

- Adams, K.L., R. Cronn, R. Percifield, and J.F. Wendel. 2003. Genes duplicated by polyploidy show unequal contributions to the transcriptome and organ-specific reciprocal silencing. *Proceedings of the National Academy of Sciences* 100: 4649-4654.
- Adams, K.L. and J.F. Wendel. 2005. Polyploidy and genome evolution in plants. *Curr. Op. In Plant Biology* 8:135-141.
- Agnieska A, PE Bayer, GC Barker, PP Edger, HR Kim, PA Martinez, CKK Chan, A Severn-Ellis, WR McCombie, IAP Parkin, AH Paterson, JC Pires, AG Sharpe, H Tang, GR Teakle, CD Town, J Batley & D. Edwards. 2016. The pangenome of an agronomically important crop plant, *Brassica oleracea*. *Nature Communications*, *Nature Communications* volume 7: 13390
- Anderson JE, J-M Michno, TJY Kono, AO Stec, BW Campbell, SJ Curtin & RM Stupar. 2016. Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. *BMC Biotechnology* 16:41
- Adams, K.L., R. Percifield, and J.F. Wendel. 2004. Organ-specific silencing of duplicated genes in a newly synthesized cotton allotetraploid. *Genetics* 168: 2217-2226.
- Akkaya, M. S., Bhagwat, A. A., and P. B. Cregan. 1992. Length polymorphisms of simple sequence repeat DNA in soybean. *Genetics*. 132:1131-1139.
- Akhunov et al., 2003. The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. *Genome Res.* 13:753-763.
- Alou, A.H., A. Azaiez, M. Jean, and F.J. Belzile. 2004. Involvement of the *Arabidopsis thaliana* AtPMS1 gene in somatic repeat instability. *Plant Molecular Biology* 56: 339- 349.
- Alves, E., I. Ballesteros, R. Linacero, and A.M. Vázquez. 2005. RYS1, a foldback transposon, is activated by tissue culture and shows preferential insertion points into the rye genome. *Theoretical and Applied Genetics* 111: 431-436.
- Anderson JE, J-M Michno, TJY Kono, AO Stec, BW Campbell, SJ Curtin, RM Stupar. 2016. Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. *BMC Biotechnology* 16:41
- Anderson LK, A Lai, SM Stack, C Rizzon, and BS Gaut. 2006. Uneven distribution of expressed sequence tag loci on maize pachytene chromosomes. *Genome Res.* 16:115-122.
- Anderson SN, MC Stitzer, AB Brohammer, P Zhou, JM Noshay, CD Hirsch, J Ross-Ibarra, CN Hirsch & NM Springer. 2019. Transposable elements contribute to dynamic genome content in maize. *BioRiv doi: https://doi.org/10.1101/547398*
- Argout, X. J. Salse, J.-M. Aury, M.J. Guiltinan, G. Droc, J. Gouzy, M. Allegre, C. Chaparro, T. Legavre, S.N Maximova, M. Abrouk, F. Murat, O. Fouet, J. Poulain, M. Ruiz, Y. Roguet, M. Rodier-Goud, J. Fernandes Barbosa-Neto, F. Sabot, D. Kudrna, J.S.S. Ammiraju, S.C. Schuster, J.E. Carlson, E. Sallet, T. Schiex, A. Dievart, M. Kramer, L. Gelley, Z. Shi, A. Bérard, C. Viot, M. Boccarda, A.M. Risterucci, V. Guignon, X. Sabau, M.J. Axtell, Z. Ma, Y. Zhang, S. Brown, M. Bourge, W. Golser, X. Song, D. Clement, R. Rivallan, M. Tahij.M. Akaza, B. Pitollat, K. Gramacho, A. D'Hont, D. Brunel, D. Infante, I. Kebe, P. Costet, R. Wing, W.R. McCombie, E. Guiderdoni, F. Quétier, O. Panaud, P. Wincker, S. Bocs and C. Lanaud. 2011. The genome of *Theobroma cacao*. *Nature Genetics* 43: 101–108.
- Arumuganathan, K. and E.D. Earle. 1991. Nuclear DNA content of some important plant species. *Plant Mol. Biol. Rep.* 9:208-218. (QH433.P52)
- Ashby, M.K., A. Warry, E.R. Bejarano, A. Khashoggi, M. Burrell, and C. Lichtenstein. 1997. Analysis of multiple copies of geminiviral DNA in the genome of four closely related *Nicotiana* species suggest a unique integration event. *Plant Mol.Biol.* 35:313-321. (QH506.P52)
- Babcock, E.B., G.L. Stebbins,Jr., and J.A. Jenkins. 1942. Genetic evolutionary processes in *Crepis*. *Amer. Nat.* 76:337-363. (QH1.A512)
- Barakat, A., G. Matassi, and G. Bernardi. 1998. Distribution of genes in the genome of *Arabidopsis thaliana* and its implications for the genome organization of plants. *Proc. Natl. Acad. Sci. USA*

- 95:10044-10049. (Q11.N275)
- Becker, J. and M. Heun. 1995. Barley microsatellites: allele variation and mapping. *Plant Mol. Biol.* 27:835-845.
- Belyayev, A., O. Raskina, A. Korol, and E. Nevo. 2000. Coevolution of A and B genomes in allotetraploid *Triticum dicoccoides*. *Genome* 43: 1021-1026.
- Bennett MD. 1971. The duration of meiosis. *Proceedings of the Royal Society of London Series B.* 178:277–299
- Bennet, MD. 1972. Nuclear DNA content and minimum generation time in herbaceous plants. *Proceedings of the Royal Society B.* 181(1063): 109-135
- Bennett MD. 1987. Variation in genomic form in plants and its ecological implications. *New Phytologist.* 106: 177–200
- Bennett, M.D. 1998. Plant genome values: How much do we know? *Proc.Natl.Acad.Sci.USA* 95:2011-2016. (Q11.N275)
- Bennett, M.D. 2000. Nuclear DNA amounts in angiosperms and their modern uses - 807 new estimates. *Ann Bot.* 86:859-909.
