 557-574. *corresponding authors.
306. Montgomery, J., Giacomini, D., **Weigel, D.**, and Tranel, P. (2021) Male-specific Y-chromosomal regions in waterhemp (*Amaranthus tuberculatus*) and Palmer amaranth (*Amaranthus palmeri*). New Phytol. *229*, 3522-3533.
307. Cambiagno, D. A., Giudicatti, A. J., Arce, A. L., Gagliardi, D., Li, L., Yuan, W., Lundberg, D. S., **Weigel, D.**, and Manavella, P. A. (2021) HASTY modulates miRNA biogenesis by linking pri-miRNA transcription and processing. Mol. Plant *14*, 426-439.
308. Symeonidi, E., Regalado, J. Schwab, R., and **Weigel, D.** (2021) CRISPR-finder: A high throughput and cost effective method for identifying successfully edited *A. thaliana* individuals. Quant. Plant Biol. *2*, e1.
309. Milani, A., Lutz, U., Galla, G. Scarabel, L., **Weigel, D.**, and Sattin, M. (2021) Population structure and evolution of resistance to acetolactate synthase (ALS)-inhibitors in *Amaranthus tuberculatus* in Italy. Pest Manag. Sci. *77*, 2971-2980.
310. Ignacio, J. C. I., Zaidem, M., Casal Jr., C., Dixit, S., Kretzschmar, T., Samaniego, J. M., Mendioro, M. S., **Weigel, D.**, and Septiningsih, E. M. (2021) Genetic mapping by sequencing more precisely detects loci responsible for anaerobic germination tolerance in rice. Plants *10*, 705.

311. Kreiner, J. M., Tranel, P. J., **Weigel, D.**, Stinchcombe, J. R., and Wright, S. I. (2021) The genetic architecture and genomic context of glyphosate resistance in *Amaranthus tuberculatus*. Mol. Ecol. *30*, 5373–5389.
312. Whiting, J. R., Paris, J. R., van der Zee, M. J., Parsons, P. J., **Weigel, D.**, and Fraser, B. A. (2021) Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies. PLoS Genet. *17*, e1009566.
313. Lundberg, D. S., Na Ayutthaya, P. P., Strauß, A., Shirsekar, G., Lo, W.-S., Lahaye, T., and **Weigel, D.** (2021) Host-associated microbe PCR (hamPCR) enables convenient measurement of both microbial load and community composition. eLife 10, *e66186*.
314. Pruitt, R. N., Locci, F., Wanke, F. Zhang, L., Saile, S. C., Joe, A., Hua, C., Karelina, D., Fröhlich, K., Wan, W.-L., Hu, M., Rao, S., Stolze, S., Harzen, A., Gust, A. A., Harter, K., Joosten, M. H. A. J., Thomma, B. P. H. K., Zhou, J.-M., Dangl, J. L., **Weigel, D.**, Nakagami, H., Oecking, C., El Kasmi, F., Parker, J. E., and Nürnberger, T. (2021) The EDS1-PAD4-ADR1 node mediates *Arabidopsis* pattern-triggered immunity. Nature *598*, 495-499.
315. Shirsekar, G., Devos, J., Latorre, S. M., Blaha, A., Queiroz Dias. M., González Hernando, A., Lundberg, D. S., Burbano, H. A., Fenster, C. B., and **Weigel, D.** (2021) Multiple sources of introduction of North American *Arabidopsis thaliana* from across Eurasia. Mol. Biol. Evol. *38*, 5328-5344.
316. Vogt, F., Shirsekar, G., and **Weigel, D.** (2022) *vcf2gwas* – Python API for comprehensive GWAS analysis using GEMMA. Bioinformatics *38*, 839-40.
317. Shalev, O., Ashkenazy, H., Neumann, M., and **Weigel, D.** (2022) Commensal *Pseudomonas* protect *Arabidopsis thaliana* from a coexisting pathogen via multiple lineage-dependent mechanisms. ISME J. *16*, 1235-1244.
318. Nunn, A., Rodríguez-Arévalo, I., Tandukar, Z., Frels, K., Contreras-Garrido, A., Carbonell-Bejerano, P., Zhang, P., Ramos-Cruz, D., Jandrasits, K., Lanz, C., Brusa, A., Mirouze, M., Dorn, K., Jarvis, B., Sedbrook, J., Wyse, D. L., Otto, C., Langenberger, D., Stadler, P. F., **Weigel, D.**, Marks, M. D., Anderson, J. A., Becker, C., and Chopra, R. (2022) Chromosome-level *Thlaspi arvense* genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. Plant Biotech. J. *20*, 944-963.
319. Monroe, J. G., Srikant, T., Carbonell-Bejerano, P., Becker, C., Lensink, M., Exposito-Alonso, M., A. Klein, M., Hildebrandt, J., Neumann, M., Kliebenstein, Weng, M.-L., Imbert, E., Ågren, J., Rutter, M. T., Fenster, C. B., and **Weigel, D.** (2022) Mutation bias reflects natural selection in *Arabidopsis thaliana*. Nature *602*, 101-105. (Correction published on July 26, 2023.)
320. Kreiner, J. M., Sandler, G., Stern, A. J. Tranel, P. J., **Weigel, D.**, Stinchcombe, J. R., and Wright, S. I. (2022) Repeated origins, gene flow, and allelic interactions of herbicide resistance mutations in a widespread agricultural weed. eLife *11*, e70242.
321. van der Zee, M. J., Whiting, J. R., Paris, J. R., Bassar, R. D., Travis, J., **Weigel, D.**, Reznick, D. N., and Fraser, B. A. (2022) Rapid genomic convergent evolution in experimental populations of Trinidadian guppies (*Poecilia reticulata*). Ecol. Lett. *6*, 149–161.
322. Shalev, O., Karasov, T., Lundberg, D. S., Ashkenazy, H., Na Ayutthaya, P. P., and **Weigel, D.** (2022) Commensal *Pseudomonas* strains facilitate protective response against pathogens in the host plant. Nat. Ecol. Evol. *6*, 383-396.

323. Fan, L., Fröhlich, K., Melzer, E., Pruitt, R. N., Albert, I., Zhang, L., Joe, A., Hua, Ch, Song, C., Albert, M., Kim, S.-T., **Weigel, D.**, Zipfel, C., Chae, E., Gust, A. A., and Nürnberger, T. (2022) Genotyping-by-sequencing-based identification of *Arabidopsis* pattern recognition receptor RLP32 recognizing proteobacterial translation initiation factor IF1. Nat. Commun. *13*, 1294.
324. Hüther, P., Hagmann, J., Nunn, A., Kakoulidou, I., Pisupati, R., Langenberger, D., **Weigel, D.**, Johannes, F., Schultheiss, S. J., and Becker, C. (2022) MethylScore, a pipeline for accurate and context-aware identification of differentially methylated regions from population-scale plant WGBS data. Quant. Plant Biol. *3*, e19.
325. Wibowo, A. T., Antunez-Sanchez, J., Dawson, A., Price, J., Meehan, C., Wrightsman, T., Collenberg, M., Bezrukov, I., Becker, C., Benhamed, M., **Weigel, D.***, and Gutierrez-Marcos, J.* (2022) Predictable and stable epimutations induced during clonal propagation with embryonic transcription factor. PLoS Genet. *18*, e1010479. *corresponding authors.
326. Kreiner, J., Latorre, S. M., Burbano, H. A., Stinchcombe, J. R., Otto, S. P., **Weigel, D.**, and Wright, S. I. (2022) Rapid weed adaptation and range expansion in response to agriculture over the last two centuries. Science *378*, 1079-1085.
327. Rabanal, F. A., Graeff, M., Lanz, C., Fritschi, K., Llaca, V., Lang, M., Carbonell-Bejerano, P., Henderson, I., and **Weigel, D.** (2022) Pushing the limits of HiFi assemblies reveals centromere diversity between two *Arabidopsis thaliana* genomes. Nucleic Acids Res. *50*, 12309-12327.
328. Lundberg, D. S., de Pedro Jové, R., Pramoj Na Ayutthaya, P., Karasov, T. L., Shalev, O., Poersch, K., Ding, W., Bollmann-Giolai, A., Bezrukov, I., and **Weigel, D.** (2022) Contrasting patterns of microbial dominance in the *Arabidopsis thaliana* phyllosphere. Proc. Natl. Acad. Sci. USA *119*, e2211881119.
329. Srikant, T., Yuan, W., Berendzen, K. W., Contreras Garrido, A., Drost, H.-G., Schwab, R., and **Weigel, D.** (2022) Canalization of genome-wide transcriptional activity in *Arabidopsis thaliana* accessions by MET1-dependent CG methylation. Genome Biol. *23*, 263.
330. Mateos, J. L., Sanchez, S. E., Legris, M., Esteve-Bruna, D., Torchio, J. C., Petrillo, E., Goretti, D., Blanco-Touriñán, N., Seymour, D. K., Schmid, M., **Weigel, D.**, Alabadí, D., and Yanovsky, M. J. (2023) PICLN modulates alternative splicing and ensures adaptation to light and temperature changes in plants. Plant Physiol. *191*, 1036-1051.
331. Arce, A. L., Mencia, R., Cambiagno, D. A., Lang, P. L., Liu, C., Burbano, H. A., **Weigel, D.**, and Manavella, P. A. (2023) Polymorphic Inverted Repeats near coding genes impact chromatin topology and phenotypic traits in *Arabidopsis thaliana*. Cell Rep. *42*, 112029.
332. Kersten, S., Rabanal, F. A., Herrmann, J., Hess, M., Kronenberg, Z. N., Schmid, K., and **Weigel, D.** (2023) Deep haplotype analyses of target-site resistance locus *ACCase* in blackgrass enabled by pool-based amplicon sequencing. Plant Biotech J. *21*, 1240-1253.
333. Kersten, S., Chang, J., Huber, C. D., Voichek, Y., Lanz, C., Hagmaier, T., Lang, P., Lutz, U., Hirschberg, I., Lerchl, J., Porri, A., Van de Peer, Y., Schmid, K., **Weigel, D.**,* and Rabanal, F. A. (2023) Standing genetic variation fuels rapid evolution of herbicide resistance in blackgrass. Proc. Natl. Acad. Sci. USA *120*, e2206808120. *corresponding author.
334. Gu, B., Parkes, T., Rabanal, F., Smith, C., Lua, F.-H., McKenzie, N., Dong, H., **Weigel, D.**, Jones, J. D. G., Cevik, V., and Bevan, M. W. (2023) The integrated LIM-peptidase domain of the CSA1-CHS3/DAR4 paired immune receptor detects changes in DA1 family peptidase inhibitors in Arabidopsis. Cell Host Microbe *31*, 949-961.

