



## UvA-DARE (Digital Academic Repository)

### Phenotypic variation in plants

*Roles for epigenetics*

Lauss, K.

#### Publication date

2017

#### Document Version

Other version

#### License

Other

[Link to publication](#)

#### Citation for published version (APA):

Lauss, K. (2017). *Phenotypic variation in plants: Roles for epigenetics*. [Thesis, fully internal, Universiteit van Amsterdam].

#### General rights

It is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

#### Disclaimer/Complaints regulations

If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: <https://uba.uva.nl/en/contact>, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.

## Bibliography

---

### Bibliography

1. Johannsen W. Elemente der exakten Erblchkeitslehre. Jena, G Fish. 1909; doi:10.1017/CBO9781107415324.004
2. Dhondt S, Wuyts N, Inzé D. Cell to whole-plant phenotyping: The best is yet to come. *Trends Plant Sci.* 2013;18: 1360–1385. doi:10.1016/j.tplants.2013.04.008
3. Alonso-Blanco C, Koornneef M. Natural variation, an underexploited resource of genetic variation for plant genetics. *Trends Plant Sci.* 2000;5: 22–29.
4. Weigel D. Natural Variation in Arabidopsis: From Molecular Genetics to Ecological Genomics. *Plant Physiol.* 2012;158: 2–22. doi:10.1104/pp.111.189845
5. Keurentjes JJB, Bentsink L, Alonso-Blanco C, Hanhart CJ, Vries HB De, Effgen S, et al. Development of a near-isogenic line population of Arabidopsis thaliana and comparison of mapping power with a recombinant inbred line population. *Genetics.* 2007;175: 891–905. doi:10.1534/genetics.106.066423
6. Campos EI, Reinberg D. Histones: annotating chromatin. *Annu Rev Genet.* 2009;43: 559–99. doi:10.1146/annurev.genet.032608.103928
7. Law J a, Jacobsen SE. Establishing, maintaining and modifying DNA methylation patterns in plants and animals. *Nat Rev Genet.* Nature Publishing Group; 2010;11: 204–20. doi:10.1038/nrg2719
8. Waddington CH. The epigenotype. *Endeavour.* 1942;1: 18–20.
9. Riggs, A.D.; Martienssen, R.A.; Russo VEA. Epigenetic Mechanisms of Gene Regulation. Cold Spring Harb Lab Press. 1996;32: 1–4.
10. Riggs, A.D.; Porter TN. Overview of epigenetic mechanisms. Cold Spring Harb Lab Press. 1996;32: 29–45.
11. Bird A. Perceptions of epigenetics. *Nature.* 2007;447: 396–8. doi:10.1038/nature05913
12. Goldberg AD, Allis CD, Bernstein E. Epigenetics: A Landscape Takes Shape. *Cell.* 2007;128: 635–638. doi:10.1016/j.cell.2007.02.006
13. Jiang D, Berger F. Histone variants in plant transcriptional regulation. *BBA - Gene Regul Mech.* Elsevier B.V.; 2016; doi:10.1016/j.bbagr.2016.07.002
14. Zink LM, Hake SB. Histone variants: Nuclear function and disease. *Curr Opin Genet Dev.* Elsevier Ltd; 2016;37: 82–89. doi:10.1016/j.gde.2015.12.002
15. Jackson JP, Lindroth AM, Cao X, Jacobsen SE. Control of CpNpG DNA methylation by the KRYPTONITE histone H3 methyltransferase. *Nature.* 2002;416: 556–60. doi:10.1038/nature731
16. Lindroth AM, Shultis D, Jasencakova Z, Fuchs J, Johnson L, Schubert D, et al. Dual histone H3 methylation marks at lysines 9 and 27 required for interaction with CHROMOMETHYLASE3. *EMBO J.* 2004;23: 4286–4296. doi:10.1038/sj.emboj.7600430
17. Matzke M, Mosher R. RNA-directed DNA methylation: an epigenetic pathway of increasing complexity. *Nat Rev Genet.* 2014;15: 394–408. doi:10.1038/nrg3683
18. Zemach A, Kim MY, Hsieh P-H, Coleman-Derr D, Eshed-Williams L, Thao K, et al.

- 
- The Arabidopsis Nucleosome Remodeler DDM1 Allows DNA Methyltransferases to Access H1-Containing Heterochromatin. *Cell*. Elsevier Inc.; 2013;153: 193–205. Available: <http://dx.doi.org/10.1016/j.cell.2013.02.033>
19. Schmitz RJ, Schultz MD, Urich MA, Nery JR, Pelizzola M, Libiger O, et al. Patterns of population epigenomic diversity. *Nature*. 2013;495: 193–198. Available: <http://www.nature.com/doi/10.1038/nature11968>
  20. Mari-Ordóñez A, Marchais A, Etcheverry M, Martin A, Colot V, Voinnet O. Reconstructing de novo silencing of an active plant retrotransposon. *Nat Genet*. Nature Publishing Group; 2013;45: 1029–39. doi:10.1038/ng.2703
  21. Kato M, Takashima K, Kakutani T. Epigenetic control of CACTA transposon mobility in *Arabidopsis thaliana*. *Genetics*. 2004;168: 961–9. doi:10.1534/genetics.104.029637
  22. Zilberman D, Gehring M, Tran RK, Ballinger T, Henikoff S. Genome-wide analysis of *Arabidopsis thaliana* DNA methylation uncovers an interdependence between methylation and transcription. *Nat Genet*. 2007;39: 61–9. doi:10.1038/ng1929
  23. Takuno S, Gaut BS. Body-methylated genes in *Arabidopsis thaliana* are functionally important and evolve slowly. *Mol Biol Evol*. 2012;29: 219–227. doi:10.1093/molbev/msr188
  24. Capuano F, Mülleder M, Kok R, Blom HJ, Ralser M. Cytosine DNA methylation is found in *Drosophila melanogaster* but absent in *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, and other yeast species. *Anal Chem*. 2014;86: 3697–3702. doi:10.1021/ac500447w
  25. Finnegan EJ, Peacock WJ, Dennis ES. Reduced DNA methylation in *Arabidopsis thaliana* results in abnormal plant development. *Proc Natl Acad Sci U S A*. 1996;93: 8449–8454. doi:10.1073/pnas.93.16.8449
  26. Kakutani T, Jeddeloh J a, Richards EJ. Characterization of an *Arabidopsis thaliana* DNA hypomethylation mutant. *Nucleic Acids Res*. 1995;23: 130–7. Available: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=306640&tool=pmcentrez&rendertype=abstract>
  27. Kakutani T, Jeddeloh JA, Flowers SK, Munakata K, Richards EJ. Developmental abnormalities and epimutations associated with DNA hypomethylation mutations. *Proc Natl Acad Sci U S A*. 1996;93: 12406–12411. doi:10.1073/pnas.93.22.12406
  28. Li Q, Eichten SR, Hermanson PJ, Zaunbrecher VM, Song J, Wendt J, et al. Genetic perturbation of the maize methylome. *Plant Cell*. 2014;26: 4602–16. doi:10.1105/tpc.114.133140
  29. Li Q, Gent JI, Zynda G, Song J, Makarevitch I, Hirsch CD, et al. RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. *Proc Natl Acad Sci U S A*. 2015; 1514680112-. doi:10.1073/pnas.1514680112
  30. Lippman Z, Gendrel A-V, Black M, Vaughn MW, Dedhia N, McCombie WR, et al.