- Bennett, M.D. 2004. Perspectives on polyploidy in plants - ancient and neo. *Biological Journal of the Linnean Society* 82: 411-423.
- Bennetzen, J.L. 1998. The structure and evolution of angiosperm nuclear genomes. *Curr.Op.Plant Biol.* 1:103-108. (N/A)
- Bennetzen, J.L. 2000. Transposable element contributions to plant gene and genome evolution. *Plant Mol Biol.* 42:251-269.
- Bennetzen, J. 2002. Opening the door to comparative plant biology. *Science.* 296:60-63.
- Bennetzen, J., and Freeling, M. 1997. The unified grass genome: synergy in synteny. *Genome Res.* 7:301-306.
- Bennetzen JK and M Park. 2018. Distinguishing friends, foes, and freeloaders in giant genomes. *Current Opinion in Genetics & Development.* 49:49-55. doi: 10.1016/j.gde.2018.02.013.
- Biscotti MA, E Olmo & JS Heslop-Harrison. 2015. Repetitive DNA is eukaryotic genomes. *Chromosome Research* 23(3): 415-420.
- Blanc, G. and K.H. Wolfe. 2004. Functional divergence of duplicated genes formed by polyploidy during *Arabidopsis* evolution. *The Plant Cell* 16: 1679-1691.
- Bock R. 2010. The give-and-take of DNA: horizontal gene transfer in plants. *Trends in Plant Science* 15:11–22.
- Bolot S, M Abrouk, U Masood-Quraishi, N Stein, J Messing, C Feuillet, and J Salse. 2009. The ‘inner circle’ of the cereal genome. *Curr Op Plant Biol* 12:119-125.
- Bonierbale, M.W., R.L. Plaisted, and S.D. Tanksley. 1988. RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato. *Genetics* 120:1095-1103. (QH431.G328)
- Bowers et al., 2005. Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. *PNAS.* 102:13206-13211.
- Brandes, A., J.S. Heslop-Harrison, A. Kamm, S.E. Kubis, R.L. Doudrick, and T. Schmidt. 1997. Comparative analysis of the chromosomal and genomic organization of *Ty1-copia*-like retrotransposons in pteridophytes, gymnosperms and angiosperms. *Plant Mol.Biol.* 33:11-21. (QH506.P52)
- Bullock, D. and A. Rayburn. 1991. Genome size variation in southwestern US Indian maize populations may be a function of effective growing season. *Maydica* (SB191.M2M38)
- Butelli E, C Licciardello, Y Zhang, J Liu, S Mackay, P Bailey, G Reforgiato-Recupero, C Martin. 2012.

- Retrotransposons control fruit-specific, cold-dependent accumulation of anthocyanins in blood oranges. *Plant Cell*, 24: 1242-1255
- Cai, X. and S Xu. 2007. Meiosis-driven variation in plants. *Current Genomics* 8:151-161.
- Canter, P.H., I. Pašakinskien , R.N. Jones, and M.W. Humphreys. 1999. Chromosome substitutions and recombination in the amphiploid *Lolium perenne* × *Festuca pratensis* cv. Prior (2n=4x=28). *Theoretical and Applied Genetics* 98: 809-814.
- Carbonell-Bejerano P, C Royo, R Torres-Pérez, J Grimplet, L Fernandez, JM Franco-Zorrilla, D Lijavetzky, E Baroja, J Martínez, E García-Escudero, J Ibáñez, JM Martínez-Zapater. 2017. Catastrophic unbalanced genome rearrangements cause somatic loss of berry color in grapevine. *Plant Physiology*, 175(2): 786-801. doi.org/10.1104/pp.17.00715
- Ceccarelli, E. Falistocco, and P.G. Cionni. 1992. Variation of genome size and organization within hexaploid *Festuca arundinacea*. *Theor. Appl. Genet.* (SB123.Z8)
- Ceccarelli, M., T. Giordani, L. Natali, A. Cavallini, and P.G. Cionni. 1997. Genome plasticity during seed germination in *Festuca arundinacea*. *Theor. Appl. Genet.* 94:309-315. (SB123.Z8)
- Chen F, J Wu, X Cai, J Liang, M Freeling, and X Wang. 2018. Gene retention, fractionation and subgenome differences in polyploid plants. *Nature Plants* 4: 258–268
- Chen, Y., R.G. Schneeberger, and C.A. Cullis. 2005. A site-specific insertion sequence in flax genotrophs induced by environment. *New Phytologist* 167: 171-180.
- Choi et al., 2004. Estimating genome conservation between crop and model legume species. *PNAS*. 101:15289-15294.
- Cohen S, A Houben and D Segal. 2008. Extrachromosomal circular DNA derived from tandemly repeated genomic sequences in plants. *Plant J.* 53:1027-1034.
- Cook et al 2012. Copy number variation of multiple genes at Rhg1 mediates nematode resistance in soybean. *Science* 338:1206-1209
- Cordesse, F., R. Cooke, D. Tremousaygue, F. Grellet, and M. Delseny. 1993. Fine structure and evolution of the rDNA intergenic spacer in rice and other cereals. *J. Mol. Evol.* 36:369-379. (QH505.A158)
- D'Hont A, F Denoeud, J-M Aury et al. 2010. The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature* volume 488, pages213–217
- Della Coletta R, Y Qiu, S Ou, MB Hufford & CN Hirsch. 2021. How the pan-genome is changing crop genomics and improvement/ *BMC Genome Biology* 22: 3
- Cullis, C.A. 2005. Mechanisms and control of rapid genomic changes in flax. *Annals of Botany* 95: 201-206.