335. Wlodzimierz, P., Rabanal, F. A., Burns, R., Naish, M., Primetis, E., Scott, A., Mandáková, T., Gorringe, N., Tock, A. J., Holland, D., Fritschi, K., Habring, A., Lanz, C., Patel, C., Schlegel, T., Collenberg, M., Mielke, M., Nordborg, M., Roux, F., Shirsekar, G., Alonso-Blanco, C., Lysak, M. A., Novikova, P. Y., Bousios, A.*, **Weigel, D.***, and Henderson, I. R.* (2023) Cycles of satellite and transposon evolution in *Arabidopsis* centromeres. Nature *618*, 557-565. *corresponding authors.
336. Yuan, W., Beitel, F., Srikant, T., Bezrukov, I., Schäfer, S., Kraft, R., and **Weigel, D.** (2023) Pervasive under-dominance in gene expression underlying emergent growth trajectories in *Arabidopsis thaliana* hybrids. Genome Biol. *24*, 200.
337. Duque-Jaramillo, A., Ulmer, N., Alseekh, S., Bezrukov, I., Fernie, A. R., Skirycz, A., Karasov, T. L., and **Weigel, D.** (2023) The genetic and physiological basis of *Arabidopsis thaliana* tolerance to *Pseudomonas viridiflava*. New Phytol. *240*, 1961-1975.
338. Wang, M.-Y.*, Chen, J.-B.*, Wu, R.*, Guo, H.-L-, Chen, Y., Li, Z.-J-, Wei, L.-Y., Liu, C., He, S.-F., Du, M.-M., Guo, Y.-L., Peng, Y.-L., Jones, J. D. G., **Weigel, D.**, Huang, J.-H., and Zhu, W-S. (2023) The immune receptor SNC1 monitors helper NLRs targeted by a bacterial effector. Cell Host Microbe *31*, 1792-1803.e7. *co-first authors; R.W. Weigel lab member.
339. Chen, J., Li, L., Kim, J. H., Neuhäuser, B., Wang, M., Thelen, M., Hilleary, R., Chi, Y., Wei, L., Venkataramani, K., Exposito-Alonso, M. A., Liu, C., Keck, J., Barragan, A. C., Schwab, R., Lutz, U., Pei, Z.-M., He, S.-Y., Ludewig, U., **Weigel, D**.*, and Zhu, W.* (2023) Small proteins modulate ion channel-like ACD6 to regulate immunity in *Arabidopsis thaliana*. Mol. Cell *83*,4386-4397.e9. *corresponding authors.
340. Saarenpää, S.*, Shalev, O.*, Ashkenazy, H.*, de Oliveira-Carlos, V., Lundberg, D. S., **Weigel, D.**, and Giacomello, S. (2024) Spatially resolved host-bacteria-fungi interactomes via spatial metatranscriptomics. Nat. Biotech., *published online November 20, 2023*. *co-first authors; O.S. and H.A. Weigel lab members.
341. Barragán, A. C., Collenberg, M., Schwab, R., Kerstens, M., Požárová, D., Bezrukov, I., Bemm, F., Kolář, F., and **Weigel, D.** (2024) Deleterious phenotypes in wild *Arabidopsis arenosa* populations are common and linked to runs of homozygosity. G3 *14*, jkad290.
342. Fernandes, J. B. Naish, M., Lian, Q., Burns, R., Tock, A. J., Rabanal, F. A., Wlodzimierz, P., Habring, A., Nicholas, R. E., **Weigel, D.**, Mercier, R., and Henderson, I. R. (2024) Structural variation and DNA methylation shape the centromere-proximal meiotic crossover landscape in Arabidopsis. Genome Biol. *25*, 30.
343. Contreras-Garrido, A., Galanti, D., Movilli, A., Becker, C., Bossdorf, O., Drost, H.-J., and **Weigel, D.** (2024) Transposon dynamics in the emerging oilseed crop *Thlaspi arvense*. PLoS Genet. *20*, e1011141.
344. Calderón, L.*, Carbonell-Bejerano, P.*, Muñoz., C., Bree, L., Sola, C., Bergamin, D., Tulle, W., Gomez-Talquenca, S., Lanz, C., Royo, C., Ibañez, J., Martinez-Zapater, J. M., **Weigel, D.**, and Lijavetzky, D. (2023) Diploid genome assembly of the Malbec grapevine cultivar enables haplotype-aware analysis of transcriptomic differences underlying clonal phenotypic variation. Hortic. Res. *11*, uhae080. *co-first authors; P.C-B. Weigel lab member.
345. Murray, K. D., Borevitz, J. O., **Weigel, D.**, and Warthmann, N. (2024) Acanthophis: a comprehensive plant hologenomics pipeline. J. Open Source Softw. *9*, 6062.
346. Karasov, T. L. *, Neumann, M., Leventhal, L., Symeonidi, E., Shirsekar, G., Hawks, A., Monroe, G., PATHODOPSIS Team, Expósito Alonso, M., Bergelson, J., **Weigel, D.***, and

Schwab, R. (2024) Continental-scale associations of *Arabidopsis thaliana* phyllosphere members with host genotype and drought. Nat. Microbiol., *accepted in principle*. *corresponding authors.

347. Mencia, R., Arce, A. L., Houriet, C., Xian, W., Contreras, A., Shirsekar, G., **Weigel, D.**, and Manavella, P. A. (2023) Transposon-triggered epigenetic chromatin dynamics modulate EFR-related pathogen response. Nat. Struct. Mol. Biol., *accepted in principle*.

*Preprints*

1. Hagmann, J., Becker, C., Müller, J., Stegle, O., Meyer, R. C., Schneeberger, K., Fitz, J., Altmann, T., Bergelson, J., Borgwardt, K., and **Weigel, D.** (2014) Century-scale methylome stability in a recently diverged *Arabidopsis thaliana* lineage. bioRxiv 009225 (published as article #224).
2. Exposito-Alonso, M., Becker, C., Schuenemann, V. J., Reitter, E., Setzer, C., Slovak, R., Brachi, B., Hagmann, J., Grimm, D. G., Jiahui, C., Busch, W., Bergelson, J., Ness, R. W., Krause, J., Burbano, H. A., and **Weigel, D.** (2016) The rate and potential relevance of new mutations in a colonizing plant lineage. bioRxiv 050203 (published as article #274).
3. Catoni, M., Griffiths, J., Becker, C., Zabet, N. R., Bayon, C., Dapp, M., Lieberman-Lazarovich, M., **Weigel, D.**, and Paszkowski, J. (2016) DNA sequence properties that predict susceptibility to epiallelic switching. bioRxiv 057794 (published as article #253).
4. Alexandre, C. M., Urton, J. R., Jean-Baptiste, K., Dorrity, M. W., Cuperus, J. C., Sullivan, A. M., Bemm, F., Jolic, D., Arsovski, A. A., Thompson, A., Nemhauser, J. L., Fields, S., **Weigel, D.**, Bubb, K. L., and Queitsch, C. (2017) Regulatory DNA in A. thaliana can tolerate high levels of sequence divergence. bioRxiv 104323 (published as article #271).
5. Exposito-Alonso, M., Vasseur F., Ding, W., Wang, G., Burbano, H. A., and **Weigel, D.** (2017) Genomic basis and evolutionary potential for extreme drought adaptation in *Arabidopsis thaliana*. bioRxiv 118067 (published as article #270).
6. Lang, P. L. M., Christie, M. D., Dogan, E., Schwab, R., Hagmann, J., Van de Weyer, A.-L., and **Weigel, D.** (2017) A role for the F-box protein HAWAIIAN SKIRT in plant miRNA function. bioRxiv 123703 (published as article #269).
7. Michael, T. P., Jupe, F., Bemm, F., Motley, S. T., Sandoval, J. P., Lanz. C., Loudet, O., **Weigel, D.,** and Ecker, J. R. (2017) High contiguity *Arabidopsis thaliana* genome assembly with a single nanopore flow cell. bioRxiv 149997 (published as article #273).
8. Seymour, D. K., Chae, E., Ariöz, B. I., Koenig, K., and **Weigel, D.** (2017) The genetic architecture of recurrent segregation distortion in *Arabidopsis thaliana*. bioRxiv 158527 (published as article #285).
9. Exposito-Alonso, M., Gámez Rodríguez, R., Barragán, C., Capovilla, G., Chae, E., Devos, J., Dogan, E. S., Friedemann, C., Gross, G., Lang, P., Lundberg, D., Middendorf, V., Kageyama, J., Karasov, T., Kersten, S., Petersen, S., Rabbani, L., Regalado, J., Reinelt, L., Rowan, B., Seymour, D. K., Symeonidi, E., Schwab, R., Tran, D. T. N., Venkataramani, K., Van de Weyer, A.-L., Vasseur, F., Wang, G., Wedegärtner, R., Weiss, F., Wu, R., Xi, W., Zaidem, M., Zhu, W., García-Arenal, F., Burbano, H. A., Bossdorf, O., and **Weigel, D.** (2017) A rainfall-manipulation experiment with 517 *Arabidopsis thaliana* accessions. bioRxiv 186767 (published as Supplementary Material to article #294).

10. Vasseur, F., Wang, G., Bresson, J., Schwab, R., and **Weigel, D.** (2017) Image-based methods for phenotyping growth dynamics and fitness components in *Arabidopsis thaliana*. bioRxiv 208512 (published as article #278).
11. Karasov, T. L., Almario, J., Friedemann, C., Ding, W., Giolai, W., Heavens, D., Kersten, S., Lundberg, D. S., Neumann, M., Regalado, J., Neher, R. A., Kemen, E., and **Weigel, D.** (2018) Stability of association between *Arabidopsis thaliana* and *Pseudomonas pathogens* over evolutionary time scales. bioRxiv 241760 (published as article #277).
12. Wibowo, A., Becker, C., Durr, J., Price, J., Staepen, S., Hilton, S., Putra, H., Papareddy, R., Saintain, Q., Harvey, S., Bending, G. D., Schulze-Lefert, P., **Weigel, D.**, and Gutierrez-Marcos, J. (2018) Incomplete reprogramming of cell-specific epigenetic marks during asexual reproduction leads to heritable phenotypic variation in plants. bioRxiv 267955 (published as article #280).
13. Vasseur, F., Exposito-Alonso, M., Ayala-Garay, O., Wang, G., Enquist, B. J., Vile, D., Violle, C., and **Weigel, D.** (2018) Adaptive diversification of growth allometry in the plant *Arabidopsis thaliana*. bioRxiv 269498 (published as article #276).
14. Zhu, W., Zaidem, M., Van de Weyer, A.-L., Gutaker, R. M., Chae, E., Kim, S.-T., Bemm, F., Li, L., Schwab, R., Unger, F., Beha, M. J., Demar, M., and **Weigel, D.** (2018) Modulation of *ACD6* dependent hyperimmunity by natural alleles of an *Arabidopsis thaliana* NLR resistance gene. bioRxiv 300798 (published as article #281).
15. Exposito-Alonso, M. A., 500 Genomes Field Experiment Team, Burbano, M. A., Bossdorf, O., Nielsen, R., and **Weigel, D.** (2018) A map of climate change-driven natural selection in *Arabidopsis thaliana*. bioRxiv 321133 (published as article #294).
16. Vasseur, F., Fouqueau, L., de Vienne, D., Nidelet, T., Violle, C., and **Weigel, D.** (2018) Non-linear phenotypic variation uncovers the emergence of heterosis in *Arabidopsis thaliana*. bioRxiv 404616 (published as article #287).
17. Koenig, D., Hagmann, J. Li, R., Bemm, F., Slotte, T., Neuffer, B., Wright, S. I., and **Weigel, D.** (2018) Long-term balancing selection drives evolution of immunity genes in *Capsella*. bioRxiv 477612 (published as article #286).
18. Kreiner, J. M., Giacomini, D., Bemm, F., Waithaka, B., Regalado, J., Lanz, C., Hildebrandt, J., Sikkema, P. H., Tranel, P. J., **Weigel, D.**, Stinchcombe, J. R., Wright, S. I. (2018) Multiple modes of convergent adaptation in the spread of glyphosate-resistant *Amaranthus tuberculatus*. bioRxiv 498519 (published as article #296).
19. Barragan, C. A., Wu, R., Kim, S.-T., Xi, W., Habring, A., Hagmann, J., Van de Weyer, A.-L., Zaidem, M., Ho, W. W. H., Wang, G., Bezrukov, I., **Weigel, D.**, and Chae, E. (2018) RPW8/HR Repeats Control NLR Activation in *A. thaliana*. bioRxiv 559864 (published as article #291).
20. Van de Weyer, A.-L., Monteiro, F., Furzer, O. J., Nishimura, M. T., Cevik, V., Witek, K., Jones, J. D. G., Dangl, J. L., **Weigel, D.**, and Bemm, F. (2019) The *Arabidopsis thaliana* pan-NLRome. bioRxiv 537001(published as article #292).
21. Lange, H., Ndecky, S. Y. A., Gomez-Diaz, C., Pflieger, D., Butel, N., Zumsteg, J., Kuhn, L., Piermaria, C., Chicher, J., Christie, M., Karaaslan, E. S., Lang, P. L. M., **Weigel, D.**, Vaucheret, H., Hammann, P., and Gagliardi, D. (2019) RST1 and RIPR connect the cytosolic RNA exosome to the Ski complex in *Arabidopsis*. bioRxiv 617894 (published as article #293).