## Bibliography

---

- Role of transposable elements in heterochromatin and epigenetic control. *Nature*. 2004;430: 471–476. doi:10.1038/nature02651
31. The Arabidopsis Genome Initiative. Analysis of the genome sequence of the Flowering plant *Arabidopsis thaliana*. *Nature*. 2000;408: 796–815. doi:10.1038/35048692
32. West PT, Li Q, Ji L, Eichten SR, Song J, Vaughn MW, et al. Genomic distribution of H3K9me2 and DNA methylation in a maize genome. *PLoS One*. 2014;9: 1–10. doi:10.1371/journal.pone.0105267
33. Gent JI, Ellis NA, Guo L, Harkess AE, Yao Y, Zhang X, et al. CHH islands: De novo DNA methylation in near-gene chromatin regulation in maize. *Genome Res*. 2013;23: 628–637. doi:10.1101/gr.146985.112
34. O'Malley RC, Ecker JR. Epiallelic variation in *Arabidopsis thaliana*. *Cold Spring Harb Symp Quant Biol*. 2012;77: 135–45. doi:10.1101/sqb.2012.77.014571
35. Weigel D, Colot V. Epialleles in plant evolution. *Genome Biol*. 2012;13: 249. doi:10.1186/gb-2012-13-10-249
36. Soppe WJ, Jacobsen SE, Alonso-Blanco C, Jackson JP, Kakutani T, Koornneef M, et al. The late flowering phenotype of *fwa* mutants is caused by gain-of-function epigenetic alleles of a homeodomain gene. *Mol Cell*. 2000;6: 791–802. Available: <http://www.ncbi.nlm.nih.gov/pubmed/11090618>
37. Stam M, Belele C, Dorweiler JE, Chandler VL. Differential chromatin structure within a tandem array 100 kb upstream of the maize *b1* locus is associated with paramutation. *Genes Dev*. 2002;16: 1906–18. doi:10.1101/gad.1006702
38. Bender J, Fink GR. Epigenetic control of an endogenous gene family is revealed by a novel blue fluorescent mutant of *Arabidopsis*. *Cell*. 1995;83: 725–34. Available: <http://www.ncbi.nlm.nih.gov/pubmed/8521489>
39. Henderson IR, Jacobsen SE. Tandem repeats upstream of the *Arabidopsis* endogene *SDC* recruit non-CG DNA methylation and initiate siRNA spreading. *Genes Dev*. 2008;22: 1597–606. doi:10.1101/gad.1667808
40. Quadrana L, Almeida J, Asís R, Duffy T, Dominguez PG, Bermúdez L, et al. Natural occurring epialleles determine vitamin E accumulation in tomato fruits. *Nat Commun*. 2014;5: 3027. doi:10.1038/ncomms5027
41. Miura K, Agetsuma M, Kitano H, Yoshimura A, Matsuoka M, Jacobsen SE, et al. A metastable *DWARF1* epigenetic mutant affecting plant stature in rice. *Proc Natl Acad Sci U S A*. 2009;106: 11218–11223. doi:10.1073/pnas.0901942106
42. Chodavarapu RK, Feng S, Ding B, Simon SA, Lopez D, Jia Y, et al. Transcriptome and methylome interactions in rice hybrids. *Proc Natl Acad Sci U S A*. Department of Molecular, Cell and Developmental Biology, University of California, Los Angeles, CA 90095, USA.; 2012;109: 12040–12045. Available: <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmed&id=22778444&retmode=ref&cmd=prlinks>
43. He G, Zhu X, Elling AA, Chen L, Wang X, Guo L, et al. Global epigenetic and

- transcriptional trends among two rice subspecies and their reciprocal hybrids. *Plant Cell*. 2010;22: 17–33. doi:10.1105/tpc.109.072041
44. Eichten SR, Swanson-Wagner R a, Schnable JC, Waters AJ, Hermanson PJ, Liu S, et al. Heritable epigenetic variation among maize inbreds. *PLoS Genet*. 2011;7: e1002372. doi:10.1371/journal.pgen.1002372
45. Barber WT, Zhang W, Win H, Varala KK, Dorweiler JE, Hudson ME, et al. Repeat associated small RNAs vary among parents and following hybridization in maize. *Proc Natl Acad Sci U S A*. Department of Crop Sciences, University of Illinois, Urbana, IL 61801, USA.; 2012;109: 10444–10449. Available: <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmed&id=22689990&retmode=ref&cmd=prlinks>
46. Regulski M, Lu Z, Kendall J, Donoghue MTA, Reinders J, Llaça V, et al. The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. *Genome Res*. 2013;23: 1651–1662. Available: <http://genome.cshlp.org/cgi/doi/10.1101/gr.153510.112>
47. Groszmann M, Greaves IK, Albertyn ZI, Scofield GN, Peacock WJ, Dennis ES. Changes in 24-nt siRNA levels in Arabidopsis hybrids suggest an epigenetic contribution to hybrid vigor. *Proc Natl Acad Sci U S A*. Commonwealth Scientific and Industrial Research Organization Plant Industry, Canberra, Australian Capital Territory 2601, Australia.; 2011;108: 2617–2622. Available: <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmed&id=21266545&retmode=ref&cmd=prlinks>
48. Shen H, He H, Li J, Chen W, Wang X, Guo L, et al. Genome-Wide Analysis of DNA Methylation and Gene Expression Changes in Two Arabidopsis Ecotypes and Their Reciprocal Hybrids. *Plant Cell*. 2012;24: 875–892. Available: <http://www.plantcell.org/cgi/doi/10.1105/tpc.111.094870>
49. Zhai J, Liu J, Liu B, Li P, Meyers BC, Chen X, et al. Small RNA-directed epigenetic natural variation in Arabidopsis thaliana. *PLoS Genet*. 2008;4: e1000056. doi:10.1371/journal.pgen.1000056
50. Moghaddam AMB, Roudier F, Seifert M, Bérard C, Magniette M-LM, Ashtiyani RK, et al. Additive inheritance of histone modifications in Arabidopsis thaliana intra-specific hybrids. *Plant J*. 2011;67: 691–700. doi:10.1111/j.1365-313X.2011.04628.x
51. Yang M, Wang X, Huang H, Ren D, Su Y, Zhu P, et al. Natural variation of H3K27me3 modification in two Arabidopsis accessions and their hybrid. *J Integr Plant Biol*. 2016;58: 466–474. doi:10.1111/jipb.12443
52. Johannes F, Porcher E, Teixeira FK, Saliba-Colombani V, Simon M, Agier N, et al. Assessing the impact of transgenerational epigenetic variation on complex traits. *PLoS Genet*. 2009;5. doi:10.1371/journal.pgen.1000530
53. Reinders J, Wulff BBH, Mirouze M, Mari-Ordonez A, Dapp M, Rozhon W, et al. Compromised stability of DNA methylation and transposon immobilization in