- Da Silva C, G Zamperin, A Ferrarini, A Minio, A Dal Molin, L Venturini, G Buson, P Tononi, C Avanzato, E Zago, E Boido, E Dellacassa, C Gaggero, M Pezzotti, F Carrau & M Delledonne. 2013. The high polyphenol content of grapevine cultivar Tannat berries is conferred primarily by genes that are not shared with the reference genome. *Plant Cell* 25:4777-4788
- De Bodt S, S Maere and Y Van de Peer. 2005. Genome duplication and the origin of angiosperms. *Trends Ecol Evol* 20:591-597.
- De Paepe, R., D. Prat and T. Huguet. 1982. Heritable nuclear DNA changes in doubled haploid plants obtained by pollen culture of *Nicotiana sylvestris*. *Plant Science Letters* 28:11-28.
- Deb SK, PP Edger, JC Pires & MR McCain. 2023. Patterns, mechanisms, and consequences of homoeologous exchange in allopolyploid angiosperms: a genomic and epigenomic perspective. *New Phytologist* 238: 2284–2304, doi: 10.1111/nph.18927
- Devos, K. 2005. Updating the 'Crop Circle'. *Curr. Opin. Plant Biol.* 8:155-162.
- Devos, K.M., J. Dubcovsky, J. Dvorák, and C.N. Chinoy. 1995. Structural evolution of wheat chromosomes 4A, 5A, and 7B and its impact on recombination. *Theor. Appl. Genet.* 91:282-288.

- Díez CM, BS Gaut, E Meca, E Scheinvar, S Montez-Hernandez, LE Eguiarte, and MI Tenaillon. 2013. Genome size variation in wild and cultivated maize along altitudinal gradients. *New Phytologist* 199: 264-276.
- J Dolezel, J Bartos, H Voglmayr, J Greilhuber. 2003. Nuclear DNA content and genome size of trout and human. *Cytometry*, 51: 127-128.
- Dooner HK, Q Wang, JT Hunga, Y Li, L He, W X, and C D, 2019. Spontaneous mutations in maize pollen are frequent in some lines and arise mainly from retrotranspositions and deletions. *PNAS*, <https://doi.org/10.1073/pnas.1903809116>
- Durrant A. 1962. The environmental induction of a heritable change in *Linum*. *Heredity* 17:27-61.
- Dvorak, J., Z.-L. Yang, F.M. You, and M.-C. Luo. 2004. Deletion polymorphism in wheat chromosome regions with contrasting recombination rates. *Genetics* 168: 1665-1675.
- Edger PP, MR McKain, KA Bird & R VanBuren. 2018. Subgenome assignment in allopolyploids: challenges and future directions. *Current Opinion in Plant Biology* 42: 76-80.
- Edger PP, R Smith, MR McKain, AM Cooley, M Vallejo-Marin, Y Yuan, AJ Bewick, L Ji, AE Platts, MJ Bowman, KL Childs, JD Washburn, RJ Schmitz, GD Smith, JC Pires & JR Puszey. 2018. Subgenome dominance in an interspecific hybrid, synthetic allopolyploid, and a 140-year-old naturally established neo-allopolyploid monkeyflower. *The Plant Cell* 29: 2150–2167.
- Edwards KD, N Fernandez-Pozo, K Drake-Stowe, M Humphrey, AD Evans, A Bombarely, F Allen, R Hurst, B White, SP Kernodle, JR Bromley, JP Sanchez-Tamburino, RS Lewis & LA Mueller. 2017. A reference genome for *Nicotiana tabacum* enables map-based cloning of homeologous loci implicated in nitrogen utilization efficiency. *BMC Genomics* 18: 448
- Eichten, S.R., J.M. Foerster, N. de Leon, Y. Kai, C.-T. Yeh, S. Liu, J.A. Jeddeloh, P.S. Schnable, S.M. Kaeplinger and N.M. Springer. 2011. B73-Mo17 near-isogenic lines demonstrate dispersed structural variation in maize. *Plant Physiol.* 156:1679-1690.
- El Baidouri M, M-C Carpentier, R Cooke, D Gao, E Lasserre, C Llauro, M Mirouze, N Picault, SA Jackson and O Panaud. 2014. Widespread and frequent horizontal transposable elements in plants. *Genome Research* 24: 831-838
- Elrouby, N. and T.E. Bureau .2010. *Bs1*, a new chimeric gene formed by retrotransposon-mediated exon shuffling in maize. *Plant Physiol.* 153: 1413-1424.
- Evans, G., A. Durrant, and H. Rees. 1966. Associated nuclear changes in induction of flax genotrophs. *Nature* 212:697-699.
- Fan C, Y Zhang, Y Yu, S Rounsley, M Long and R Wing. 2008. The subtelomere of *Orzyza sativa* chromosome 3 short arm as a hot bed of new gene origination in rice. *Mol Plant* 1:839-850.
- Freeling, M. 1984. Plant transposable elements and insertion sequences. *Ann. Rev. Plant Physiol.* 35:277-298.
- Flavell R. 1980. The molecular characterization and organization of plant chromosomal sequences. *Annual Review of Plant Physiology*. 31: 569-596
- Flavell R.B. 1985. Repeated sequences and genome change. In: B Hohn & ES Dennis (ed). *Genetic Flux in Plants*. Springer-Verlag, Wien, New York, pp 139-156.
- Fleischmann A, TP Michael, F Rivadavia, A Souza, W Wang, EM Temsch, J Greilhuber, KF Müller, G Heubl. 2014. Evolution of genome size and chromosome number in the carnivorous plant genus *Genlisea* (Lentibulariaceae), with a new estimate of the minimum genome size in angiosperms. *Annals of Botany*, 114(8): 1651–1663
- Freeling M, E Lyons, B Pedersen, M Alam, R Ming and D Lisch. 2008. Many or most genes in *Arabidopsis* transposed after the origin of the order Brassicales. *Genome Res* 18: 1924-1937.
- Fu, H. and H.K. Dooner. 2002. Intraspecific violation of genetic colinearity and its implications in maize.

- PNAS 99:9573-9578.
- Fuchs, J., A. Brandes, and I. Schubert. 1995. Telomere sequence localization and karyotype evolution in higher plants. *Plant Syst. Evol.* 196:227-241.