22. Rowan, R. A., Heavens, D., Feuerborn, T. R., Tock, A. J., Henderson, I. R., and **Weigel, D.** (2019) An ultra high-density *Arabidopsis thaliana* crossover map that refines the influences of structural variation and epigenetic features. bioRxiv 665083 (published as article #295).
23. Li, L., Habring, A., Wang, K., and **Weigel, D.** (2019) Oligomerization of the NLR immune receptor RPP7 triggered by the atypical resistance protein RPW8/HR as a ligand. bioRxiv 682807 (published as article #298).
24. Palatnik, J. F., and **Weigel, D.** (2019) Specific Regulation of *TCP* genes by miR319. bioRxiv 747790 (correction for article #84).
25. Srikant, T., Wibowo, A., Schwab, R., and **Weigel, D.** (2019) Position-dependent effects of cytosine methylation on *FWA* expression in *Arabidopsis thaliana*. bioRxiv 774281.
26. Price, J., Antunez-Sanchez, J., Hussain, N. Wibowo, A., Papareddy, R., Becker, C., Teakle, G., Barker, G., **Weigel, D.**, and Gutierrez-Marcos, J. (2019) Importance of parental genome balance in the generation of novel yet heritable epigenetic and transcriptional states during doubled haploid breeding. bioRxiv 812347.
27. Voichek, Y., and **Weigel, D.** (2019) Finding genetic variants in plants without complete genomes, bioRxiv 818096 (published as article #299).
28. Regalado, J., Lundberg, D. S., Deusch, O., Kersten. S., Karasov, T. L.., Poersch, K., Shirsekar, G., and **Weigel, D.** (2019) Combining whole genome shotgun sequencing and rDNA amplicon analyses to improve detection of microbe-microbe interaction networks in plant leaves. bioRxiv 823492 (published as article #300).
29. Karasov, T. L., Neumann, M., Duque-Jaramillo, A., Kersten, S., Bezrukov, I., Schröppel, B., Symeonidi, E., Lundberg, D. S., Regalado, J., Shirsekar, G., Bergelson, J., and **Weigel, D.** (2019) The relationship between microbial biomass and disease in the *Arabidopsis thaliana* phyllosphere. bioRxiv 828814.
30. Antunez-Sanchez, J., Naish, M., Ramirez-Prado. J. S., Ohno, S., Huang, Y., Dawson, A., Opassathian, K., Manza-Mianza, D., Ariel, F., Raynaud, C., Wibowo, A., Daron, J., Ueda, M., Latrasse, D., Slotkin, K., **Weigel, D.,** Benhamed, M., and Gutierrez-Marcos, J. (2020) A new role for histone demethylases in the maintenance of plant genome integrity. bioRxiv 972752 (published as article #305).
31. Rabbani, L., Mueller, J., and **Weigel, D.** (2020) An algorithm to build a multi-genome reference. bioRxiv 036871.
32. Barragan, A. C., Collenberg, M., Wang, J., Lee, R. R. Q., Yuan Cher, W., Rabanal, F. A., Ashkenazy, H., **Weigel, D.,** and Chae, E. (2020) A singleton NLR of recent origin causes hybrid necrosis in *Arabidopsis thaliana*. bioRxiv 101451 (published as article #304).
33. Lundberg, D. S., Na Ayutthaya, P. P., Strauß, A., Shirsekar, G., Lo, W.-S., Lahaye, T., and **Weigel, D.** (2020) Host-associated microbe PCR (hamPCR): accessing new biology through convenient measurement of both microbial load and community composition. bioRxiv 103937 (published as article #313).
34. Monroe, J. G., Srikant, T., Carbonell-Bejerano, P., Exposito-Alonso, M., Weng, M.-L., Rutter, M. T., Fenster, C. B., and **Weigel, D.** (2020) Mutation bias shapes gene evolution in *Arabidopsis thaliana*. bioRxiv 156752 (published as article #319).
35. Fraser, B. A., Whiting, J. R., Paris, J. R., Weadick, C. J., Parsons, P. J., Charlesworth, D., Bergero, R., Bemm, F., Hoffmann, M., Verena A Kottler, Liu, C., Dreyer, C., and **Weigel, D.**

(2020) Improved reference genome uncovers novel sex-linked regions in the guppy (*Poecilia reticulata*). bioRxiv 240986 (published as article #303).

36. Symeonidi, E., Regalado, J. Schwab, R., and **Weigel, D.** (2020) CRISPR-finder: A high throughput and cost effective method for identifying successfully edited *A. thaliana* individuals. bioRxiv 171538 (published as article #307).
37. Whiting, J. R., Paris, J. R., van der Zee, M. J., Parsons, P. J., **Weigel, D.**, and Fraser, B. A. (2020) Drainage-structuring of ancestral variation and a common functional pathway shape limited genomic convergence in natural high- and low-predation guppies. bioRxiv 339333 (published as article #312).
38. Pruitt, R. N., Zhang, L., Saile, S. C., Karelina, D., Fröhlich, K., Wan, W.-L., Rao, S., Gust, A. A., Locci, F., Joosten, M. H. A. J., Thomma, B. P. H. K., Zhou, J.-M., Dangl, J. L., **Weigel, D.**, Parker, J. E., El Kasmi, F., and Nürnberger, T. (2020) *Arabidopsis* cell surface LRR immune receptor signaling through the EDS1-PAD4-ADR1 node. bioRxiv 391516 (published as article #314).
39. Shirsekar, G., Devos, J., Latorre, S. M., Blaha, A., Queiroz Dias. M., González Hernando, A., Lundberg, D. S., Burbano, H. A., Fenster, C. B., and **Weigel, D.** (2021) Fine-scale population structure of North American *Arabidopsis thaliana* reveals multiple sources of introduction from across Eurasia. bioRxiv 427575 (published as article #315).
40. Barragan, A. C., Collenberg, M., Schwab, R., Kerstens, M., Bezrukov, I., Bemm, F., Požárová, D., Kolář, F., and **Weigel, D.** (2021) Homozygosity at its limit: Inbreeding depression in wild *Arabidopsis arenosa* populations. bioRxiv 427284 (published as article #341).
41. Zhu, W., Li, L., Neuhäuser, B., Thelen, M., Wang, M., Chen, J., Wei, L., Venkataramani, K., Exposito-Alonso, M., Liu, C., Keck, J., Barragan, A. C., Schwab, R., Lutz, U., Ludewig, U., and **Weigel, D.** (2021) Small peptides modulate the immune function of the ion channel-like protein ACD6 in Arabidopsis thaliana. bioRxiv 428077 (published as article #340).
42. van der Zee, M. J., Whiting, J. R., Paris, J. R., Bassar, R. D., Travis, J., **Weigel, D.**, Reznick, D. N., and Fraser, B. A. (2021) Rapid genomic convergent evolution in experimental populations of Trinidadian guppies (*Poecilia reticulata*). bioRxiv 430609 (published as article #321).
43. Kreiner, J. M., Tranel, P. J., **Weigel, D.**, Stinchcombe, J. R., and Wright, S. I. (2021) The genetic architecture and genomic context of glyphosate resistance in *Amaranthus tuberculatus*. bioRxiv 257972 (published as article #311).
44. Fan, L., Fröhlich, K., Melzer, E., Albert, I., Pruitt, R. N., Zhang, L., Albert, M., Kim, S.-T., Chae, E., **Weigel, D.**, Gust, A. A., and Nürnberger, T. (2021) Genotyping-by-sequencing-based identification of *Arabidopsis* pattern recognition receptor RLP32 recognizing proteobacterial translation initiation factor IF1. bioRxiv 433884 (published as article #323).
45. Shalev, O., Karasov, T., Lundberg, D. S., Ashkenazy, H., and **Weigel, D.** (2021) Protective host-dependent antagonism among *Pseudomonas* in the *Arabidopsis* phyllosphere. bioRxiv 438928 (published as article #322).
46. Lundberg, D. S., de Pedro Jové, R., Pramoj Na Ayutthaya, P., Karasov, T. L., Shalev, O., Poersch, K., Ding, W., Bollmann-Giolai, A., Bezrukov, I., and **Weigel, D.** (2021) Contrasting patterns of microbial dominance in the *Arabidopsis thaliana* phyllosphere. bioRxiv 438366 (published as article #329).

47. Kreiner, J. M., Sandler, G., Stern, A. J. Tranel, P. J., **Weigel, D.**, Stinchcombe, J. R., and Wright, S. I. (2021) Repeated origins, gene flow, and allelic interactions of herbicide resistance mutations in a widespread agricultural weed. bioRxiv 443516 (published as article #320).
48. Vogt, F., Shirsekar, G., and **Weigel, D.** (2021) *vcf2gwas* – Python API for comprehensive GWAS analysis using GEMMA. bioRxiv 446586 (published as article #316).
49. Nunn, A., Rodríguez-Arévalo, I., Tandukar, Z., Frels, K., Contreras-Garrido, A., Carbonell-Bejerano, P., Zhang, P., Ramos-Cruz, D., Jandrasits, K., Lanz, C., Brusa, A., Mirouze, M., Dorn, K., Jarvis, B., Sedbrook, J., Wyse, D. L., Otto, C., Langenberger, D., Stadler, P. F., **Weigel, D.**, Marks, M. D., Anderson, J. A., Becker, C., and Chopra, R. (2021) Chromosome-level *Thlaspi arvense* genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. bioRxiv 454478 (published as article #318).
50. Kersten, S., Chang, J., Huber, C. D., Voichek, Y., Lanz, C., Hagmaier, T., Lang, P., Lutz, U., Hirschberg, I., Lerchl, J., Porri, A., Van de Peer, Y., Schmid, K., **Weigel, D.***, and Rabanal, F. A. (2021) Standing genetic variation fuels rapid evolution of herbicide resistance in blackgrass. bioRxiv 472587 (published as article #333). *corresponding author.
51. Hüther, P., Hagmann, J., Nunn, A., Kakoulidou, I., Pisupati, R., Langenberger, D., **Weigel, D.**, Johannes, F., Schultheiss, S. J., and Becker, C. (2022) MethylScore, a pipeline for accurate and context-aware identification of differentially methylated regions from population-scale plant WGBS data. bioRxiv 475031 (published as article #324).
52. Rabanal, F. A., Gräff, M., Lanz, C., Fritschi, K., Llaca, V., Lang, M., Carbonell-Bejerano, P., Henderson, I., and **Weigel, D.** (2022) Pushing the limits of HiFi assemblies reveals centromere diversity between two *Arabidopsis thaliana* genomes. bioRxiv 480579 (published as article #328).
53. Yuan, W., Beitel, F., Srikant, T., Bezrukov, I., Schäfer, S., Kraft, R., and **Weigel, D.** (2022) Pervasive under-dominance in gene expression as unifying emergent growth trajectories in *Arabidopsis thaliana* hybrids. bioRxiv 482808 (published as article #336).
54. Kreiner, J., Latorre, S. M., Burbano, H. A., Stinchcombe, J. R., Otto, S. P., **Weigel, D.**, and Wright, S. I. (2022) Rapid adaptation and range expansion in response to agriculture over the last two centuries. bioRxiv 482047 (published as article #327).
55. Czech, L., Peng, Y., Spence, J. P., Lang, P. L. M., Bellagio, T., Hildebrandt, J., Fritschi, K., Schwab, R., Rowan, B. A., GrENE-net Consortium, **Weigel, D.**, Scheepens, J. F., Vasseur, F., and Exposito-Alonso, M. (2022) Monitoring rapid evolution of plant populations at scale with Pool-Sequencing. bioRxiv 477408.
56. Wibowo, A. T., Antunez-Sanchez, J., Dawson, A., Price, J., Meehan, C., Wrightsman, T., Collenberg, M., Bezrukov, I., Becker, C., Benhamed, M., **Weigel, D.***, and Gutierrez-Marcos, J.* (2022) Predictable and stable epimutations induced during clonal propagation with embryonic transcription factors. bioRxiv 484412 (published as article #325). *corresponding authors.
57. Karasov, T. L., Neumann, M., Shirsekar, G. Monroe, G., PATHODOPSIS Team, **Weigel, D.**, and Schwab, R. (2022) Drought selection on *Arabidopsis* populations and their microbiomes. bioRxiv 487684.
58. Mateos, J. L., Sanchez, S. E., Legris, M., Esteve-Bruna, D., Torchio, J. C., Petrillo, E., Goretti, D., Blanco-Touriñán, N., Seymour, D. K., Schmid, M., **Weigel, D.**, Alabadí, D., and

Yanovsky, M. J. (2022) PICLN modulates alternative splicing and ensures adaptation to light and temperature changes in plants. bioRxiv 496170 (published as article #325).