## Bibliography

---

- mosaic Arabidopsis epigenomes. *Genes Dev.* 2009;23: 939–950. doi:10.1101/gad.524609
54. Mathieu O, Reinders J, Čaikovski M, Smathajitt C, Paszkowski J. Transgenerational Stability of the Arabidopsis Epigenome Is Coordinated by CG Methylation. *Cell.* 2007;130: 851–862. doi:10.1016/j.cell.2007.07.007
55. Roux F, Colomé-Tatché M, Edelist C, Wardenaar R, Guerche P, Hospital F, et al. Genome-wide epigenetic perturbation jump-starts patterns of heritable variation found in nature. *Genetics.* 2011;188: 1015–7. doi:10.1534/genetics.111.128744
56. Cortijo S, Wardenaar R, Colomé-Tatché M, Gilly A, Etcheverry M, Labadie K, et al. Mapping the epigenetic basis of complex traits. *Science.* 2014;343: 1145–1148. doi:10.1126/science.1248127
57. Kooke R, Johannes F, Wardenaar R, Becker F, Etcheverry M, Colot V, et al. Epigenetic Basis of Morphological Variation and Phenotypic Plasticity in Arabidopsis thaliana. *Plant Cell.* 2015;27: 337–348. doi:10.1105/tpc.114.133025
58. Dapp M, Reinders J, Bédiée A, Balsera C, Bucher E, Theiler G, et al. Heterosis and inbreeding depression of epigenetic Arabidopsis hybrids. *Nat Plants.* Macmillan Publishers Limited; 2015;1: 15092. doi:10.1038/nplants.2015.92
59. Hauben M, Haesendonckx B, Standaert E, Kelen K Van Der, Azmi A, Breusegem F Van, et al. Energy use efficiency is characterized by an epigenetic component that can be directed. *Proc Natl Acad Sci U S A.* 2009;106: 20109–14. doi:10.1073/pnas.0908755106
60. Verkest A, Byzova M, Martens C, Willems P, Verwulgen T, Slabbinck B, et al. Selection for Improved Energy Use Efficiency and Drought Tolerance in Canola Results in Distinct Transcriptome and Epigenome Changes. [Internet]. *Plant physiology.* 2015. doi:10.1104/pp.15.00155
61. Soltis PS, Soltis DE. The Role of Hybridization in Plant Speciation. *Annu Rev Plant Biol.* 2009;60: 561–88. doi:10.1146/annurev.arplant.043008.092039
62. Chen ZJ. Molecular mechanisms of polyploidy and hybrid vigor. *Trends Plant Sci.* 2010;15: 57–71. doi:10.1016/j.tplants.2009.12.003
63. Chen ZJ. Genomic and epigenetic insights into the molecular bases of heterosis. *Nat Rev Genet.* Nature Publishing Group; 2013;14: 471–82. doi:10.1038/nrg3503
64. Wendel JF, Cronn RC. Polyploidy and the Evolutionary history of Cotton. *Adv Agron.* 2003;78: 139–186.
65. Salamini F, Ozkan H, Brandolini A, Schäfer-Pregl R, Martin W. Genetics and geography of wild cereal domestication in the near east. *Nat Rev Genet.* 2002;3: 429–441. doi:10.1038/nrg817
66. Maheshwari S, Barbash D a. The Genetics of Hybrid Incompatibilities. *Annu Rev Genet.* 2011;45: 331–355. doi:10.1146/annurev-genet-110410-132514
67. Schnable PS, Springer NM. Progress toward understanding heterosis in crop plants. *Annu Rev Plant Biol.* 2013;64: 71–88. doi:10.1146/annurev-arplant-042110-103827

68. Darwin CR. The effects of Cross and Self Fertilization in the Vegetable Kingdom. John Murray, London. 1876;
69. East EM. Heterosis. *Genetics*. 1936;21: 336–397.
70. Shull GH. The Composition of a Field of Maize. 1905; 296–301.
71. Duvick DN. Biotechnology in the 1930s: the development of hybrid maize. *Nat Rev Genet*. 2001;2: 69–74. doi:10.1038/35047587
72. Groszmann M, Greaves IK, Fujimoto R, James Peacock W, Dennis ES. The role of epigenetics in hybrid vigour. *Trends Genet*. 2013;29: 684–690. Available: <http://linkinghub.elsevier.com/retrieve/pii/S016895251300125X>
73. Bruce AB. The Mendelian Theory of Heredity and the Augmentation of Vigor. *Science*. 1910;32: 627–628.
74. Jones DF. Dominance of linked Factors as a means of accounting for Heterosis. *Genetics*. 1917;2: 466–479.
75. Yu SB, Li JX, Xu CG, Tan YF, Gao YJ, Li XH, et al. Importance of epistasis as the genetic basis of heterosis in an elite rice hybrid. *Proc Natl Acad Sci U S A*. 1997;94: 9226–31. Available: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=23127&tool=pmcentrez&rendertype=abstract>
76. Chen F, He G, He H, Chen W, Zhu X, Liang M, et al. Expression analysis of miRNAs and highly-expressed small RNAs in two rice subspecies and their reciprocal hybrids. *J Integr Plant Biol*. 2010;52: 971–80. doi:10.1111/j.1744-7909.2010.00985.x
77. Shivaprasad P V, Dunn RM, Santos BA, Bassett A, Baulcombe DC. Extraordinary transgressive phenotypes of hybrid tomato are influenced by epigenetics and small silencing RNAs. *EMBO J*. Nature Publishing Group; 2012;31: 257–266. doi:10.1038/emboj.2011.458
78. Rigal M, Becker C, Pélissier T, Pogorelcnik R, Devos J, Ikeda Y, et al. Epigenome confrontation triggers immediate reprogramming of DNA methylation and transposon silencing in *Arabidopsis thaliana* F1 epihybrids. *Proc Natl Acad Sci*. 2016; 201600672. doi:10.1073/pnas.1600672113
79. Greaves IK, Groszmann M, Ying H, Taylor JM, Peacock WJ, Dennis ES. Trans chromosomal methylation in *Arabidopsis* hybrids. *Proc Natl Acad Sci U S A*. 2012;109: 3570–3575. doi:10.1073/pnas.1201043109
80. Chandler VL. Paramutation: From Maize to Mice. *Cell*. 2007;128: 641–645. doi:10.1016/j.cell.2007.02.007
81. Hövel I, Pearson NA, Stam M. Cis-acting determinants of paramutation. *Semin Cell Dev Biol*. Elsevier Ltd; 2015; doi:10.1016/j.semcdb.2015.08.012
82. Giacomelli BJ, Hollick JB. Trans-Homolog Interactions Facilitating Paramutation in Maize. *Plant Physiol*. 2015;168: 1226–1236. doi:10.1104/pp.15.00591
83. Bateson W, Pellew C. On the genetics of “rogues” among culinary peas (*Pisum sativum*). *J Genet*. 1915;5: 15–36.