- Gaeta R.T., and J.C. Pires. 2009. Homoeologous recombination in allopolyploids: the polyploid ratchet. *New Phytologist* 186:18-28.
- Gaines TA, W Zhang, D Wang, B Bukun, ST Chislom, DL Shaner, SJ Nielsen, WL Patzoldt, PJ Tranel, AS Culpepper, TL Grey, TM Webster, WK Vencill, RD Sammons, J Jiang, CPreson, JE Leach & P Westra. 2009. Gene amplification confers glyphosate resistance in *Amaranthus palmeri*. *PNAS* 107 (3) 1029-1034;
- Gale, M.D. and K.M. Devos. 1998. Plant comparative genetics after 10 years. *Science* 282:656-659.
- Gao L, I Gonda, H Sun, Q Ma, K Bao, DM Tieman, EA Burzynski-Chang, TL Fish, KA Stromberg, GL Sacks, TW Thannhauser, MJ Foolad, MJ Diez, J Blanca, J Canizares, Y Xu, E van der Knaap, S Huan, HJ Klee, JJ Giovannoni & Z Fei. 2019. The tomato pan-genome uncovers new genes and a rare allele regulating fruit flavor. *Nature Genetics*. 51: 1044–105
- Gaut BS, SI Wright, C Rizzon, J Dvorak and LK Anderson. 2007. Recombination: An underappreciated factor in the evolution of plant genomes. *Nat. Rev. Genet* 8: 77-84.
- Geering ADW, F Maumus, D Copetti, N Choisne, DJ Zwicki, M Zytnicki, AR McTaggart, S Scalabrin, S Vezzulli, RA Wing, H Quesneville and P-Y Teycheyney. 2014. Endogenous floroviruses are a major components of plant genomes and hallmarks of virus evolution. *Nature Communications* 5(5269) doi:10.1038/ncomms6269.
- Giroux MJ, J Shaw, G Barry, BG Cobb, T Greene, T Okita and LC Hannah LC. 1996. A single gene mutation that increases maize seed weight. *Proc Natl Acad Sci U S A* 93: 5824-5829
- Gordon SP, B Contreras-Moreira, DP Woods, DL Des Marais, D Burgess, S Shu, C Stritt, AC Roulin, W Schackwitz, L Tyler, J Martin, A Lipzen, N Dochy, J Phillips, K Barry, K Geuten, H Budak, TE Juenger, R Amasino, AL Caicedo, D Goodstein, P Davidson, LAJ Mur, M Figueroa, M Freeling, P Catalan & JP Vogel. 2017. Extensive gene content variation in the *Brachypodium distachyon* pan-genome correlates with population structure. *Nature Communications*, 8, Article number: 2184
- Grandbastien, M. A. 1998. Activation of plant retrotransposons under stress conditions. *Trends Plant Sci.* 3: 181-187.
- Greibelhuber, J. 2005. Intraspecific variation in genome size in angiosperms: Identifying its existence. *Annals of Botany* 95: 91-98.
- Greibelhuber, J., T. Borsch, K. Müller, A. Worberg, S. Porembski, and W. Barthlott. 2006. Smallest angiosperm genomes found in Letibulariaceae, with chromosomes of bacterial size. *Plant Biology* 8:770-777.
- Golicz A. A., Bayer P. E., et al. 2016. The pangenome of an agronomically important crop plant *Brassica oleracea*. *Nature* 13390
- Gu C, L Wang, W Wang, H Zhou, B Ma, H Zheng, T Fang, C Ongutu, S Vimolmangkang & Y Han. 2016. Copy number variation of a gene cluster encoding endopolygalacturonase mediates flesh texture and stone adhesion in peach. *Journal of Experimental Botany* 67(6): 1993–2005
- Gu, Y.Q., D. Coleman-Derr, X. Kong, and O.D. Anderson. 2004. Rapid genome evolution revealed by comparative sequence analysis of orthologous regions from four Triticeae genomes. *Plant Physiology* 135: 459-470.
- Guo W, L Comai & I Henry. 2023. Chromoanagenesis in plants: triggers, mechanisms, and potential impact. 39(1): 34-45. <https://doi.org/10.1016/j.tig.2022.08.003>
- Han, F., G. Fedak, W. Guo, and B. Liu. 2005. Rapid and repeatable elimination of a parental genotype-specific DNA repeat (pGc1R-1a) in newly synthesized wheat allopolyploids. *Genetics* 170:1239-1245.

- Han F, Lamb JC, Birchler JA (2006) High frequency of centromere inactivation resulting in stable dicentric chromosomes of maize. *Proc Natl Acad Sci USA* 103:3238–3243
- Han Y, Z Zhang, C Liu, J Liu S Huang, J Jiang, and W Jin. 2009. Centromere repositioning in curcurbit species: implication of the genomic impact centromere activation and inactivation. *PNAS* 106:14937-14941.
- Hanada K, V Vallejo, K Nobuta, RK Slotkin, D Lisch D, BC Meyers, S-H Shiu and N Jiang N. 2009. The functional role of Pack-MULEs in rice inferred from purifying selection and expression profile. *Plant Cell* 21: 25-38
- Hawkins JS, SR Proulx, RA Rapp and JF Wendel. 2009. Rapid DNA loss as a counterbalance to genome expansion through retrotransposon proliferation in plants. *PNAS* 106:17811-17816.
- He, P., B.R. Fribe, B.S. Gill, and J.-M. Zhou. 2003. Allopolyploidy alters gene expression in the highly stable hexaploid wheat. *Plant Molecular Biology* 52: 401-414.
- Heslop-Harrison, J.S. and T. Schwarzacher. 2011. Organization of the plant genome in chromosomes. *The Plant Journal* 66:18-33.
- Hibdige SGS, P Raimondeau, P-A Christin & LT Dunning. 2021. Widespread lateral gene transfer among grasses. *New Phytologist*, 230(6): 2474-2486.