59. Kersten, S., Rabanal, F. A., Herrmann, J., Hess, M., Kronenberg, Z. N., Schmid, K., and **Weigel, D.** (2022) Deep haplotype analyses of target-site resistance locus *ACCase* in blackgrass enabled by pool-based amplicon sequencing. bioRxiv 496946 (published as article #332).
60. Srikant, T., Yuan, W., Berendzen, K. W., Contreras Garrido, A., Drost, H.-G., Schwab, R., and **Weigel, D.** (2022) Canalization of genome-wide transcriptional activity in *Arabidopsis thaliana* accessions by MET1-dependent CG methylation. bioRxiv 500095 (published as article #329).
61. Arce, A. L., Mencia, R., Cambiagno, D. A., Lang, P. L., Liu, C., Burbano, H. A., **Weigel, D.**, and Manavella, P. A. (2022) Polymorphic Inverted Repeats near coding genes impact chromatin topology and phenotypic traits in *Arabidopsis thaliana*. bioRxiv 98814 (published as article #331).
62. Saarenpää, S.*, Shalev, O.*, Ashkenazy, H.*, de Oliveira-Carlos, V., Lundberg, D. S., **Weigel, D.**, and Giacomello, S. (2022) Spatially resolved host-bacteria-fungi interactomes via spatial metatranscriptomics. bioRxiv 496977. *co-first authors; O.S. and H.A. Weigel lab members (published as article #338).
63. Monroe, J. G., Murray, K. D., Xian, W., Carbonell-Bejerano, P., Fenster, C. B., and **Weigel, D.** (2022) Report of mutation biases mirroring selection in *Arabidopsis thaliana* unlikely to be entirely due to variant calling errors. bioRxiv 504682.
64. Vasseur, F., Baldrich, P., Jiménez-Góngora, T., Villar-Martin, L., **Weigel, D.**, and Rubio-Somoza, I. (2022) miR472 deficiency enhances *Arabidopsis thaliana* defence without reducing seed production. bioRxiv 520224.
65. Duque-Jaramillo, A., Ulmer, N., Alseekh, S., Bezrukov, I., Fernie, A. R., Skirycz, A., Karasov, T. L., and **Weigel, D.** (2023) The genetic and physiological basis of *Arabidopsis thaliana* tolerance to *Pseudomonas viridiflava*. bioRxiv 533268 (published as article #337).
66. Wang, M.-Y.*, Chen, J.-B.*, Wu, R.*, Guo, H.-L-, Chen, Y., Li, Z.-J-, Wei, L.-Y., Liu, C., He, S.-F., Du, M.-M., Guo, Y.-L., Peng, Y.-L., Jones, J. D. G., **Weigel, D.**, Huang, J.-H., and Zhu, W-S. (2023) The immune receptor SNC1 monitors helper NLRs targeted by a bacterial effector. bioRxiv 533910. *co-first authors; R.W. Weigel lab member (published as article #339).
67. Contreras-Garrido, A., Galanti, D., Movilli, A., Becker, C., Bossdorf, O., Drost, H.-J., and **Weigel, D.** (2023) Transposon dynamics in the emerging oilseed crop *Thlaspi arvense*. bioRxiv 542068 (published as article #343).
68. Fernandes, J. B. Naish, M., Lian, Q., Burns, R., Tock, A. J., Rabanal, F. A., Wlodzimierz, P., Habring, A., Nicholas, R. E., **Weigel, D.**, Mercier, R., and Henderson, I. R. (2023) Structural variation and DNA methylation shape the centromere-proximal meiotic crossover landscape in Arabidopsis. bioRxiv 544545 (published as article #342).
69. Mencia, R., Arce, A. L., Houriet, C., Xian, W., Contreras, A., Shirsekar, G., **Weigel, D.**, and Manavella, P. A. (2023) Transposon-triggered epigenetic chromatin dynamics modulate EFR-related pathogen response. bioRxiv 561201.
70. Voichek, Y., Hristova, G., Mollá-Morales, A., **Weigel, D.**, and Nordborg, M. (2023) Widespread transcriptional regulation from within transcribed regions in plants. bioRxiv 557872.

71. Yeaman, S., Whiting, J., Booker, T., Rougeux, C., Lind, B., Singh, P., Lu, M., Huang, K., Whitlock, M., Aitken, S., Andrew, R., Borevitz, J., Bruhl, J. J., Collins, T., Fischer, M., Hodgins, K., Holliday, J., Ingvarsson, P. K., Janes, J., Khandaker, M., Koenig, D., Kreiner, J., Kremer, A., Lascoux, M., Leroy, T., Milesi, P., Murray, K., Rellstab, C., Rieseberg, L., Roux, F., Stinchcombe, J., Telford, I. R. H., Todesco, M., Wang, B., Weigel, D., Willi, Y., Wright, S., Zhou, L. (2023) Core genes driving climate adaptation in plants. ResearchSquare 3434061.
72. Calderón, L.*, Carbonell-Bejerano, P.*, Muñoz., C., Bree, L., Sola, C., Bergamin, D., Tulle, W., Gomez-Talquenca, S., Lanz, C., Royo, C., Ibañez, J., Martinez-Zapater, J. M., **Weigel, D.**, and Lijavetzky, D. (2023) Diploid genome assembly of the Malbec grapevine cultivar enables haplotype-aware analysis of transcriptomic differences underlying clonal phenotypic variation. bioRxiv 569420. *co-first authors; P.C-B. Weigel lab member. (published as article #344).
73. Tao, Y., Xian, W., Rabanal F., Movilli, A., Lanz, C., Shirsekar, G., and **Weigel, D.** (2023) Atlas of telomeric repeat diversity in *Arabidopsis thaliana*. bioRxiv 572118.
74. Xian, W., and **Weigel, D.** (2024) TIPP_plastid: A user-friendly tool for de novo assembly of plastid genomes. bioRxiv 577798.
75. Vorbrugg, S., Bezrukov, I., Bao, Z., and **Weigel, D.** (2024) Gretl - Variation GRaph Evaluation TooLkit. bioRxiv 580974.
76. Igolkina, A. A., Vorbrugg, S., Rabanal, F. A., Liu, H.-J., Ashkenazy, H., Kornienko, A. E., Fitz, J., Collenberg, M., Kubica, C., Mollá Morales, A., Jaegle, B., Wrightsman, T., Voloshin, V., Llaca, V., Nizhynska, V., Lanz, C., Bemm, F., Flood, P. J., Nemomissa, S., Hancock, A., Guo, Y.-L., Kersey, P., **Weigel, D.***, and Nordborg, M.* (2024) Towards an unbiased characterization of genetic polymorphism. bioRxiv 596703. *corresponding authors.

*Other articles*

1. **Weigel, D.**, and Jäckle, H. (1989) Novel homeotic genes of *Drosophila*. Biochem. Cell Biol. *67*, 393-396.
2. Jäckle, H., Gaul, U., Nauber, U., Gerwin, N., Pankratz, M. J., Schuh, R., and **Weigel, D.** (1989) Musterbildung bei *Drosophila*. Naturwissenschaften *76*, 512-517.
3. **Weigel, D.**, and Jäckle, H. (1990) The fork head domain, a novel DNA-binding motif of eucaryotic transcription factors? Cell *63*, 455-456.
4. Meyerowitz, E. M., Bowman, J. L., Brockman, L. L., Drews, G. N., Jack, T., Sieburth, L. E., and **Weigel, D.** (1991) A genetic and molecular model for flower development in *Arabidopsis thaliana*. Development (Suppl. *1*), 157-167.
5. Drews, G. N., **Weigel, D.**, and Meyerowitz, E. M. (1991) Floral patterning. Curr. Opin. Genet. Dev. *1*, 174-178.
6. **Weigel, D.**, and Meyerowitz, E. M. (1993) *LEAFY* controls meristem identity in *Arabidopsis*. In *Cellular Communication in Plants* (ed. Amasino, R.), pp. 115-122. Plenum Press, New York.
7. **Weigel, D.**, and Meyerowitz, E. M. (1993) Genetic hierarchy controlling flower development. In *Molecular Basis of Morphogenesis* (ed. Bernfield, M.), pp. 91-105. Wiley-Liss, New York.
8. **Weigel, D.** (1993) Patterning the *Arabidopsis* embryo. Curr. Biol. *3*, 443-445.

9. **Weigel, D.**, and Meyerowitz, E. M. (1994) The ABCs of floral homeotic genes. Cell *78*, 203-209.
10. **Weigel, D.** (1994) The SECrets of *Arabidopsis* embryogenesis. Curr. Biol. *4*, 1040-1042.
11. **Weigel, D.** (1995) The APETALA2 domain is related to a novel type of DNA binding domain. Plant Cell *7*, 388-389.
12. **Weigel, D.** (1995) How genes control flower development. Futura *10*, 96-102.
13. **Weigel, D.** (1995) The genetics of flower development: from floral induction to ovule morphogenesis. Annu. Rev. Genet. *29*, 19-39.
14. **Weigel, D.**, and Doerner, P. (1996) Cell-cell interactions: taking cues from the neighbors. Curr. Biol. *6*, 10-12.
15. **Weigel, D.**, and Clark, S. E. (1996) Sizing up the floral meristem. Plant Physiol. *112*, 5-10.
16. Nilsson, O., and **Weigel, D.** (1997) Manipulating the timing of flowering. Curr. Opin. Biotech. *8*, 195-199.
17. **Weigel, D.** (1997) Repressing reproduction. Curr. Biol. *7*, R373-R375.
18. **Weigel, D.** (1998) From floral induction to floral shape. Curr. Opin. Plant Biol. *1*, 55-59.
19. Sessions, A., Yanofsky, M. F., and **Weigel, D.** (1998) Patterning the floral meristem. Sem. Cell Dev. Biol. 9, 221-226
20. Lee, I., **Weigel, D.**, and Parcy, F. (1998) Genetic control of floral induction and floral patterning. In *Arabidopsis* (eds. J. A. Roberts and M. Anderson). Sheffield Academic Press, Sheffield, UK. pp. 298-330.
21. Christensen, S., and **Weigel, D.** (1998) The making of a leaf. Curr. Biol. *8*, R643-R645.
22. Blázquez, M. A., **Weigel, D.**, and Gocal, G. F. W. (1998) Gibberellins and flowering of *Arabidopsis*. Flowering Newsletter *26*, 29-35.
23. **Weigel, D.** (1998) Plant development. In *McGraw-Hill Yearbook of Science and Technology 1999*. McGraw-Hill, New York. pp. 289-291.
24. Chory, J., Ecker, J. R., Briggs, S., Caboche, M., Coruzzi, G. M., Cook, D., Dangl, J., Grant, S., Guerinot, M. L., Henikoff, S., Martienssen, R., Okada, K., Raikhel, N. V., Somerville, C. R., and **Weigel, D.** (2000). National Science Foundation-Sponsored Workshop Report: “The 2010 Project” Functional genomics and the virtual plant. A blueprint for understanding how plants are built and how to improve them. Plant Physiol. *123*, 423-426.
25. Maloof, J. N., Borevitz, J. O., **Weigel, D.**, and Chory, J. (2000) Natural variation in phytochrome signaling. Sem. Cell Dev. Biol. *11*, 523-530.
26. Benfey, P. N., and **Weigel, D.** (2001) Transcriptional networks in plant development. Plant Physiol. *125*, 109-111.
27. Wigge, P. A., and **Weigel, D.** (2001) *Arabidopsis* genome: Life without Notch. Curr. Biol. *11*, R112-R114.
28. Bisseling, T., and **Weigel, D.** (2001) Meeting Report: Plant development: From cell fate to organ formation. Plant Cell *13*, 221-227.
29. **Weigel, D.**, and Dean, C. (2002) Editorial: development, evolution and adaptation. Curr. Opin. Plant Biol. *5*, 11-13.
30. Wu, X., **Weigel, D.**, and Wigge, P. A. (2002) Intercellular signaling in plants by RNA and protein movement. Genes Dev. *15*, 151-158.