## Bibliography

---

84. Hagemann R. Somatic conversion in *Lycopersicon esculentum* Mill. *Zeitschrift fuer Vererbungslehre*. 1958;89: 587–613.
85. de Vanssay A, Bougé A-L, Boivin A, Hermant C, Teyssset L, Delmarre V, et al. Paramutation in *Drosophila* linked to emergence of a piRNA-producing locus. *Nature*. 2012;490: 112–115. doi:10.1038/nature11416
86. Rassoulzadegan M, Grandjean V, Pierre G, Stephane V, Isabelle G, Francois C. RNA-mediated non-mendelian inheritance of an epigenetic change in the mouse. *Nature*. 2006;441: 469–474. doi:10.1038/nature04674
87. Greaves IK, Groszmann M, Dennis ES, Peacock WJ. Trans-chromosomal Methylation. *Epigenetics*. 2012;7: 800–805.
88. Chandler VL, Stam M. Chromatin conversations: mechanisms and implications of paramutation. *Nat Rev Genet*. 2004;5: 532–544. doi:10.1038/nrg1378
89. Chandler VL, Eggleston WB, Dorweiler JE. Paramutation in maize. *Plant Mol Biol*. 2000;43: 121–145. doi:10.1023/A:1006499808317
90. Patterson G, Thorpe C, Chandler V. Paramutation, an allelic interaction, is associated with a stable and heritable reduction of transcription of the maize b regulatory gene. *Genetics*. 1993;135: 881–894.
91. Haring M, Bader R, Louwers M, Schwabe A, Van Driel R, Stam M. The role of DNA methylation, nucleosome occupancy and histone modifications in paramutation. *Plant J*. 2010;63: 366–378. doi:10.1111/j.1365-313X.2010.04245.x
92. Alleman M, Sidorenko L, McGinnis K, Seshadri V, Dorweiler JE, White J, et al. An RNA-dependent RNA polymerase is required for paramutation in maize. *Nature*. 2006;442: 295–298. doi:10.1038/nature04884
93. Sidorenko L, Dorweiler JE, Cigan AM, Arteaga-Vazquez M, Vyas M, Kermicle J, et al. A dominant mutation in mediator of paramutation2, one of three second-largest subunits of a plant-specific RNA polymerase, disrupts multiple siRNA silencing processes. *PLoS Genet*. 2009;5. doi:10.1371/journal.pgen.1000725
94. Erhard KFJ, Stonaker JL, Parkinson SE, Lim JP, Hale CJ, Hollick JB. RNA Polymerase IV Functions in Paramutation in *Zea mays*. *Science*. 2009;323: 1201–1205.
95. Sloan AE, Sidorenko L, McGinnis KM. Diverse gene silencing mechanisms with distinct requirements for RNA polymerase subunits in *Zea mays*. *Genetics*. 2014;198: 1031–1042.
96. Stonaker JL, Lim JP, Erhard KF, Hollick JB. Diversity of Pol IV function is defined by mutations at the maize *rmr7* locus. *PLoS Genet*. 2009;5: e1000706. doi:10.1371/journal.pgen.1000706
97. Nobuta K, Lu C, Shrivastava R, Pillay M, Paoli E De, Accerbi M, et al. Distinct size distribution of endogenous siRNAs in maize : Evidence from deep sequencing in the *mop1-1* mutant. *PNAS*. 2008;105: 14958–14963.
98. Gent JI, Madzima TF, Bader R, Kent MR, Zhang X, Stam M, et al. Accessible DNA and Relative Depletion of H3K9me2 at Maize Loci Undergoing RNA-Directed DNA Methylation. *Plant Cell*. 2014;26: 4903–4917. doi:10.1105/tpc.114.130427



99. Arteaga-Vazquez M, Sidorenko L, Rabanal F a, Shrivistava R, Nobuta K, Green PJ, et al. RNA-mediated trans-communication can establish paramutation at the b1 locus in maize. *Proc Natl Acad Sci U S A*. 2010;107: 12986–12991. doi:10.1073/pnas.1007972107
100. Belele CL, Sidorenko L, Stam M, Bader R, Arteaga-Vazquez M a., Chandler VL. Specific Tandem Repeats Are Sufficient for Paramutation-Induced Trans-Generational Silencing. *PLoS Genet*. 2013;9: e1003773. doi:10.1371/journal.pgen.1003773
101. Bologna NG, Voinnet O. The Diversity, Biogenesis, and Activities of Endogenous Silencing Small RNAs in Arabidopsis. *Annu Rev Plant Biol*. 2014;65: 473–503. doi:10.1146/annurev-arplant-050213-035728
102. Xu C, Tian J, Mo B. siRNA-mediated DNA methylation and H3K9 dimethylation in plants. *Protein Cell*. 2013;4: 656–663. doi:10.1007/s13238-013-3052-7
103. Springer NM. Epigenetics and crop improvement. *Trends Genet*. Elsevier Ltd; 2013;29: 241–247. doi:10.1016/j.tig.2012.10.009
104. Richards EJ. Natural epigenetic variation in plant species: a view from the field. *Curr Opin Plant Biol*. Elsevier Ltd; 2011;14: 204–9. doi:10.1016/j.pbi.2011.03.009
105. Finer S, Holland ML, Nanty L, Rakyan VK. Review Article The Hunt for the Epiallele. 2011;11. doi:10.1002/em
106. Colomé-Tatché M, Cortijo S, Wardenaar R, Morgado L, Lahouze B, Sarazin A, et al. Features of the Arabidopsis recombination landscape resulting from the combined loss of sequence variation and DNA methylation. *Proc Natl Acad Sci National Acad Sciences*; 2012;109: 16240–16245. Available: <http://www.pnas.org/content/109/40/16240.short>
107. Massonnet C, Vile D, Fabre J, Hannah M a., Caldana C, Lisek J, et al. Probing the Reproducibility of Leaf Growth and Molecular Phenotypes: A Comparison of Three Arabidopsis Accessions Cultivated in Ten Laboratories. *Plant Physiol*. 2010;152: 2142–2157. doi:10.1104/pp.109.148338
108. Rieseberg LH, Archer M a, Wayne RK. Transgressive segregation, adaptation and speciation. *Heredity (Edinb)*. 1999;83 ( Pt 4): 363–372. doi:10.1038/sj.hdy.6886170
109. Paterson AH, Lander ES, Hewitt JD, Peterson S, Lincoln SE, Tanksley SD. Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. *Nature*. 1988. pp. 721–726. doi:10.1038/335721a0
110. VAN Ooijen JW. Multipoint maximum likelihood mapping in a full-sib family of an outbreeding species. *Genet Res (Camb)*. 2011;93: 343–349. doi:10.1017/S0016672311000279
111. Lander ES, Botstein D. Mapping Mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics*. 1989;121: 185–199.
112. Churchill GA, Doerge RW. Empirical Threshold Values for Quantitative Trait