- Hirsch CN et al. 2016. Draft assembly of elite inbred line PH207 provides insights into genomic and transcriptome diversity in maize. *The Plant Cell* 28:2700-2714.
- Huang CY, MA Ayliffe and JN Timmis. 2003. Direct measurement of the transfer rate of chloroplast DNA into the nucleus. *Nature* 422:72-76.
- Huang CY, MA Ayliffe and JN Timmis. 2004. Simple and complex nuclear loci created by newly transferred chloroplast DNA in tobacco. *PNAS* 101: 9710-9715
- Hüber S, N Bercovich, M Todesco, JR Mandel, J Odenheimer, E Ziegler, JS Lee, GJ Baute, GL Owens, CJ Grassa, DP Ebert, KL Ostevik, BT Moyers, S Yakimoski, RR Masalia, L Gao, I Calic, JE Bowers, NC Kane, DZK Swanevelder, T Kubach, S Muños, NB Langdale, JM Burke & LH Rieseberg. 2019. Sunflower pan-genome analysis shows that hybridization altered gene content and disease resistance. *Nature Plants* 5: 54–62
- Ibarra -Laclatee E, E Lyons, G Hernández-Guzmán, CA Pérez-Torres, L Carretano-Paulette, T-H Chang, T Lan, AJ Welch, MJ Abraham Juárez, J Simpson, A Fernández-Cortés, M Arteaga-Vázquez, E Góngora-Castillo, G Acevedo-Hernández, SC Schuster, H Himmelbauer, AE Minoche, S Xu, M Lynch, A Oropeza-Aburto, SA Cervantes-Pérez, MdJ Ortega-Estrada, JI Cervantes-Luevano, TP Michael, T Mockler, D Bryant, and A Herrera-Estrella, VA Albert, L Herrera-Estrella. 2013. Architecture and evolution of a minute plant genome. *Nature* 498: 94–98.
- International Rice Genome Sequencing Project. 2005. The map-based sequence of the rice genome. *Nature* 436:793
- Iovone M, T Zhang, Q Lou, CR Buell and J Jiang. 2013. Copy number variation in potato - an asexually propagated autotetraploid species. *The Plant Journal* 75:80-89.
- Jackson, R.C. 1971. The karyotype in systematics. *Ann. Rev. Ecol. Syst.* 2:327-368. (QH540.A53)
- Jaillon CO et al. 2007. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. *Nature* 449:463-467.
- Jiang N, Z Bao, X Zhang, H Hirochika, SR Eddy, SR McCouch & SR Wessler. 2003. An active DNA transposon family in rice. *Nature* 421(6919): 163-167
- Jiao, V., N.J. Wickett, S. Ayyampalayam, A.S. Chanderbali, L. Landherr, P.E. Ralph, L.P. Tomsho, Y. Hu, H. Liang, P.S. Soltis, S.W. Clifton, S.E. Schlarbaum, S.C. Schuster, H. Ma, J. Leebens-Mack and C.W. dePamphilis. 2011. Ancestral polyploidy in seed plants and angiosperms. *Nature* 473:97-100.
- Jo C & S Kim. 2020. Transposition of a non-autonomous DNA transposon in the gene coding for a bHLH

- transcription factor results in a white bulb color of onions (*Allium cepa* L.). *Theor Appl Genetics*, 133: 317-328.
- Joachimiak, A. And T. Ilnicki. 2003. Nuclear morphology, polyploidy, and chromatin elimination in tissue culture of *Allium fistulosum* L. *Acta Societatis Botanicorum Poloniae* 72: 11-17.
- Jones, J.D.G. and R. Flavell. 1982. The mapping of highly-repeated DNA families and their relationship to C-bands in chromosomes of *Secale cereale*. *Chromosoma* 86: 595-612.
- Kashkush, K., M. Feldman, and A.A. Levy. 2002. Gene loss, silencing and activation in a newly synthesized wheat allotetraploid. *Genetics* 160: 1651-1659.
- Kahn AW, V Garg, M Roorkiwal, AA Golycz, D Edwards & RK Varshney. 2019. Super-pangenome by integrating the wild side of a species for accelerated crop improvement. *Trends in Plant Sciene* 25: 148-158.
- Kato A, JC Lamb and JA. Birchler 2004. Chromosome painting using repetitive DNA sequences as probes for somatic chromosome identification in maize. *PNAS* 101:13554-13559
- Kermin RE, J Hart, PD Fiesel, Y-R Lou, P Fan, AD Jones & R L. Last. 2024. Tomato root specialized metabolites evolved through gene duplication and regulatory divergence within a biosynthetic gene cluster. *Science Advances*, 10(17) DOI: 10.1126/sciadv.adn3991
- Kobayashi S, N Goto-Yamamoto & H Hirochika. 2004. Retrotransposon-induced mutations in grape skin color. *Science*, 304:998. DOI: 10.1126/science.1095011
- Komarova, N.Y., T. Grabe, D.J. Huigen, V. Hemleben, and R.A. Volkov. 2004. Organization, differential expression and methylation of rDNA in artificial *Solanum* allopolyploids. *Plant Molecular Biology* 56: 439-463.
- Koo D-H, M Jugulam, K Putta, IB Cuvaca, DE Peterson, RS Currie, B Fribe, & BS Gill. 2018 Gene duplication and aneuploidy trigger rapid evolution of herbicide resistance in common waterhemp. *Plant Physiol* 176: 1932–1938
- Knight CA & JM Beaulieu. 2008. Genome size scaling through phenotypic space. *Annals of Botany* 101: 759-766.
- Knight, C.A., N.A. Molinari, and D.A. Petrov. 2005. The large genome constraint hypothesis: Evolution, ecology and phenotype. *Annals of Botany* 95: 177-190.
- Kubis, S.E., J.S. Heslop-Harrison, C. Desel, and T. Schmidt. 1998. The genomic organization of non-LTR retrotransposons (LINEs) from three *Beta* species and five other angiosperms. *Plant Mol.Biol.* 36:821-831. (QH506.P52)
- Kumar, A. and J.L. Bennetzen. 1999. Plant retrotransposons. *Annu. Rev. Genet.* 33:479-532.