31. Lohmann, J. U., and **Weigel, D.** (2002) Building beauty: the genetic control of floral patterning. Dev. Cell *2*, 135–142.
32. **Weigel, D.**, and Jürgens, G. (2002) Stem cells that make stems. Nature *415*, 751-754.
33. Lohmann, J. U., and **Weigel, D.** (2004) From tough nuts to touch-me-nots. Cell *116*, 763-764.
34. **Weigel, D.**, and Jürgens, G. (2005) Hotheaded healer. Nature *434*, 443.
35. **Weigel, D.**, and Nordborg, M. (2005) Natural variation in *Arabidopsis thaliana*: How do we find the causal genes? Plant Physiol., *138*, 567-568.
36. **Weigel, D.**, and Izaurralde, E. (2006) A tiny helper lightens the maternal load. Cell *124*, 1117-1118.
37. **Weigel, D.** (2007) Q&A. Curr. Biol. *17*, R227-R228.
38. Bomblies, K., and **Weigel, D.** (2007) Hybrid necrosis: autoimmunity as a potential gene-flow barrier in plant species. Nat. Rev. Genet. *8*, 382-393.
39. Kobayashi, Y., and **Weigel, D.** (2007) Move on up, it's time for change – mobile signals controlling photoperiod-dependent flowering. Genes Dev. *21*, 2371-2384.
40. Bomblies, K., and **Weigel, D.** (2007) *Arabidopsis* – a model genus for speciation. Curr. Opin. Genet. Dev. *17*, 500-504.
41. **Weigel, D.**, and Dangl, J. L. (2007) 10 years of *Current Opinion in Plant Biology* 1997 to 2007. Curr. Opin. Plant Biol. *10*, 543-545.
42. Jones, A. M., Chory, J., Dangl, J. L., Estelle, M., Jacobsen, S. E., Meyerowitz, E. M., Nordborg, M., **Weigel, D.** (2008) The impact of *Arabidopsis* on human health research: Diversifying our portfolio. Cell *133*, 939-943.
43. Nordborg, M., and **Weigel, D.** (2008) Next-generation genetics in plants. Nature *456*, 720-723.
44. Meyers, B. C., Axtell, M. J., Bartel, D. P., Baulcombe, D., Bowman, J. L., Cao, X., Carrington, J. C., Chen, X., Green, P. J., Griffiths-Jones, S., Jacobsen, S. E., Mallory, A. C., Martienssen, R. A., Poethig, R. S., Qi, Y., Vaucheret, H., Voinnet, O., **Weigel, D.**, and Zhu, J.-K. (2008) Criteria for annotation of plant microRNAs. Plant Cell *20*, 3186-3190.
45. **Weigel. D.**, and Mott, R. (2009) The 1001 Genomes project for *Arabidopsis thaliana*. Genome Biol. *10*, 107.
46. Rubio-Somoza, I., Cuperus, J., **Weigel, D.**, and Carrington, J. C. (2009) Regulation and functional specialization of small RNA-target nodes during plant development. Curr. Opin. Plant Biol. *12*, 622-627.
47. de Felippes, F. F., and **Weigel, D.** (2010) Transient assays for the analysis of miRNA processing and function. Methods Mol. Biol. *592*, 255-264.
48. Schwab, R., Ossowski, S., Warthmann. N., **Weigel, D.** (2010) Directed gene silencing with artificial microRNAs. Methods Mol. Biol. *592*, 71-88.
49. Wollmann, H., and **Weigel, D.** (2010) Small RNAs in flower development. Eur. J. Cell Biol. *89*, 250-257.
50. Tautz, D, Ellegren, H., and **Weigel, D.** (2010) Next generation molecular ecology. Mol. Ecol. *19 (Suppl. 1)*, 1-3.
51. Bomblies, K., and **Weigel, D.** (2010) *Arabidopsis* as a model for the study of genetic and genomic incompatibilities. Proc. R. Soc. London B *65*, 1815-1812.

52. Gleick, P.H., (242 authors), **Weigel, D.**, (11 authors) (2010). Climate change and the integrity of science. Science *328*, 689-690.
53. Heard, E., Tishkoff, S., Todd, J. A., Vidal, M., Wagner, G. P., Wang, J., **Weigel, D.**, and Young R. (2010) Ten years of genetics and genomics: What have we achieved and where are we heading? Nat. Genet. *11*, 723-733.
54. **Weigel, D.** (2011) What developmental biologists can learn from plant pathogens. Dev. Cell *20*, e2.
55. Schneeberger, K., and **Weigel, D.** (2011) Fast-forward genetics enabled by new sequencing technologies. Trends Plant Sci. *16*, 282-288.
56. Rubio-Somoza, I., and **Weigel, D.** (2011) MicroRNA networks and developmental plasticity in plants. Trends Plant Sci. *16*, 258-224.
57. Manavella, P. A., **Weigel, D.**, and Wu, L. (2011) Argonaute10 as a miRNA locker. Cell *145*, 173-174.
58. Rowan, B., **Weigel, D.**, and Koenig, D. (2011) Developmental genetics and new sequencing technologies: the rise of non-model organisms. Dev. Cell *21*, 65-76.
59. Rubio-Somoza, I., **Weigel, D.**, Franco-Zorilla, J.-M., García, J. A., and Paz-Ares, J. (2011) ceRNAs: miRNA target mimic mimics. Cell *147*, 1431-1432.
60. **Weigel, D.** (2012) Natural variation in Arabidopsis: from molecular mechanisms to ecological genomics. Plant Physiol. 158, 2-22.
61. Smith, L. M., and **Weigel, D.** (2012) On epigenetics and epistasis: hybrids and their non-additive interactions. EMBO J. *31*, 249-250.
62. The EPIC Planning Committee: Berger, F., Cao, X. F., Chandler, V., Dennis, L., Martienssen, R., Meyers, B., Pikaard, C., Peacock, J., Richards, E., Wagner, D., **Weigel, D.**, Colot, V., Deal, R., Dean, C., Ecker, J., Gehring, M., Gong, Z., Gregory, B., Rodrigo, G., Gutierrez-Marcos, J., Hasebe, M., Hwang, I.-D., Jacobsen, S., Kakutani, T., Li, J., Michaels, S., Noh, Y.-S., Provart, N., Vaughn, M. (2012). Reading the second code: Mapping epigenomes to understand plant growth, development, and adaptation to the environment. Plant Cell *24*, 2257-2261.
63. Becker, C., and **Weigel, D.** (2012) Epigenetic variation: origin and transgenerational inheritance. Curr. Opin. Plant Biol., *15*, 562-567.
64. **Weigel, D.**, and Colot, V. (2012) Epialleles in plant evolution. Genome Biol. *13*, 249.
65. Schekman, R., Patterson, M., Watt, F., and **Weigel, D.** (2012) Launching *eLife*, part 1. eLife *1*, e00270.
66. Schekman, R., Watt, F., and **Weigel, D.** (2012) Launching *eLife*, part 2. eLife *1*, e00365.
67. Warthmann, N., Ossowski, S., Schwab, R., and **Weigel, D.** (2013) Artificial microRNAs for specific gene silencing in rice. Methods Mol. Biol. *956*, 131-149.
68. Schekman, R., Watt, F., and **Weigel, D.** (2013) The eLife approach to peer review. eLife *2*, e00799.
69. Doolittle, W. F., Fraser, P., Graveley, B. R., Gerstein, M. B., Henikoff, S., Huttenhower, C., Oshlack, A., Ponting, C. P., Rinn, J. L., Schatz, M. C., Ule, J., **Weigel, D.**, and Weinstock, G. M. (2013) Sixty years of genome biology. Genome Biol. *14*, 113.
70. **Weigel, D.** (2013) QnAs with Detlef Weigel. Interview by Sandeep Ravindran. Proc. Natl. Acad. Sci. USA *110*, 11216.

71. **Weigel, D.**, and Lang, P. (2013) Kontrolle der Pflanzenentwicklung durch mikroRNAs. BioSpektrum *19*, 622-624.
72. **Weigel, D.**, Schekman, R., and Watt, F. M. (2013) A year in the life of eLife. eLife *2*, e01516.
73. Yoshida, K., Burbano, H. A., Krause, J., Thines, M., **Weigel, D.**, and Kamoun, S. (2014) Mining herbaria for plant pathogen genomes: back to the future. PLoS Pathog. *10*, e1004028.
74. Patterson, M., Schekman, R., Watt, F. M., and **Weigel, D.** (2014) Advancing research. eLife *3*, e03980.
75. Brockington, S. F., Moyroud, E., Sayou, C., Monniaux, M., Nanao, M. H., Thévenon, E., Chahtane, H., Warthmann, N., Melkonian, M., Zhang, Y., Ka-Shu Wong, G., **Weigel, D.**, Dumas, R., and Parcy, F. (2015) Response to Comment on "A promiscuous intermediate underlies the evolution of LEAFY DNA binding specificity." Science *347*, 621.
76. Schekman, R., **Weigel, D.**, and Watt, F. M. (2015) Scientific publishing: recognizing the importance of new tools and resources for research. eLife *4*, e7083.
77. Koenig, D., and **Weigel, D.** (2015) Beyond the thale: comparative genomics and genetics of *Arabidopsis* relatives. Nat. Rev. Genet. *16*, 285-298.
78. Liu, C., and **Weigel, D.** (2015) Chromatin in 3D: progress and prospects for plants. Genome Biol. *16*, 170.
79. **Weigel, D.**, and Nordborg, M. (2015) Population genomics for understanding adaptation in wild plant species. Annu. Rev. Genet. Genomics *49*, 315-338.
80. Huang, S., **Weigel, D.**, Beachy, R. N., and Li, J. (2016) A proposed regulatory framework for genome-edited crops. Nat. Genet. *48*, 109-111.
81. Bergelson, J., Buckler, E. S., Ecker, J. R., Nordborg, M., and **Weigel, D.** (2016) A proposal regarding best practices for validating the identity of genetic stocks and the effects of genetic variants. Plant Cell *28*, 606-609.
82. Chae, E., Tran, D. T. N., and **Weigel, D.** (2016) Cooperation and conflict in the plant immune system. PLoS Pathogens *12*, e1005452.
83. **Weigel, D.** (2016) Why I love genetics. Genetics *204*, 841-843.
84. Rowan, B. A., Seymour, D. K., Chae, E., Lundberg, D. S., and **Weigel, D.** (2017) Methods for Genotyping-by-Sequencing. Methods Mol Biol. *1492*, 221-242.
85. **Weigel, D.**, and Lang, P. (2017) Geneditierung in der Pflanzenzüchtung. Laborjournal *7-8/2017*, 62-64.
86. **Weigel, D.** (2019) All in the family: the first whole-genome survey of NLR genes. Plant Cell *31*, 1212-1213.
87. Exposito-Alonso, M., Drost, H.-G., Burbano, H., and **Weigel, D.** (2020) The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. Plant J. *102*, 222-229.
88. Caetano-Andrade, V. L., Clement, C. R., **Weigel, D.**, Trumbore, S., Boivin, N., Schöngart, J., and Roberts, R. (2020) Tropical trees as time capsules of anthropogenic activity. Trends Plant Sci. *25*, 369-380.
89. Eisen, M. B., Akhmanova, A., Behrens, T. E., and **Weigel, D.** (2020) Publishing in the time of COVID-19. eLife *9*, e57162.

90. Karasov, T. L., Shirsekar, G., Schwab, R., and **Weigel, D.** (2020) What natural variation can teach us about resistance durability. Curr. Opin. Plant Biol. *56*, 89-98.
91. Eisen, M. B., Akhmanova, A., Behrens, T. E., Harper, D. M., **Weigel, D.**, and Zaidi, M. (2020) Implementing a "publish, then review" model of publishing. eLife *9*, e64910.
92. Barragan, A. C., and **Weigel, D.** (2021) Plant NLR diversity: the known unknowns of pan-NLRomes. Plant Cell *33*, 814-831.
93. Monroe, J. G., McKay, J. K., **Weigel, D.**, and Flood, P. (2021) The population genomics of adaptive loss of function. Heredity *126*, 383-395.
94. Li, L., and **Weigel, D.** (2021) One hundred years of hybrid necrosis: hybrid autoimmunity as a window into the mechanisms and evolution of plant–pathogen interactions. Annu. Rev. Phytopathol. *59*, 213-237.
95. Zaidi, M., Harper, D. M., Akhmanova, A., **Weigel, D.**, Behrens, T., and Eisen, M. (2021) eLife and medicine: Rigorous review and editorial oversight of clinical preprints. eLife *10*, e67528.
96. Eisen, M. B., Akhmanova, A., Behrens, T. E., Diedrichsen, J., Harper, D. M., Iordanova, M. D., **Weigel, D.**, and Zaidi, M. (2022) Peer review without gatekeeping. eLife *11*, e83889.
97. Hirt, H., Al-Babili, S., Almeida-Trapp, M., Martin, A., Aranda, M., Bartels, D., Bennett, M., Blilou, I., Boer, D., Boulouis, A., Bowler, C., Brunel-Muguet, S., Chardon, F., Colcombet, J., Colot, V., Daszkowska-Golec, A., Dinneny, J. R., Field, B., Froehlich, K., Gardener, C. H., Gojon, A., Gomès, E., Gómez-Álvarez, E. M., Gutierrez, C., Havaux, M., Hayes, S., Heard, E., Hodges, M., Alghamdi, A. K., Laplaze, L., Lauersen, K. J., Leonhardt, N., Johnson, X., Jones, J., Kollist, H., Kopriva, S., Krapp, A., Lopez-Portillo Masson, M., McCabe, M. F., Merendino, L., Molina, A., Moreno Ramirez, J. L., Müller-Röber, B., Nicolas, M., Nir, I., Olivas Orduna, I., Pardo, J. M., Reichheld, J.-P., Rodriguez Egea, P. L., Rouached, H., Saad, M. M., Schlögelhofer, P., Shekhawat, K., De Smet, I., Stanschewski, C., Stra, A., Tester, M., Walshe, C., Weber, A. P. M., **Weigel, D.**, Wigge, P., Wrzaczek, M., Wulff, B., Young, I. M. (2023) PlantACT! – how to tackle the climate crisis. Trends Plant Sci. *28*, 537-543.
98. Monroe, J. G., Murray, K. D., Xian, W., Srikant, T., Carbonell-Bejerano, P., Becker, C., Lensink, M., Exposito-Alonso, M., Klein, M., Hildebrandt, J., Neumann, M. Kliebenstein, Weng, M.-L., Imbert, E., Ågren, J., Rutter, M. T., Fenster, C. B., and **Weigel, D.** (2023) Reply to: Re-evaluating evidence for adaptive mutation rate variation. Nature *619*, E57–E60.
99. Vanderschuren, H., Chatukuta, P., **Weigel, D.**, and Mehta, D. (2023) A new chance for genome editing in Europe. Nat. Biotech. *41*, 1378-1380.
100. Khaipho-Burch, M., Cooper, M., Crossa, J., de Leon, N., Holland, J., Lewis, R., McCouch, S., Murray, S. C., Rabbi, I., Ronald, P., Ross-Ibarra, J., **Weigel, D.**, and Buckler, E. S. (2023) Genetic modification can improve crop yields – but stop overselling it. Nature *621*, 470-473.
101. Behrens, T., Dalal, Y. Harper, D. M., and **Weigel, D.** (2024) The first year of a new era. eLife *13*, e96413.