## Bibliography

---

- Mapping. *Genetics*. 1994;138: 963–971. Available: <Go to ISI>://WOS:A1994PP05000036
113. Dubin MJ, Zhang P, Meng D, Remigereau M-S, Osborne EJ, Paolo Casale F, et al. DNA methylation in *Arabidopsis* has a genetic basis and shows evidence of local adaptation. *Elife*. 2015;4: e05255. doi:10.7554/eLife.05255
114. Rajeevkumar S, Anunanthini P, Sathishkumar R. Epigenetic silencing in transgenic plants. *Front Plant Sci*. 2015;6: 693. doi:10.3389/fpls.2015.00693
115. McGinnis KM. RNAi for functional genomics in plants. *Briefings Funct Genomics Proteomics*. 2010;9: 111–117. doi:10.1093/bfpg/elp052
116. Kungulovski G, Jeltsch A. Epigenome Editing: State of the Art, Concepts, and Perspectives. *Trends Genet*. Elsevier Ltd; 2015;32: 101–113. doi:10.1016/j.tig.2015.12.001
117. Meyer RC, Toerjek O, Becher M, Altmann T. Heterosis of Biomass Production in *Arabidopsis*. Establishment during Early Development. *PLANT Physiol*. 2004;134: 1813–1823. doi:10.1104/pp.103.033001.hybrid
118. Crow JF. Anecdotal, Historical and Critical Commentaries on Genetics 90 Years Ago : The Beginning of Hybrid Maize. *Genetics*. 1998;148: 923–928.
119. Crow JF. Alternative Hypotheses of Hybrid Vigor. *Genetics*. 1948;33: 477–487. Available: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1209419&tool=pmc-entrez&rendertype=abstract>
120. Ni Z, Kim E-D, Ha M, Lackey E, Liu J, Zhang Y, et al. Altered circadian rhythms regulate growth vigour in hybrids and allopolyploids. *Nature*. Nature Publishing Group; 2009;457: 327–333. doi:10.1038/nature07523
121. Greaves IK, Groszmann M, Wang A, Peacock WJ, Dennis ES. Inheritance of Trans Chromosomal Methylation patterns from *Arabidopsis* F1 hybrids. *Proc Natl Acad Sci U S A*. 2014;111: 2017–2022. doi:10.1073/pnas.1323656111
122. Vongs A, Kakutani T, Martienssen RA, Richards EJ. *Arabidopsis thaliana* DNA methylation mutants. *Science*. 1993;260: 1926–1928. doi:10.1126/science.8316832
123. Groszmann M, Gonzalez-Bayon R, Greaves IK, Wang L, Huen AK, Peacock WJ, et al. Intraspecific *Arabidopsis* hybrids show different patterns of heterosis despite the close relatedness of the parental genomes. *Plant Physiol*. 2014;166: 265–280. doi:10.1104/pp.114.243998
124. Wang L, Greaves IK, Groszmann M, Wu LM, Dennis ES, Peacock WJ. Hybrid mimics and hybrid vigor in *Arabidopsis*. *Proc Natl Acad Sci*. 2015;112: E4959–E4967. doi:10.1073/pnas.1514190112
125. Bennett E, Roberts J a., Wagstaff C. Manipulating resource allocation in plants. *J Exp Bot*. 2012;63: 3391–3400. doi:10.1093/jxb/err442
126. Tsukahara S, Kobayashi A, Kawabe A, Mathieu O, Miura A, Kakutani T. Bursts of retrotransposition reproduced in *Arabidopsis*. *Nature*. Nature Publishing Group;

- 
- 2009;461: 423–427. doi:10.1038/nature08351
127. Rosado A, Li R, van de Ven W, Hsu E, Raikhel N V. Arabidopsis ribosomal proteins control developmental programs through translational regulation of auxin response factors. *Proc Natl Acad Sci U S A*. 2012;109: 19537–19544. doi:10.1073/pnas.1214774109
128. Pinon V, Etchells JP, Rossignol P, Collier S a, Arroyo JM, Martienssen R a, et al. Three PIGGYBACK genes that specifically influence leaf patterning encode ribosomal proteins. *Development*. 2008;135: 1315–1324. doi:10.1242/dev.016469
129. Gachomo EW, Jimenez-Lopez JC, Baptiste LJ, Kotchoni SO. GIGANTUS1 (GTS1), a member of Transducin/WD40 protein superfamily, controls seed germination, growth and biomass accumulation through ribosome-biogenesis protein interactions in Arabidopsis thaliana. *BMC Plant Biol. BMC Plant Biology*; 2014;14: 1–17. doi:10.1186/1471-2229-14-37
130. Oikawa K, Kasahara M, Kiyosue T, Kagawa T, Suetsugu N. CHLOROPLAST UNUSUAL POSITIONING1 Is Essential for proper Chloroplast positioning. 2003;15: 2805–2815. doi:10.1105/tpc.016428.tions.
131. Stroud H, Do T, Du J, Zhong X, Feng S, Johnson L, et al. Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. *Nat Struct Mol Biol*. 2014;21: 64–72. doi:10.1038/nsmb.2735
132. Chen X, Zhou D-X. Rice epigenomics and epigenetics: challenges and opportunities. *Curr Opin Plant Biol. Elsevier Ltd*; 2013;16: 164–9. doi:10.1016/j.pbi.2013.03.004
133. Lister R, O'Malley RC, Tonti-Filippini J, Gregory BD, Berry CC, Millar AH, et al. Highly Integrated Single-Base Resolution Maps of the Epigenome in Arabidopsis. *Cell. Elsevier Inc.*; 2008;133: 523–536. Available: <http://linkinghub.elsevier.com/retrieve/pii/S0092867408004480>
134. Stroud H, Greenberg MVC, Feng S, Bernatavichute Y V, Jacobsen SE. Comprehensive analysis of silencing mutants reveals complex regulation of the Arabidopsis methylome. *Cell. Elsevier Inc.*; 2013;152: 352–64. doi:10.1016/j.cell.2012.10.054
135. Cokus SJ, Feng S, Zhang X, Chen Z, Merriman B, Haudenschild CD, et al. Shotgun bisulphite sequencing of the Arabidopsis genome reveals DNA methylation patterning. *Nature. Nature Publishing Group*; 2008;452: 215–219. Available: <http://www.nature.com/nature/journal/v452/n7184/abs/nature06745.html>
136. Zhang X, Yazaki J, Sundaresan A, Cokus S, Chan SWL, Chen H, et al. Genome-wide High-Resolution Mapping and Functional Analysis of DNA Methylation in Arabidopsis. *Cell*. 2006;126: 1189–1201. doi:10.1016/j.cell.2006.08.003
137. Saze H, Mittelsten Scheid O, Paszkowski J. Maintenance of CpG methylation is essential for epigenetic inheritance during plant gametogenesis. *Nat Genet*. 2003;34: 65–9. doi:10.1038/ng1138