- Kyndt T, D Quispe, H Zhai, R Jarret, M Ghislain, Q Liu, G Gheysen & JF Freuze. 2015. The genome of cultivated sweet potato contains *Agrobacterium* T-DNAs with expressed genes: An example of a naturally transgenic crop. *Proc. Natl. Acad Sci USA* 112:5844-5849
- Lai, J., Y. Li, J. Messing, and H. K. Dooner. 2005. Gene movement by Helitron transposons contributes to the haplotype variability of maize. *PNAS*. 102: 9068-9073.
- Lai, J., R. Li, X. Xu, W. Jin, M. Xu, H. Zhao, Z. Xiang, W. Song, K. Ying, M. Zhang, Y. Jiao, P. Ni, J. Zhang, D. Li, X. Guo, K. Ye, M. Jian, B. Wang, H. Zheng, H. Liang, X. Zhang, S. Wang, S. Chen, J. Li, Y. Fu, N.M. Springer, H. Yang, J. Wang, J. Dai, P.S. Schnable, J. Wang. 2010. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nature Genetics* 42: 1027-1030.
- Lam, H-M., X. Xu. X. Liu, W. Chen, G. Yang, F.-L. Wong, M.-W. Li, W. He, N. Qin, B. Wang, J. Li, M. Jian, J. Wang, G. Shao, J. Wang, S. S.-M. Sun and G. Zhang. 2010. Resequencing of 31 wild and cultivated soybean genomes identifies patterns of genetic diversity and selection. *Nature Genetics* 42: 1053-1059.
- Lavergne S, NJ Muenke and J Molfasky. 2010. Genome size reduction can trigger rapid phenotypic

- evolution in invasive plants. *Annals of Botany* 105: 109-116.
- Lei K, E Goltsman, D Goodstein, GA Wu, DS Rokhsar & JP Vogel. 2021. Plant pan-genomics comes of age. *Annual Rev. of Plant Biology.* 72: 27.1-27.25
- Leitch, I.J., and M.D. Bennett. 2004. Genome downsizing in polyploid plants. *Biological Journal of the Linnean Society* 82: 651-663.
- Levy, A.A. and M. Feldman. 2002. The impact of polyploidy on grass genome evolution. *Plant Physiology* 130: 1587-1593.
- Levy, A.A. and M. Feldman. 2004. Genetic and epigenetic reprogramming of the wheat genome upon allopolyploidization. *Biological Journal of the Linnean Society* 82: 607-613.
- Li X, Y Wang, C Cai, J Ji, F Han, L Zhang, S Chen, L Zhang, Y Yang, Q Tang, J Bucher, X Wang, L Yang, M Zhuang, K Zhang, H Lv, G Bonnema, Y Zhang & Feng Cheng. 2024. Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in *Brassica oleracea*. *Nature Genetics.* 56: 517–529. doi.org/10.1038/s41588-024-01655-4
- Li, Y-h, G Zhou, J Ma, W Jiang, L-g Jin, Z Zhang, Y Guo, J Zhang, Y Sui, L Zheng, S-s Zhang, Q Zuo, X-h Shi, Y-f Li, W-k Zhang, Y Hu, G Kong, H-I Hong, B Tan, J Song, Z-x Liu, Y Wang, H Ruan, CKL Yeung, J Liu, H Wang, L-j Zhang, R-x Guan, K-j Wang, W-b Li, S-y Chen, R-z Chang, Z Jiang, S A Jackson, R Li & L-j Qiu. 2010. De novo assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits. *Nature Biotechnology* 32, 1045–1052.
- Li Z, MTW McKibben, GS Finch, PD Blischak, BL Sutherland & MS Barker. 2021. Patterns and processes of diploidization in land plants. *Annual Review of Plant Biology.* 72: 72:18.1–18.24
- Lim, K.Y, R. Matyášek, A. Kova ík, and A.R. Leitch. 2004. Genome evolution in allotetraploid *Nicotiana*. *Biological Journal of the Linnean Society* 82: 599-606.
- Lisch D. 2013. How important are transposons for plant evolution? *Nature Reviews Genetics* 14:49-60
- Liu, B. and J.F. Wendel. 2000. Retrotransposon activation followed by rapid repression in introgressed rice plants. *Genome* 43:874-880.
- Liu R, KO Koyanagi, S Chen & Y Kishima. 2012. Evolutionary force of AT-rich repeats to trap genomic and episomal DNAs into the rice genome: lessons from endogenous pararetrovirus. *Plant J.* 72: 817-828
- Long Q, S Cao, G Huang, X Wang, Z Liu, W Liu, Y Wang, H Xiao, Y Peng & Y Zhou. 2024. Population comparative genomics discovers gene gain and loss during grapevine domestication. *Plant Physiology.* 195(2): 1401–1413, https://doi.org/10.1093/plphys/kiae039
- Luo MC, KR Deal, ED Akhunov, AR Akhunova, OD Anderson, JA Anderson, N Blake, MT Clegg, D Coleman-Derr, EJ Conley, CC Crossman, J Dubcovsky, BS Gill, YQ Gu, J Hadam, HY Heo, N Huo, G Lazo, Y Ma, DE Matthews, PE McGuire, PL Morrell, CO Qualset, J Renfro, D Tabanao, LE Talbert, C Tian, M Toleno, ML Warburton, FM You, W Zhang, and J Dvorak. 2009. Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. *PNAS* 106:15780-15785.