## Books

1. Weigel, D., and Glazebrook, J. (2001) *Arabidopsis* – A Laboratory Manual. 357 pp. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

## Trainees

| | Name | | Period | Fellowship | Last Known Position |
|---|---|---|---|---|---|
| 1 | Lara N. Soowal | PhD | 1993-1998 | - | Research Instructor, UC San Diego, CA |
| 2 | Ilha Lee | Postdoc | 1995-1998 | - | Professor, Seoul University, Korea |
| 3 | Ove Nilsson | Postdoc | 1995-1997 | HFSPO | Professor & Director, Umeå Plant Science Center, Sweden |
| 4 | Igor V. Kardailsky | Postdoc | 1995-1997 | Noble Fd. | Research Officer, News South Wales Department of Planning, Industry and Environment, Sydney, Australia |
| 5 | Susan K. Christensen | Postdoc | 1996-2000 | NSF | Unknown |
| 6 | François Parcy | Postdoc | 1996-1998 | HFSPO | Directeur de Récherche, CNRS, France |
| 7 | Miguel A. Blázquez | Postdoc | 1996-2000 | HFSPO | Professor, CSIC, Valencia, Spain |
| 8 | Maximilian A. Busch | Postdoc | 1996-2000 | HFSPO | Product Manager, Tecniplast, Germany |
| 9 | Gregory F. Gocal | Postdoc | 1997-2000 | - | Chief Scientific Officer, Cibus Genetics, San Diego, CA |
| 10 | Vipula Shukla | Postdoc | 1997-1999 | - | Sr. Program Officer, Bill & Melinda Gates Foundation, Seattle, WA |
| 11 | R. Allen Sessions | Postdoc | 1997-2000 | LSRF | Senior Principal Scientist, BASF, Research Triangle Park, NC |
| 12 | Jasmine T. Nguyen | MS | 1998-1999 | - | Principal Scientist, Mirati Therapeutics, San Diego, CA |
| 13 | Takuji Wada | Postdoc | 1998-2001 | HFSPO/JSPS | Staff Scientist, Hiroshima University, Japan |
| 14 | Ji Hoon Ahn | Postdoc | 1998-2001 | KOSEF | Professor, Korea University, Korea |
| 15 | Julin N. Maloof | Postdoc | 1998-2001 | Helen Hay Whitney | Professor, UC Davis, CA |
| 16 | Ray L. Hong | PhD | 1998-2002 | - | Professor, California State University Northridge, CA |
| 17 | Jonathan D. Werner | PhD | 1999-2004 | NSF | Principal Lab Systems Engineer, Symantec, Mountain View, CA |
| 18 | Jan U. Lohmann | Postdoc | 1999-2002 | HFSPO | Professor, University of Heidelberg, Germany |
| 19 | Markus Schmid | Postdoc | 2000-2002 | DFG | Professor, Umeå University, Sweden |
| 20 | Philip A. Wigge | Postdoc | 2000-2002 | Wellcome Trust | Director, Leibniz Institute of Veg. & Ornament. Crops, Großbeeren, Germany |
| 21 | Xuelin Wu | Postdoc | 2000-2007 | LSRF | Staff Scientist, Salk Institute, La Jolla, CA |
| 22 | José R. Dinneny | PhD | 2001-2005 | HHMI | Associate Professor, Stanford University, Stanford, CA |
| 23 | François Godard | Postdoc | 2001-2002 | - | Deceased |
| 24 | Javier F. Palatnik | Postdoc | 2001-2005 | HFSPO | Head of Laboratory, IBR (CONICET), Rosario, Argentina |
| 25 | Sandra Stehling-Sun | PhD | 2001-2002 | - | Research Scientist, Univ. of Washington, Seattle, WA |

| | | | | | |
|---|---|---|---|---|---|
| 26 | N. Henriette Uhlenhaut | MS | 2001-2002 | - | Professor, Technical University Munich, Germany |
| 27 | Norman Warthmann | MS/PhD | 2001-2012 | German Nt. Acad. Fd. | Staff Scientist, International Atomic Energy Agency, Seibersdorf, Austria |
| 28 | Alexis Maizel | Postdoc | 2002-2005 | Marie Curie | Professor, University of Heidelberg, Germany |
| 29 | Sureshkumar Balasubramanian | Postdoc | 2002-2007 | EMBO | Professor, Monash University, Melbourne, Australia |
| 30 | Carla Schommer | Postdoc | 2002-2006 | - | Staff Scientist, CONICET, Rosario, Argentina |
| 31 | Anandita Singh | Postdoc | 2002-2004 | - | Professor, TERI Univ., New Delhi, India |
| 32 | Sandip Das | Postdoc | 2002-2004 | - | Lecturer, Hamdard University, New Delhi, India |
| 33 | Rebecca Schwab | PhD | 2002-2006 | - | Group Leader, MPI for Developmental Biology, Tübingen, Germany |
| 34 | Min Chul Kim | Postdoc | 2002-2005 | KOSEF, EMBO | Professor, Gyeongsang National University, Korea |
| 35 | Janne Lempe | PhD | 2002-2006 | - | Staff Scientist, Julius Kühn Institute, Dresden, Germany |
| 36 | Yasushi Kobayashi | Postdoc | 2003-2010 | HFSPO, JSPS | Unknown |
| 37 | Timothy Davison | Postdoc | 2004-2005 | - | Chief Technology Officer, BrainWaveBank, Belfast, UK |
| 38 | Heike Wollmann | MS/PhD | 2004-2009 | Boehringer Ingelh. Fd. | Special Consultant, DanStem, Copenhagen, Denmark |
| 39 | Richard Clark | Postdoc | 2004-2008 | - | Professor, University of Utah, Salt Lake City, UT |
| 40 | Kirsten Bomblies | Postdoc | 2004-2009 | NIH | Professor, ETH, Zurich, Switzerland |
| 41 | Stephan Ossowski | PhD | 2005-2010 | - | Professor, Universität Tübingen, Germany |
| 42 | Georg Zeller | MS/PhD | 2005-2009 | - | Teamleader, EMBL, Heidelberg, Germany |
| 43 | Gabriele Schweikert | PhD | 2005-2009 | - | Lecturer, Dundee University, UK |
| 44 | Jiawei Wang | Postdoc | 2005-2011 | EMBO | Professor & Deputy Director, SIPPE, CAS, Shanghai, China |
| 45 | Yalong Guo | Postdoc | 2005-2011 | - | Professor, Institute of Botany, CAS, Beijing, China |
| 46 | Felipe Felippes | PhD | 2005-2010 | DAAD | Sr. Research Associate, Queensland Univ. of Technology, Brisbane, Australia |
| 47 | Marco Todesco | PhD | 2005-2009 | - | Assistant Professor, University of British Columbia, Vancouver, Canada |
| 48 | Schallum Werner | PhD | 2006-2010 | - | Executive Director, Heidelberg Academy of Sciences, Heidelberg, Germany |
| 49 | Patrice Salomé | Postdoc | 2006-2013 | EMBO | Science Editor, The Plant Cell, ASPB, Washington, DC |
| 50 | Sascha Laubinger | Postdoc | 2006-2009 | DFG | Professor, University of Halle, Germany |
| 51 | Korbinian Schneeberger | MS/PhD | 2006-2010 | - | Professor, Ludwig Maximilian University, Munich, Germany |
| 52 | Ignacio Rubio-Somoza | Postdoc | 2006-2015 | Sp.. M. Ed. & Sci., EMBO | Associate Professor, CRAG, Barcelona, Spain |
| 53 | Sarah Lechner | MS | 2006-2007 | - | Staff Scientist, CeGaT, Tübingen, Germany |

| | | | | | |
|---|---|---|---|---|---|
| 54 | Sridevi Sureshkumar | PhD | 2006-2007 | - | Group Leader, Monash University, Melbourne, Australia |
| 55 | Hezi Tenenboim | MS | 2007-2008 | - | CEO, Greenshift Labs, Potsdam, Germany |
| 56 | Roosa Laitinen | Postdoc | 2007-2011 | Finn. Acad. Sci., HFSPO | Associate Professor, University of Helsinki, Finland |
| 57 | Lisa Smith | Postdoc | 2007-2013 | Marie Curie, EMBO | Lecturer, University of Sheffield, UK |
| 58 | Eunyoung Chae | Postdoc | 2007-2017 | - | Assistant Professor, National University of Singapore, Singapore, Singapore |
| 59 | Sang-tae Kim | Postdoc | 2007-2014 | - | Assistant Professor, The Catholic University of Korea, Gyeonggi, South Korea |
| 60 | Jun Cao | Postdoc | 2007-2012 | - | Staff Scientist, Corteva Agriscience, Indianapolis, IN |
| 61 | William Ho | PhD | 2008-2012 | Croucher Fd. | Staff Scientist, Peter MacCallum Cancer Centre, Melbourne, Australia |
| 62 | Jörg Hagmann | MS/PhD | 2008-2015 | - | Product Manager, Computomics, Tübingen, Germany |
| 63 | Felix Ott | PhD | 2008-2013 | - | Staff Scientist, CeGaT, Tübingen, Germany |
| 64 | Pablo Manavella | Postdoc | 2008-2013 | HFSPO | Group Leader, CONICET, Cordoba, Argentina |
| 65 | Beth Rowan | Postdoc | 2009-2016 | A. v. Humboldt Fd. | Project Scientist, UC Davis Genome Center, Davis, CA |
| 66 | Maricris Zaidem | PhD | 2010-2016 | - | Staff Scientist, Oxford University, Oxford, UK |
| 67 | Claude Becker | Postdoc | 2010-2016 | - | Professor, Ludwig Maximilian University, Munich, Germany |
| 68 | Subhashini Muralidharan | PhD | 2010-2015 | - | Scientific Writer, London, UK |
| 69 | Daniel Koenig | Postdoc | 2010-2015 | HFSPO | Assistant Professor, UC Riverside, Riverside, CA |
| 70 | George Wang | Postdoc | 2010-2016 | - | Self-employed, Davis, CA |
| 71 | Johannes Kaut | MS | 2010-2012 | - | Self-employed, Reutlingen, Germany |
| 72 | Liang Wu | Postdoc | 2010-2011 | - | Professor, Zhejiang University, Zhejiang, China |
| 73 | Darya Karelina | PhD | 2010-2015 | - | Self-employed, Tübingen, Germany |
| 74 | Jian-Feng Mao | Postdoc | 2010-2012 | - | Associate Professor, Umeå University, Sweden |
| 75 | Jorge Kageyama | PhD | 2011-2016 | - | Principal Scientist, Genentech, South San Francisco, CA |
| 76 | Xi Wang | Postdoc | 2011-2014 | - | Senior Staff Scientist, BASF, Ghent, Belgium |
| 77 | Diep Ngoc Thi Tran | PhD | 2011-2016 | - | Staff Scientist, Institut Gustave Roussy, Paris, France |
| 78 | Danelle Seymour | PhD | 2011-2015 | - | Assistant Professor, UC Riverside, Riverside, CA |
| 79 | Hernán Burbano | Postdoc | 2012-2014 | - | Assistant Professor, University College London, London, UK |
| 80 | Michael Christie | Postdoc | 2012-2014 | - | Patent Attorney, Shelston IP, Sydney, Australia |
| 81 | Congmao Wang | Postdoc | 2012-2015 | - | Director, OrigiMed, Shanghai, China |