## Bibliography

---

138. Mirouze M, Reinders J, Bucher E, Nishimura T, Schneeberger K, Ossowski S, et al. Selective epigenetic control of retrotransposition in Arabidopsis. *Nature*. Nature Publishing Group; 2009;461: 1–5. doi:10.1038/nature08328
139. Kato M, Miura A, Bender J, Jacobsen SE, Kakutani T. Role of CG and non-CG methylation in immobilization of transposons in Arabidopsis. *Curr Biol*. 2003;13: 421–426. doi:10.1016/S0960-9822(03)00106-4
140. Schmitz RJ, Schultz MD, Urich MA, Nery JR, Pelizzola M, Libiger O, et al. Patterns of population epigenomic diversity. *Nature*. 2013;495: 193–8. doi:10.1038/nature11968
141. Li Q, Eichten SR, Hermanson PJ, Springer NM. Inheritance Patterns and Stability of DNA Methylation Variation in Maize Near-Isogenic Lines. *Genetics*. 2013; Available: papers2://publication/doi/10.1534/genetics.113.158980
142. Eichten SR, Briskine R, Song J, Li Q, Swanson-Wagner R, Hermanson PJ, et al. Epigenetic and Genetic Influences on DNA Methylation Variation in Maize Populations. *Plant Cell*. 2013;25: 2783–2797. Available: <http://www.plantcell.org/cgi/doi/10.1105/tpc.113.114793>
143. Li X, Zhu J, Hu F, Ge S, Ye M, Xiang H, et al. Single-base resolution maps of cultivated and wild rice methylomes and regulatory roles of DNA methylation in plant gene expression. *BMC Genomics*. 2012;13: 300. doi:10.1186/1471-2164-13-300
144. Garg R, Narayana Chevala V, Shankar R, Jain M. Divergent DNA methylation patterns associated with gene expression in rice cultivars with contrasting drought and salinity stress response. *Sci Rep*. Nature Publishing Group; 2015;5: 14922. doi:10.1038/srep14922
145. Foerster AM, Dinh HQ, Sedman L, Wohlrab B, Scheid OM. Genetic rearrangements can modify chromatin features at epialleles. *PLoS Genet*. 2011;7. doi:10.1371/journal.pgen.1002331
146. Zhang Q, Wang D, Lang Z, He L, Yang L, Zeng L, et al. Methylation interactions in Arabidopsis hybrids require RNA-directed DNA methylation and are influenced by genetic variation. 2016; doi:10.1073/pnas.1607851113
147. Ji L, Sasaki T, Sun X, Ma P, Lewis ZA, Schmitz RJ. Methylated DNA is over-represented in whole-genome bisulfite sequencing data. *Front Genet*. 2014;5: 1–10. doi:10.3389/fgene.2014.00341
148. Ahmed I, Sarazin A, Bowler C, Colot V, Quesneville H. Genome-wide evidence for local DNA methylation spreading from small RNA-targeted sequences in Arabidopsis. *Nucleic Acids Res*. 2011;39: 6919–31. doi:10.1093/nar/gkr324
149. Joly-Lopez Z, Bureau TE. Diversity and evolution of transposable elements in Arabidopsis. *Chromosome Res*. 2014;22: 203–16. doi:10.1007/s10577-014-9418-8
150. Nocker S Van, Ludwig P. The WD-repeat protein superfamily in Arabidopsis : conservation and divergence in structure and function. 2003;11: 1–11.
151. Li CW, Lee SH, Chieh PS, Lin CS, Wang YC, Chan MT. Arabidopsis Root-Abundant

- Cytosolic Methionine Sulfoxide Reductase B Genes MsrB7 and MsrB8 are Involved in Tolerance to Oxidative Stress. *Plant Cell Physiol.* 2012;53: 1707–1719. doi:10.1093/pcp/pcs114
152. Groszmann M, Gonzalez-Bayon R, Lyons RL, Greaves IK, Kazan K, Peacock WJ, et al. Hormone-regulated defense and stress response networks contribute to heterosis in Arabidopsis F1 hybrids. *Proc Natl Acad Sci U S A.* 2015;112: E6397-406. doi:10.1073/pnas.1519926112
153. Zhang Q, Li Y, Xu T, Srivastava AK, Wang D, Zeng L, et al. The chromatin remodeler DDM1 promotes hybrid vigor by regulating salicylic acid metabolism. *Cell Discov.* 2016;2: 16027. doi:10.1038/celldisc.2016.27
154. Creasey KM, Zhai J, Borges F, Van Ex F, Regulski M, Meyers BC, et al. miRNAs trigger widespread epigenetically activated siRNAs from transposons in Arabidopsis. *Nature.* Nature Publishing Group; 2014;508: 411–5. doi:10.1038/nature13069
155. Bennetzen JL, Wang H. The contributions of transposable elements to the structure, function, and evolution of plant genomes. *Annu Rev Plant Biol.* 2014;65: 505–530. doi:10.1146/annurev-arplant-050213-035811
156. Fujimoto R, Sasaki T, Ishikawa R, Osabe K, Kawanabe T, Dennis ES. Molecular mechanisms of epigenetic variation in plants. *Int J Mol Sci.* 2012;13: 9900–9922. doi:10.3390/ijms13089900
157. Lockton S, Gaut BS. The contribution of transposable elements to expressed coding sequence in arabidopsis thaliana. *J Mol Evol.* 2009;68: 80–89. doi:10.1007/s00239-008-9190-5
158. Krieger U, Lippman ZB, Zamir D. The flowering gene SINGLE FLOWER TRUSS drives heterosis for yield in tomato. 2010;42. doi:10.1038/ng.550
159. Jiang K, Liberatore KL, Park SJ, Alvarez JP, Lippman ZB. Tomato Yield Heterosis Is Triggered by a Dosage Sensitivity of the Florigen Pathway That Fine-Tunes Shoot Architecture. *PLoS Genet.* 2013;9. doi:10.1371/journal.pgen.1004043
160. Martin M. Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet.* 17: 10–12.
161. Guo W, Fiziev P, Yan W, Cokus S, Sun X, Zhang MQ, et al. BS-Seeker2: a versatile aligning pipeline for bisulfite sequencing data. *BMC Genomics.* 2013;14: 774. doi:10.1186/1471-2164-14-774
162. Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. *Nat Methods.* 2012;9: 357–359. doi:10.1038/nmeth.1923
163. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics.* 2009;25: 2078–2079. doi:10.1093/bioinformatics/btp352
164. Gordon A. FASTX-Toolkit. [http://hannonlab.cshl.edu/fastx\\_toolkit/index.html](http://hannonlab.cshl.edu/fastx_toolkit/index.html) (Accessed January 19, 2016). 2016;
165. Bolger AM, Lohse M, Usadel B. Trimmomatic: A flexible trimmer for Illumina