- Lough AN, LM Roark, A. Kato, TS Ream, JC Lamb, JA Birchler & KJ Newton. 2008. Mitochondrial DNA transfer to the nucleus generates extensive insertion site variation in maize. *Genetics* 178:47–55
- Lovell JT, A Sreedasyam, ME Schranz, M Wilson, JW Carlson, A Harkness, D Emms, DM Goodstein & Jeremy Schmutz. 2022. GENESPACE tracks regions of interest and gene copy number variation across multiple genomes. *eLife* 11 :e78526. doi.org/10.7554/eLife.78526
- Lysak MA. 2022. Celebrating Mendel, McClintock, and Darlington: On end-to-end chromosome fusions and nested chromosome fusions. *The Plant Cell*, 34(7): 2475-2491.
- Lysak MA, A Berr, A Pecinka, R Schmidt, K McBreen, and I Schubert. 2006. Mechanisms of chromosome number reduction in *Arabidopsis thaliana* and related Brassicaceae species. *PNAS* 103:5224-5229.
- Makarevitch I, Waters AJ, West PT, Stitzer M, Hirsch CN, et al. (2015) Transposable Elements Contribute

- to Activation of Maize Genes in Response to Abiotic Stress. PLoS Genet 11(1): e1004915. doi:10.1371/journal.pgen.1004915.
- Malacarne G, M Perazzolli, A Cestaro, L Sterck, P Fontana, Y Van de Peer, R Viola, R Velasco and F Salamini. 2012. Deconstruction of the (paleo)polyploid grapevine genome based on the analysis of transposition events involving NBS resistance genes. PloS ONE 7: e29762.
- Mandáková et al, 2010. Fast diploidization in close mesopolyploid relatives of arabidopsis. Plant Cell 22:2277-2290
- Mandáková T & MA Lysak. 2018. Post-polyploid diploidization and diversification through dysploid changes. Current Opinion in Biology. 42: 55-65.
- Mayrose I & MA Lysak. 2021. The evolution of chromosome numbers: mechanistic models and experimental approaches. Genome Biology & Evolution, 13(2): evaa220
- Matyášek, R., K.Y. Lim, A. Kovařík, and A.R. Leitch. 2003. Ribosomal DNA evolution and gene conversion in *Nicotiana rustica*. Heredity 91: 268-275.
- McClintock B. 1984. The significance of responses of the genome to challenge. Science 226: 792-801.
- McHale LK, WJ Haun, WW Xu, PB Bhaskar, JE Anderson, DL Hyten, DG Gerhardt, JA Jeddeloh, and RM Stupar. Plant Physiology 159:1295-1308.
- McMurphy LM & AL Rayburn. 1991. Genome size variation in maize populations selected for cold tolerance. Plant Breeding, 106: 190–195
- Ming R, S Hou et al. 2008. The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus). Nature 452:991-996.
- Montenegro JD, AA Golicz, PE Bayer, B Hurgobin, HT Lee, C-KK Chan, P Visendi, K Lai, J Dolezel, J Batley & D Edwards. 2017. The pangenome of hexaploid bread wheat. The Plant Journal 90(5): 1007-1013.
- Montgomery JS, N Soni, SM Hill, S Morran, EL Patterson, SA Edwards, S Ranayake, Y-H Hung, PH Pandesha, RK Slotkin, F Dayan & Todd Gaines. 2024. A transposable element insertion in IAA16 interrupts normal splicing and generates a novel dicamba resistance allele in *Bassia scoparia*. Biorxiv. doi.org/10.1101/2024.07.19.604363
- Moore, G., K. M. Devos, Z. Wang, and M. D. Gale. 1995. Grasses, line up and form a circle. Curr. Biol. 5:737-739.
- Moore RC and MD Purugganan. 2005. The evolutionary dynamics of plant duplicate genes. Current Opinion in Plant Biology 8:122-128.
- Mukherjee, S. and A. Sharma. 1990. Intraspecific variation of nuclear DNA in Capsicum annuum L. Proceedings of the Indian Academy of Science 100 1-6.
- Murat F, A Armero, C Pont, C Klopp & J Salse. 2017. Reconstructing the genome of the most common recent ancestor of flowering plants. Nature Genetics 49: 490-496.
- Murray, B.G. 2005. When does intraspecific C-value variation become taxonomically significant? Annals of Botany 95: 119-125.
- Nagl, W. 1990. Gene amplification and related events. p. 154-201. In: Y.P.S. Bajaj (ed.) Biotechnology in Agriculture and Forestry, Vol. 11. Somaclonal Variation in Crop Improvement. Springer-Verlag, Berlin Heidelberg. (N/A)
- Navrátilová A, A Koblízková and J Macas. 2008. Survey of extrachromosomal circular DNA derived from plant satellite repeats. BMC Plant Biology 8:90-103
- Nelson, J.C., M.E. Sorrells, A.E. Van Deynze, Y.H. Lu, M. Atkinson, M. Bernard, P. Leroy, J.D. Faris, and J.A. Anderson. 1995. Molecular mapping of wheat: major genes and rearrangements in homoeologous groups 4, 5, and 7. Genetics, 141:721-731. (QH431.G328)
- Ohri D. 2008. Climate and growth form: The consequences for genome size in plants. Plant Biology 7(5a) 449-458.

- Orozco-Arias S, G Isaza & R Guyot. 2019. Retrotransposons in plant genomes: structure, identification, and classification through bioinformatics and machine learning. In. J. Mol. Sci. 20: 3837.
- Palaisa, K.A., M. Morgante, M. Williams, and A. Rafalski. 2003. Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci. Plant Cell 15: 1795-1806.
- Paterson et al., 1995. Convergent domestication of cereal crops by independent mutations at corresponding genetic loci. Science. 269:1714-1717.
- Paterson, A.H., J.E. Bowers, R.Bruggmann, I. Dubchak, J. Grimwood, H.Gundlach, .G. Haberer, U. Hellsten, T. Mitros, A. Poliakov, J.Schmutz, M. Spannagl, H. Tang, X. Wang, T. Wicker, A.K. Bharti, J. Chapman, F.A. Feltus, U. Gowik, I.V. Grigoriev, E.L., C.A. Maher, M. Martis, A. Narechania, R.P. O'Neill, B.W. Penning, A. A. Salamov, Y. Wang, L. Zhang, N.C. Carpita, M. Freeling, A.R. Gingle, C.T. Hash, B. Keller, P. Klein, S. Kresovich, M.C. McCann, R. Ming, D.G. Peterson, M. -ur-Rahman, D. Ware, P. Westhoff, K.F.X. Mayer, J. Messing and D.S. Rokhsar. 2009. The *Sorghum bicolor* genome and the diversification of grasses. Nature 457: 551-556.