| | | | | | |
|---|---|---|---|---|---|
| 82 | Eun-Cheon Lim | PhD | 2012-2016 | - | Research Director, able edutech, South Korea |
| 83 | Patricia Lang | PhD | 2012-2016 | - | Assistant Professor, UC Berkeley, Berkeley, CA |
| 84 | Emanuele Scacchi | Postdoc | 2012-2017 | SNF, EMBO | Research Associate, University of Tübingen, Tübingen, Germany |
| 85 | Chang Liu | Postdoc | 2012-2015 | Marie Curie | Junior Professor, University of Hohenheim, Germany |
| 86 | Yonca Ural-Blimke | MS | 2012-2013 | | Team Leader, BASF, Ludwigshafen, Germany |
| 87 | François Vasseur | Postdoc | 2013-2016 | - | Staff Scientist, CNRS, Montpellier, France |
| 88 | Jane Devos | MS/PhD | 2013-2016 | - | Staff Scientist, Symrise, Madagascar |
| 89 | Wanyan Xi | Postdoc | 2013-2016 | - | Staff Scientist, Max Planck Institute for Biology Tübingen, Tübingen, Germany |
| 90 | Gautam Shirsekar | Postdoc | 2013-2024 | - | Assistant Professor, University of Tennessee, Knoxville, TN |
| 91 | Efthymia Simeonidi | PhD | 2014-2018 | - | Postdoc, University of Utah, UT |
| 92 | Leila Rabbani | PhD | 2014-2017 | - | Staff Scientist, Karolinska Institute, Stockholm, Sweden |
| 93 | Wangsheng Zhu | Postdoc | 2014-2019 | - | Associate Professor, Chinese Agricultural University, Beijing, China |
| 94 | Derek Lundberg | Postdoc | 2014-2022 | HFSPO | Group Leader, SLU, Uppsala, Sweden |
| 95 | Julian Regalado Perez | PhD | 2014-2019 | - | Postdoc, GLOBE Institute, Copenhagen, Denmark |
| 96 | Anna Lena Van de Weyer | PhD | 2014-2018 | - | Staff Scientist, LaboKlin, Bad Kissingen, Germany |
| 97 | Felix Bemm | Postdoc | 2014-2018 | - | Group Leader, KWS Saat SE, Einbeck, Germany |
| 98 | Rui Wu | Postdoc | 2014-2018 | Marie Curie | Staff Scientist, University of Copenhagen, Denmark |
| 99 | Moisés Expósito Alonso | PhD | 2014-2018 | - | Assistant Professor, UC Berkeley, Berkeley, CA |
| 100 | Sebastián Gomez Petersen | MS | 2015-2016 | - | Program Officer, Syngenta Fd. for Sustainable Agriculture, Basel, Switzerland |
| 101 | Cristina Barragán | MS/PhD | 2015-2020 | - | Strategy Officer, EMBL, Heidelberg, Germany |
| 102 | Talia Karasov | Postdoc | 2015-2020 | EMBO, HFSPO | Assistant Professor, University of Utah, Salt Lake City, UT |
| 103 | Maximilian Collenberg | PhD | 2016-2022 | - | GMP Expert, csi, Schorndorf, Germany |
| 104 | Alba Gonzalez | PhD | 2016-2020 | - | Project Manager, University of Utah, Salt Lake City, UT |
| 105 | Patrick Hüther | MS | 2016-2016 | - | Graduate Student, Gregor Mendel Institute, Vienna, Austria |
| 106 | Or Shalev | PhD | 2016-2021 | DAAD | Postdoc, University of Tübingen, Germany |
| 107 | Wei Yuan | Postdoc | 2016- | - | |
| 108 | Ezgi Süheyla Doğan | MS | 2016 | - | Project Manager, ThermoFisher Scientific, Germany |
| 109 | Bridgit Waithaka | PhD | 2016-2022 | - | Self-employed, Toronto, Canada |

| | | | | | |
|---|---|---|---|---|---|
| 110 | Christian Kubica | PhD | 2016-2022 | | Analyst, Computomics, Tübingen, Germany |
| 111 | Lei Li | Postdoc | 2016-2021 | EMBO, HFSPO | Principal Investigator, Institute for Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China |
| 112 | Anjar Wibowo | Postdoc | 2016-2019 | Marie Curie | Associate Professor, Airlangga University, Surabaya, Indonesia |
| 113 | Ulrich Lutz | Postdoc | 2016-2024 | - | Self-employed |
| 114 | Fernando Rabanal | Postdoc | 2017- | Marie Curie, HFSPO | |
| 115 | Thanvi Srikant | PhD | 2017-2021 | - | Postdoc, ETH, Zurich, Switzerland |
| 116 | Yoav Voichek | Postdoc | 2018-2019 | Marie Curie | Postdoc, Gregor Mendel Institute, Vienna, Austria |
| 117 | Oliver Deusch | Postdoc | 2018-2020 | - | Chief Business Development Officer, HB Technologies, Tübingen, Germany |
| 118 | Haim Ashkenazy | Postdoc | 2018- | A. v. Humboldt Fd. | |
| 119 | Adrián Contreras | PhD | 2018-2024 | - | Postdoc, CNRS, Lille, France |
| 120 | Pablo Carbonell Bejerano | Postdoc | 2018-2022 | Marie Curie | Senior Scientist, CSIC, Instituto de Ciencias de la Vid y del Vino, Logroño, Spain |
| 121 | Alejandra Duque | PhD | 2018-2022 | - | Graduate School Coordinator, MPI for Biology Tübingen, Tübingen, Germany |
| 122 | Sebastian Vorbrugg | MS/PhD | 2018-2024 | - | |
| 123 | Hua Wang | Postdoc | 2019-2021 | - | Associate Professor, Huazhong Agricultural University, Wuhan, China |
| 124 | Pratchaya Pamoj Na Ayutthaya | MS | 2019-2020 | - | Graduate Student, Max Planck Institute for Plant Breeding, Cologne, Germany |
| 125 | Grey Monroe | Postdoc | 2019-2020 | - | Assistant Professor, UC Davis, Davis, CA |
| 126 | Katerina Romanova | PhD | 2020- | - | |
| 127 | Miriam Lucke | PhD | 2020- | - | |
| 128 | Luisa Teasdale | Postdoc | 2020- | - | |
| 129 | Kevin Murray | Postdoc | 2020- | Marie Curie | |
| 130 | Maike Gräff | MS | 2020-2021 | - | Graduate researcher, Max Delbrück Center, Berlin, Germany |
| 131 | Wenfei Xian | PhD | 2021- | - | |
| 132 | Andrea Movilli | PhD | 2021- | - | |
| 133 | Yueqi Tao | PhD | 2021- | - | |
| 134 | Pin-Jou Wu | PhD | 2021- | - | |
| 135 | Shanshan Wang | Postdoc | 2021- | - | |
| 136 | Patience Chatukuta | Postdoc | 2021-2023 | A. v. Humboldt Fd. | Project leader, Max Planck Institute for Biology Tübingen, Tübingen, Germany |

| | | | | | |
|---|---|---|---|---|---|
| 137 | Gal Ofir | Postdoc | 2022- | EMBO, HFSPO | |
| 138 | Laura Bader | MS | 2022 | - | Graduate student, Crick Institute, London, UK |
| 139 | Zhigui Bao | PhD | 2022- | - | |
| 140 | Sheila Roitman | Postdoc | 2023- | CNV Fd., EMBO | |
| 141 | Li He | Postdoc | 2023- | - | |
| 142 | Svitlana Sushko | PhD | 2023- | - | |
| 143 | Eirik Lågeide | PhD | 2024- | - | |
| 144 | Anita Bollmann-Giolai | Postdoc | 2024- | - | |

## Grants Held

*Past:*

| | |
|---|---|
| IBN 94-06948 (Weigel) | 08/01/1994-07/31/1997 |
| **NSF** | $310,000 |
| Role: PI | Salk Institute |
| Role of *LEAFY* in determining floral identity | |
| MCB 94-58210 (Weigel) | 08/01/1994-07/31/1999 |
| **NSF** | $312,500 |
| Role: PI | Salk Institute |
| NSF Young Investigator | |
| 95-37301-2038 (Weigel) | 09/01/1995-08/31/1998 |
| **USDA** | $210,000 |
| Role: PI | Salk Institute |
| Induction of flowers in transgenic plants | |
| OIA 96-02612 (Weigel) | 04/15/1997-01/31/1998 |
| **NSF** | $100,000 |
| Role: PI | Salk Institute |
| Renovation and consolidation of Salk Institute plant growth facilities | |
| Sponsored Research Agreement (Weigel) | 04/01/1997-03/31/2000 |
| **Agritope** | $200,000 |
| Role: PI | Salk Institute |
| LEAFY | |
| Sponsored Research Agreement (Weigel) | 05/01/1997-04/30/1999 |
| **ForBio** | $150,000 |
| Role: PI | Salk Institute |
| LEAFY | |
| RG 303/97 (Weigel) | 05/01/1997-04/30/2000 |
| **HFSPO** | $630,000 ($157,500 to Weigel) |
| Role: PI | Salk Institute |
| Genetic and molecular control of flowering time | |
| IBN 97-23818 (Weigel) | 08/01/1997-07/31/2000 |
| **NSF** | $330,000 |
| Role: PI | Salk Institute |
| The role of meristem-identity genes in floral patterning | |
| MCB-9723823 (Weigel) | 09/01/1997-08/31/2000 |
| **NSF** | $345,000 |
| Role: PI | Salk Institute |
| Genetic and molecular analysis of floral induction | |

| | |
|---|---|
| DE-FG03-98ER20317 (Weigel) | 09/01/1998-08/31/2001 |
| **DOE** | $645,000 |
| Role: PI | Salk Institute |
| Regulation of the floral homeotic gene *AGAMOUS* | |

| | |
|---|---|
| 99-35301-8047 (Weigel) | 09/01/1999-08/31/2002 |
| **USDA** | $280,150 |
| Role: PI | Salk Institute |
| Induction of flowers in transgenic plants | |

| | |
|---|---|
| Sponsored Research Agreement (Weigel) | 07/01/2000-06/30/2002 |
| **Agrinomics/Exelixis Plant Sciences** | $687,120 |
| Role: PI | Salk Institute |
| Activation tagging | |

| | |
|---|---|
| IBN-0078273 (Weigel) | 09/01/2000-08/31/2003 |
| **NSF** | $340,125 |
| Role: PI (terminated 12/31/2002) | Salk Institute |
| The role of the F-box protein UFO in flower development | |

| | |
|---|---|
| MCB-0078277 (Weigel) | 09/01/2000-08/31/2003 |
| **NSF** | $450,000 |
| Role: PI (terminated 12/31/2002) | Salk Institute |
| Gibberellins and floral induction in *Arabidopsis* | |

| | |
|---|---|
| 1 R01 GM62932-01 (Weigel) | 04/01/2001-03/31/2005 |
| **NIH/NIGMS** | $1,425,648 |
| Role: PI (from 01/01/2003, Co-Investigator) | Salk Institute |
| Transcriptional regulation in early flower development | |

| | |
|---|---|
| RGP0235/2001-M (Weigel) | 05/01/2001-04/30/2004 |
| **HFSPO** | $187,500 (to Weigel) |
| Role: PI | Salk Institute/MPI |
| Control of plant architecture by a new signaling pathway | |

| | |
|---|---|
| SFB446 (Jürgens) | 07/01/2003-06/30/2006 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €75,600 (to Weigel) |
| Role: Co-Investigator | MPI |
| Transport of transcription factors between plant cells | |

| | |
|---|---|
| (Nover) | 10/01/2003-09/30/2004 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €190,418 (to Weigel) |
| Role: Co-Investigator | MPI |
| AtGenExpress: A multinational coordinated effort to uncover the transcriptome of the multicellular model organism *Arabidopsis thaliana* | |