## Bibliography

---

- sequence data. *Bioinformatics*. 2014;30: 2114–2120. doi:10.1093/bioinformatics/btu170
166. Kersey PJ, Allen JE, Armean I, Boddu S, Bolt BJ, Carvalho-Silva D, et al. Ensembl Genomes 2016: more genomes, more complexity. *Nucleic Acids Res*. 2015;44: D574-80. doi:10.1093/nar/gkv1209
167. Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol*. 2013;14: R36. doi:10.1186/gb-2013-14-4-r36
168. Langmead B, Trapnell C, Pop M, Salzberg S. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol*. 2009;10: R25. doi:10.1186/gb-2009-10-3-r25
169. Trapnell C, Hendrickson DG, Sauvageau M, Goff L, Rinn JL, Pachter L. Differential analysis of gene regulation at transcript resolution with RNA-seq. *Nat Biotechnol*. Nature Publishing Group; 2013;31: 46–53. doi:10.1038/nbt.2450
170. Kooke R, Keurentjes JJB. Epigenetic variation contributes to environmental adaptation of *Arabidopsis thaliana*. *Plant Signal Behav*. 2015;10: e1057368. doi:10.1080/15592324.2015.1057368
171. Jablonka E. Epigenetic inheritance and plasticity: The responsive germline. *Prog Biophys Mol Biol*. Elsevier Ltd; 2013;111: 99–107. doi:10.1016/j.pbiomolbio.2012.08.014
172. Heard E, Martienssen R a. Transgenerational epigenetic inheritance: Myths and mechanisms. *Cell*. Elsevier Inc.; 2014;157: 95–109. doi:10.1016/j.cell.2014.02.045
173. Brink R a. A Genetic Change Associated with the R Locus in Maize Which Is Directed and Potentially Reversible. *Genetics*. 1956;41: 872–889.
174. Pilu R, Panzeri D, Cassani E, Cerino Badone F, Landoni M, Nielsen E. A paramutation phenomenon is involved in the genetics of maize low phytic acid1-241 (*lpa1-241*) trait. *Heredity (Edinb)*. 2009;102: 236–45. doi:10.1038/hdy.2008.96
175. Stam M, Belele C, Ramakrishna W, Dorweiler JE, Bennetzen JL, Chandler VL. The regulatory regions required for B' paramutation and expression are located far upstream of the maize b1 transcribed sequences. *Genetics*. 2002;162: 917–930.
176. Hövel I. Novel insights into gene silencing mechanisms in *Zea mays* and *Arabidopsis thaliana*. Thesis. 2016;
177. Louwers M, Bader R, Haring M, van Driel R, de Laat W, Stam M. Tissue- and expression level-specific chromatin looping at maize b1 epialleles. *Plant Cell*. 2009;21: 832–42. doi:10.1105/tpc.108.064329
178. Belele CL, Sidorenko L, Stam M, Bader R, Arteaga-Vazquez M a., Chandler VL. Specific Tandem Repeats Are Sufficient for Paramutation-Induced Trans-Generational Silencing. *PLoS Genet*. 2013;9: e1003773. doi:10.1371/journal.pgen.1003773
179. Sekhon RS, Lin H, Childs KL, Hansey CN, Robin Buell C, De Leon N, et al. Genome-

- wide atlas of transcription during maize development. *Plant J.* 2011;66: 553–563. doi:10.1111/j.1365-313X.2011.04527.x
180. Baulcombe DC, Dean C. Epigenetic regulation in plant responses to the environment. *Cold Spring Harb Perspect Biol.* 2014;6: a019471. doi:10.1101/cshperspect.a019471
181. Gutiérrez-Marcos JF, Costa LM, Prà MD, Scholten S, Kranz E, Perez P, et al. Epigenetic asymmetry of imprinted genes in plant gametes. *Nat Genet.* 2006;38: 876–878. doi:10.1038/ng1828
182. Chitwood DH, Timmermans MCP. Small RNAs are on the move. *Nature.* Nature Publishing Group; 2010;467: 415–419. doi:10.1038/nature09351
183. Nogueira FTS, Chitwood DH, Madi S, Ohtsu K, Schnable PS, Scanlon MJ, et al. Regulation of small RNA accumulation in the maize shoot apex. *PLoS Genet.* 2009;5. doi:10.1371/journal.pgen.1000320
184. Ghosh Dastidar M, Mosiolek M, Bleckmann A, Dresselhaus T, Nodine MD, Maizel A. Sensitive whole mount *in situ* localization of small RNAs in plants. *Plant J.* 2016; doi:10.1111/tpj.13270
185. Fahlgren N, Sullivan CM, Kasschau KD, Chapman EJ, Cumbie JS, Montgomery TA, et al. Computational and analytical framework for small RNA profiling by high-throughput sequencing. *RNA (New York, NY).* 2009;15: 992–1002. doi:10.1261/rna.1473809
186. Moritoh S, Eun CH, Ono A, Asao H, Okano Y, Yamaguchi K, et al. Targeted disruption of an orthologue of DOMAINS REARRANGED METHYLASE 2, OsDRM2, impairs the growth of rice plants by abnormal DNA methylation. *Plant J.* 2012;71: 85–98. doi:10.1111/j.1365-313X.2012.04974.x
187. Eichten SR, Ellis NA, Makarevitch I, Yeh CT, Gent JI, Guo L, et al. Spreading of Heterochromatin Is Limited to Specific Families of Maize Retrotransposons. *PLoS Genet.* 2012;8. doi:10.1371/journal.pgen.1003127
188. Goettel W, Messing J. Epiallele biogenesis in maize. *Gene.* Elsevier B.V.; 2013;516: 8–23. doi:10.1016/j.gene.2012.12.034
189. Goettel W, Messing J. Divergence of gene regulation through chromosomal rearrangements. *BMC Genomics.* 2010;11: 678. doi:10.1186/1471-2164-11-678
190. Chhibber A, Schroeder BG. Single-molecule polymerase chain reaction reduces bias: Application to DNA methylation analysis by bisulfite sequencing. *Anal Biochem.* 2008;377: 46–54. doi:10.1016/j.ab.2008.02.026
191. Wojdacz TK, Hansen LL, Dobrovic A. A new approach to primer design for the control of PCR bias in methylation studies. *BMC Res Notes.* 2008;1: 54. doi:10.1186/1756-0500-1-54
192. Moskalev EA, Zavgorodnij MG, Majorova SP, Vorobjev IA, Jandaghi P, Bure I V., et al. Correction of PCR-bias in quantitative DNA methylation studies by means of cubic polynomial regression. *Nucleic Acids Res.* 2011;39: 1–12. doi:10.1093/nar/gkr213