1R13GM070207-01 (Weigel) 01/01/2004-02/01/2004
**NIH/NIGMS** $30,000
Role: PI Keystone Symposia
Keystone Conference: Variation and quantitative genetics in model organisms

(Weigel) 10/01/2004-09/30/2005
**Max Planck Society Innovation Funds** €1,000,000
Role: PI MPI
Whole-genome study of intraspecific variation: Re-sequencing the *Arabidopsis thaliana* genome

GABI-REGULATORS (Coupland) 10/01/2004-09/30/2007
**BMBF** €210,000 (to Weigel)
Role: Co-Investigator MPI
Exploiting inter-species conservation in promoter sequences to identify regulators of reproductive development and physiological performance

SY-STEM (Traas) 01/01/2006-12/31/2008
**European Commission Framework Programme 6** €203,223 (to Weigel)
Role: Co-Investigator MPI
Marie Curie Research Training Network: Systems biology of plant stem cells

824/04 (Ori, Eshed, Weigel) 01/01/2006-12/31/2008
**German-Israeli Foundation for Scientific Research** €66,666 (to Weigel)
Role: Co-Investigator MPI
Genetic dissection of dissected leaves

(Hess) 01/01/2006-12/31/2008
**Foundation of the State of Baden-Württemberg** €44,000 (to Weigel)
Role: Co-Investigator MPI
RNAi and regulatory RNA in the genome-wide analysis of gene function of green organisms

1 R01 GM62932-05 (Chory) 04/01/2005-03/31/2009
**NIH/NIGMS** $1,609,979
Role: Co-Investigator Salk Institute
Molecular mechanisms of natural variation in *Arabidopsis*

SFB446 (Jürgens) 07/01/2006-06/30/2009
**DFG (Deutsche Forschungsgemeinschaft)** €174,000 (to Weigel)
Role: Co-Investigator MPI
Integration of flowering time control and primordium formation by microRNAs

ARelatives (Weigel) 04/01/2007-03/31/2010
**European Research Area-Plant Genome (DFG)** €226,800 (to Weigel)
Role: PI MPI
Leveraging the genome sequences of two *Arabidopsis* relatives for evolutionary and ecological genomics

| | |
|---|---|
| ARABRAS (Koornneef) | 04/01/2007-03/31/2010 |
| **European Research Area-Plant Genome (BMBF)** | €230,000 (to Weigel) |
| Role: Co-Investigator | MPI |

Identifying candidate genes for improving plant growth under abiotic stress conditions in *Brassica* crops

| | |
|---|---|
| GABI-GNADE (Koornneef) | 09/01/2007-08/31/2010 |
| **BMBF** | €148,000 (to Weigel) |
| Role: Co-Investigator | MPI |

Exploring the possibility of genome-wide exploitation of natural diversity, across the entire *Arabidopsis* population

| | |
|---|---|
| RGP 57/2007 (Weigel) | 07/01/2007-06/30/2011 |
| **HFSPO** | $337,500 (to Weigel) |
| Role: PI | MPI |

Reproductive isolation and autoimmunity in plants

| | |
|---|---|
| SIROCCO (Baulcombe) | 01/01/2007-09/30/2011 |
| **European Commission Framework Programme 6** | €421,290 (to Weigel) |
| Role: Co-Investigator | MPI |

Integrated Project: Silencing RNAs: organizers and coordinators of complexity in eukaryotic organisms

| | |
|---|---|
| AGRON-OMICS (Hilson) | 10/01/2006-09/30/2011 |
| **European Commission Framework Programme 6** | €615,235 (to Weigel) |
| Role: Co-Investigator | MPI |

Integrated Project: Arabidopsis growth network integrating omics technologies

| | |
|---|---|
| PLANT-KBBE-TRANSNET (Coupland) | 04/01/2009-03/31/2012 |
| **BMBF** | €270,000 (to Weigel) |
| Role: Co-Investigator | MPI |

Transcriptional networks and their evolution in the *Brassicaceae*

| | |
|---|---|
| AENEAS (Varotto) | 04/01/2009-03/31/2013 |
| **European Commission Framework Programme 7** | €449,481 (to Weigel) |
| Role: Co-Investigator | MPI |

Acquired environmental epigenetics advances: from *Arabidopsis* to maize

| | |
|---|---|
| (Weigel) | 07/01/2007-06/30/2014 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €2,500,000 |
| Role: PI | MPI |

Gottfried Wilhelm Leibniz Award

| | |
|---|---|
| SPP1530 Flowering Time Control (Jung) | 08/01/2011-07/31/2014 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €189,530 (to Weigel) |
| Role: Co-Investigator | MPI |

Comparative analysis of miRNA networks regulating flowering

SPP1529 Adaptomics (Kraemer) 08/01/2011-07/31/2014
**DFG (Deutsche Forschungsgemeinschaft)** €203,226 (to Weigel)
Role: Co-Investigator MPI
Phenotypic and genetic variation in *Biscutella didyma* and adaptation to environmental change – a combined ecological-genomic approach

SPP1529 Adaptomics (Kraemer) 12/01/2011-11/30/2014
**DFG (Deutsche Forschungsgemeinschaft)** €287,980 (to Weigel)
Role: Co-Investigator MPI
Starting from scratch: adaptation to variable environments after an extreme bottleneck

GABI-Innovativ-NuGGET (Altmann) 08/01/2011-01/31/2015
**BMBF** €467,622 (to Weigel)
Role: Co-Investigator MPI
Next generation forward genetics for crop plants

(Weigel) 08/01/2011-07/31/2014
**State of Baden Württemberg** €100,000
Role: PI MPI
State Research Prize 2011

SFB1101 (Harter) 04/01/2014-03/31/2017
**DFG (Deutsche Forschungsgemeinschaft)** €211,320 (to Weigel)
Role: Co-Investigator MPI
Regulation of microRNA biogenesis and activity

SPP1529 Adaptomics (Kraemer) 01/01/2015-12/31/2017
**DFG** €214,596 (to Weigel)
Role: Co-Investigator MPI
Starting from scratch: adaptation to variable environments after an extreme bottleneck

ImmuNemesis (Weigel) 03/01/2014-11/30/2019
**ERC** €2,499,900
Role: PI MPI
Advanced Grant: The Plant Immune System: Epistasis and Fitness-Tradeoffs

SPP1529 Adaptomics (Kraemer) 08/01/2014-07/31/2017
**DFG** €188,481 (to Weigel)
Role: Co-Investigator MPI
Phenotypic and genetic variation in *Biscutella didyma* and other Brassicaceae and adaptation to environmental change - a combined ecological-genomic approach

SPP1530 Flowering Time Control (Jung) 10/01/2014-09/30/2017
**DFG** €84,710 (to Weigel)
Role: Co-Investigator MPI
Determination of the relationship between allelic constitution and the flowering time phenotype in grapevine

| | |
|---|---|
| (2Blades) | 7/01/2015-06/30/2018 |
| **Gordon and Betty Moore Foundation** | $436,624 (to Weigel) |
| Role: Co-Investigator | MPI |

1001 NB-LRRomes: discovery and definition of plant immune receptor diversity and evolution

| | |
|---|---|
| Regional Research Alliance (Ludewig) | 10/01/2016-09/30/2019 |
| **State of Baden-Württemberg** | €79,005 (to Weigel) |
| Role: Co-Investigator | MPI |

Heterosis and environmental stability in amaranth hybrids

| | |
|---|---|
| Epidiverse (Verhoeven) | 09/01/2017-02/28/2022 |
| **European Commission Horizon 2020** | €249,216 (to Weigel) |
| Role: Co-Investigator | MPI |

Marie Skłodowska Curie ITN: Epigenetic diversity in ecology

| | |
|---|---|
| SPP2125 DECRyPT (Zuccaro) | 07/01/2018-06/30/2021 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €174,785 (to Weigel) |
| Role: Co-Investigator | MPI |

Effects of microbiome, host and pathogen genotype, and environment on the interaction between *Pseudomonas* isolates and plants

| | |
|---|---|
| SFB1101 (Harter) | 01/01/2018-12/31/2021 |
| **DFG (Deutsche Forschungsgemeinschaft)** | €279,600 (to Weigel) |
| Role: Co-Investigator | MPI |

Specificity in (auto)immune signalling by the atypical resistance protein RPW8

| | |
|---|---|
| AUREATE (Weigel) | 06/01/2018-11/30/2021 |
| **ERA-Coordinating Action in Plant Sciences (DFG)** | €334,550 (to Weigel) |
| Role: PI | MPI |

AUgmented REsilience After Transmission of Epimutations

| | |
|---|---|
| 1001G+ (Nordborg) | 11/01/2018-01/31/2022 |
| **ERA-Coordinating Action in Plant Sciences (DFG)** | €334,550 (to Weigel) |
| Role: Co-Investigator | MPI |

1001 Genomes Plus

*Active:*

| | |
|---|---|
| Novozymes Prize (Weigel) | 01/01//2021-12/31/2025 |
| **Novo Nordisk Foundation** | €605,124 |
| Role: PI | MPI |

Novozymes Prize

| | |
|---|---|
| PATHOCOM (Weigel) | 07/01//2021-06/30/2027 |
| **ERC** | €2,742,525 (to Weigel) |
| Role: Corresponding PI | MPI |

Synergy Grant: Understanding and predicting PATHOgen COMmunities

SPP2125 DECRyPT (Zuccaro) 01/01/2022-12/31/2024
**DFG (Deutsche Forschungsgemeinschaft)** €84,000 (to Weigel)
Role: Co-Investigator MPI
Effects of other microbes and the host on the interaction and eco-logical function of Pseudomonas and Sphingomonas isolates with plants

SFB1101 (Harter) 01/01/2022-12/31/2025
**DFG (Deutsche Forschungsgemeinschaft)** €279,600 (to Weigel)
Role: Co-Investigator MPI
Specificity in (auto)immune signalling by the atypical resistance protein RPW8

TRR356 (Parniske) 01/01/2023-12/31/2026
**DFG (Deutsche Forschungsgemeinschaft)** €320,400 (to Weigel)
Role: Co-Investigator MPI
Genomic and geographic maps of NLRs and matching effectors in the *A. thaliana - H. arabidopsidis* pathosystem

*Pending:*

EC (Ralser) 01/01//2025-12/31/2028
**European Commission Horizon 2020** €280,000 (to Weigel)
Role: Co-Investigator MPI
INFRA-Strain: A platform that integrates distributed natural strains and species collections with multi-omics data for biodiscovery applications

salk®
Where cures begin.

# Salk Adjunct Service/Contributions Form

**Name:** Detlef Weigel **Appointment Start Date:** 2003
**Sponsors:** J. Chory, J. Ecker

To be eligible for appointment and reappointment in the Adjunct series, appointees are expected to be engaged in **at least two** Institute-related activities outlined below. If you are being considered for your first Adjunct Professor appointment, provide information about your plans to engage in the Salk community and select any of the activities you would be interested in below. If you are being considered for reappointment, select your ongoing activities and give a brief summary of your engagement in each activity during the past appointment period. Also provide a summary of your plans to engage in the Salk activities during the next appointment period.

**Salk Activities (list the course/seminar titles, committees, and student names if known)**
** Please note research collaborations with a Salk Faculty sponsor(s) do not qualify as Institute-related activities expected for an Adjunct position*

☒ Giving Seminars, such as those hosted by Sponsors or by the Institute
☐Teaching in Salk-organized courses
☐ Serving on UCSD Student Review committees and/or Thesis Committees in Salk Labs
☐ Reviewing Postdoctoral and other Internal Grants
☐Participating in Salk's outreach and educational efforts to recruit underrepresented minority student applicants

☒Consulting on Salk scientific initiatives or multi-PI grants
☐Serving on Faculty Review Committees
☐Promoting award and nomination opportunities for Salk Faculty
☐ Organizing or participating on Salk Meetings or Conferences
☒ Other

**Salk Service Summary & Plans:** Describe your plans to engage in the activities marked above during the next appointment period (i.e.: Salk Course or Seminar Titles, names of Student or Faculty review committee, description of contributions to grants, etc. if unable to fit above). If you are being considered for reappointment, also describe your engagement in the Salk activities during the last appointment period. You may attach a supplemental letter with these activities as needed.

Apart from discussing my science at invited seminars, I'm giving feedback on the Plant Biology research program, especially the Harnessing Plants Initiative, and I'm serving as mentor in Salk's postdoc mentoring program.