## Bibliography

---

193. McCormick KP, Willmann MR, Meyers BC. Experimental design, preprocessing, normalization and differential expression analysis of small RNA sequencing experiments. *Silence*. BioMed Central Ltd; 2011;2: 2. doi:10.1186/1758-907X-2-2
194. Nobuta, K., McCormick, K., Nakano, M., Meyers, B. Bioinformatics Analysis of Small RNAs in Plants Using Next Generation Sequencing Technologies. *Plant MicroRNAs*. 2010;592: 89–106.
195. Gruntman E, Qi Y, Slotkin RK, Roeder T, Martienssen RA, Sachidanandam R. Kismeth: Analyzer of plant methylation states through bisulfite sequencing. *BMC Bioinformatics*. 2008;9: 371. Available: <http://www.biomedcentral.com/1471-2105/9/371>
196. Lewontin R. The Genotype/Phenotype Distinction. *The Stanfo*.
197. Alonso-blanco C, Aarts MGM, Bentsink L, Keurentjes JJB, Reymond M. What Has Natural Variation Taught Us about Plant Development , Physiology , and Adaptation ? *Plant Cell*. 2009;21: 1877–1896. doi:10.1105/tpc.109.068114
198. Taudt A, Colomé-Tatché M, Johannes F. Genetic sources of population epigenomic variation. *Nat Rev Genet*. Nature Publishing Group; 2016; doi:10.1038/nrg.2016.45
199. Becker C, Hagmann J, Müller J, Koenig D, Stegle O, Borgwardt K, et al. Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. *Nature*. 2011;480: 245–9. doi:10.1038/nature10555
200. Jiang C, Mithani A, Belfield EJ, Mott R, Hurst LD, Harberd NP. Environmentally responsive genome-wide accumulation of de novo Arabidopsis thaliana mutations and epimutations. *Genome Res*. 2014;24: 1821–1829. doi:10.1101/gr.177659.114
201. Schmitz RJ, Schultz MD, Lewsey MG, O'Malley RC, Urich MA, Libiger O, et al. Transgenerational Epigenetic Instability Is a Source of Novel Methylation Variants. *Science*. 2011;334: 369–373. Available: <http://www.sciencemag.org/cgi/doi/10.1126/science.1212959>
202. Ossowski S, Schneeberger K, Lucas-Lledó JI, Warthmann N, Clark RM, Shaw RG, et al. The rate and molecular spectrum of spontaneous mutations in Arabidopsis thaliana. *Science*. 2010;327: 92–94. doi:10.1126/science.1180677
203. van der Graaf A, Wardenaar R, Neumann DA, Taudt A, Shaw RG, Jansen RC, et al. Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. *Proc Natl Acad Sci U S A*. 2015;112: 6676–81. doi:10.1073/pnas.1424254112
204. Ma X, Zhang Q, Zhu Q, Liu W, Chen Y, Qiu R, et al. A Robust CRISPR/Cas9 System for Convenient, High-Efficiency Multiplex Genome Editing in Monocot and Dicot Plants. *Mol Plant*. Elsevier Ltd; 2015;8: 1274–1284. doi:10.1016/j.molp.2015.04.007
205. Lowder LG, Zhang D, Baltes NJ, Paul JW, Tang X, Zheng X, et al. A CRISPR/Cas9 Toolbox for Multiplexed Plant Genome Editing and Transcriptional Regulation. *Plant Physiol*. 2015;169: 971–85. doi:10.1104/pp.15.00636



206. Baubec T, Dinh HQ, Pecinka A, Rakic B, Rozhon W, Wohlrab B, et al. Cooperation of multiple chromatin modifications can generate unanticipated stability of epigenetic states in Arabidopsis. *Plant Cell*. 2010;22: 34–47. doi:10.1105/tpc.109.072819
207. Andorf S, Gaertner T, Steinfath M, Witucka-Wall H, Altmann T, Repsilber D. Towards systems biology of heterosis: A hypothesis about molecular network structure applied for the Arabidopsis metabolome. *Eurasip J Bioinforma Syst Biol*. 2009; doi:10.1155/2009/147157
208. Andorf S, Selbig J, Altmann T, Poos K, Witucka-Wall H, Repsilber D. Enriched partial correlations in genome-wide gene expression profiles of hybrids (*A.thaliana*): A systems biological approach towards the molecular basis of heterosis. *Theor Appl Genet*. 2010;120. Available: DOI: 10.1007/s00122-009-1214-z
209. Robertson FW, Reeve ECR. Heterozygosity, environmental variation and Heterosis. 1952. p. 286.
210. Meng D, Dubin M, Zhang P, Osborne EJ, Stegle O, Clark RM, et al. Limited Contribution of DNA Methylation Variation to Expression Regulation in Arabidopsis thaliana. *PLOS Genet*. 2016;12: e1006141. doi:10.1371/journal.pgen.1006141
211. Kawakatsu T, Huang SC, Jupe F, Sasaki E, Schmitz RJ, Urich MA, et al. Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. *Cell*. 2016;166: 492–505. doi:http://dx.doi.org/10.1016/j.cell.2016.06.044
212. Johannes F, Colot V, Jansen RC. Epigenome dynamics: a quantitative genetics perspective. *Nat Rev Genet*. 2008;9: 883–890. doi:10.1038/nrg2467
213. Crop Production 2012. Food Agric Organ United Nations. 2012;
214. Petroni K, Pilu R, Tonelli C. Anthocyanins in corn: a wealth of genes for human health. *Planta*. 2014;240: 901–911. doi:10.1007/s00425-014-2131-1
215. Winkel-Shirley B. Biosynthesis of flavonoids and effects of stress biosynthesis of flavonoids and effects of stress. *Curr Opin Plant Biol*. 2002;5: 218–223. doi:10.1016/S1369-5266(02)00256-X
216. Dooner HK, Robbins TP, Jorgensen RA. Genetic and Developmental control of Anthocyanin Biosynthesis. *Annu rev Genet*. 1991;25: 173–99.
217. Chan SWL, Zhang X, Bernatavichute Y V., Jacobsen SE. Two-step recruitment of RNA-directed DNA methylation to tandem repeats. *PLoS Biol*. 2006;4: 1923–1933. doi:10.1371/journal.pbio.0040363
218. Foolad MR. Genome mapping and molecular breeding of tomato. *Int J Plant Genomics*. 2007;2007. doi:10.1155/2007/64358
219. Zhou R, Wu Z, Cao X, Jiang FL. Genetic diversity of cultivated and wild tomatoes revealed by morphological traits and SSR markers. 2015;14: 13868–13879. doi:10.4238/2015.October.29.7
220. Giovannoni J. Harnessing epigenome modifications for better crops. *J Exp Bot*.

## Bibliography

---

- 2016;67: 2535–2537. doi:10.1093/jxb/erw143
221. Hagemann R. Somatische Konversion ( Paramutation ) am sulfurea Locus von Lycopersicon esculentum Mill . 1969;305.
222. Gouil Q, Novák O, Baulcombe DC. *SLTAB2* is the paramutated *SULFUREA* locus in tomato. J Exp Bot. 2016; erw096. doi:10.1093/jxb/erw096
223. Ehlert B, Schoettler MA, Tischendorf G, Ludwig-Mueller J, Bock R. The paramutated *SULFUREA* locus of tomato is involved in auxin biosynthesis. J Exp Bot. 2008;59: 3635–3647. doi:10.1093/jxb/ern213