- Patterson EL, CA Saski, DB Sloan, PJ Tranel, P Westra, & TA Gaines. 2019. The draft genome of Kochia scoparia and the mechanism of glyphosate resistance via 3 transposon-ediated EPSPS tandem gene duplication. BioRxiv doi: <https://doi.org/10.1101/600072>
- Pellicer, J., M.F. Fay, and I.J. Leitch. 2010. The largest eukaryotic genome of them all? Botanical Journal of the Linnean Society 104:10-15.
- Pellicer J & IJ Leitch. 2020. The Plant DNA C-values database (release 7.1): an updated online repository of plant genome size data for comparative studies. New Phytologist. 226: 301-305.
- Peng Y, Y Wang, Y Liu, X Fang, L Chen, Q Long, D Su, T Zhang, X Shi, X Xy, Q Xu, N Wang, F Zhang, Z Liu, J Yao, L Tian, W Hu, S Chen, H Wang, S Huang, BS Gaut & Y Zhou. 2025. The genomic and epigenomic landscapes of hemizygous genes across crops with contrasting reproductive systems. PNAS 122 (6) e2422487122. /doi.org/10.1073/pnas.2422487122.
- Piegù B, R Guyot, N Picault, A Roulin, A Saniyal, H Kim, K Collura, DS Brar, S Jackson, RA Wing and O Penaud. 2007. Doubling of genome size without polyploidization: dynamics of retrotransposition-driven genomic expansions in *Oryza australiensis*, a wild relative of rice. Genome Res 16:1262-1269.
- Pires, J.C., K.Y. Lim, A. Kova ík, R. Matyášek, A. Boyd, A.R. Leitch, I.J. Leitch, M.D. Bennett, P.S. Soltis, and D.E. Soltis. 2004a. Molecular cytogenetic analysis of recently evolved *Tragopogon* (Asteraceae) allopolyploids reveal a karyotype that is additive of the diploid progenitors. Am J Bot 91: 1022-1035.
- Pires, J.C., J. Zhao, M.E. Schranz, E.J. Leon, P.A. Quijada, L.N. Lukens, and T.C. Osborn. 2004b. Flowering time divergence and genomic rearrangements in newly synthesized *Brassica* polyploids (Brassicaceae). Biological Journal of the Linnean Society 82: 675- 688.
- Pont C, S Wagner, A Kremer, L Orlando, C Plomion & J Salse. 2019. Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. Genome Biology 20:29
- Potato Genome Sequencing Consortium. 2011. Genome sequence and analysis of the tuber crop potato. Nature. 475:189–195.
- Rafalski, J. A. and S. T. Tingey. 1993. Genetic diagnostics in plant breeding: RAPDs, microsatellites and machines. Trends in Genet. 8:275-280.
- Rasmussen DC & RL Phillips. 1997. Plant breeding progress and genetic diversity from de novo variation and elevated epistasis. Crop Sci. 37:303-310.
- Rayburn, A.L., J.A. Auger, E.A. Benzinger EA, and A.G. Hepburn. 1989. Detection of intraspecific DNA content variation in *Zea-mays-L* by flow-cytometry. J. Expt. Bot. 40:1179-1183.
- Rayburn AL, DP Biradar, RL Nelson, R McCloskey, and KM Yeater. 2004. Documenting intraspecific genome size variation in soybean. Crop Science 44: 262-264

- Reed SM and JA Burns. 1989. Cytological consequences of DNA amplification in an anther culture-derived doubled haploid line of *Nicotiana tabacum*. American Journal of Botany. 76: 958-965.
- Reed SM, JA Burns, and EA Wernsman. 1992. Cytological comparison of amplified chromosome segments in four tobacco doubled haploids. Crop Sci. 32:362-366.
- Rejmánek M. 1996. A theory of seed plant invasiveness: the first sketch. Biological Conservation 78: 171-181.
- Roark LM, AY Hui, L Donnelly, JA Birchler & KJ Newton. 2010. Recent and frequent insertions of chloroplast DNA into maize nuclear chromosomes. Cytogenet Genome Res 129:17–23 DOI: 10.1159/000312724
- Saliva C. D., et al. 2013. The high polyphenol content of grapevine cultivar tannat berries is conferred primarily by genes that are not shared with the reference genome. The Plant Cell 12: 4777-4788
- Salse J. 2012. In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. Current Opinion in Plant Biology. 15:122-130.
- Salse J, M Abrouk, S Bolot, N Guihot, E Courcelle, T Farout, R Waugh, TJ Close, J Messing, and C Feuillet. 2009. Reconstruction of monocotyledoneous proto-chromosomes reveals faster evolution in plants than in animals. PNAS 106:14908-14913.
- San Miguel, P., B.S. Gaut, A. Tikhonov, Y. Nakajima, and J.L. Bennetzen. 1998. The paleontology of intergene retrotransposons of maize. Nat. Genet. 20:43-45. (QH426.N37)
- Schmidt, A., R. L. Doudrick, J. S. Heslop-Harrison, T. Schmidt. 2000. The contribution of short repeats of low sequence complexity to large conifer genomes. TAG. 101:7-14.
- Schmidt, T. and J.S. Heslop-Harrison. 1998. Genomes, genes and junk: the large-scale organization of plant chromosomes. Trends Plant Sci 3:195-199. (Q11.N275)
- Schmutz, J., S.B. Cannon, J. Schlueter, J. Ma, T. Mitros, W. Nelson, D.L. Hyten, Q. Song, J.J. Thelen, J. Cheng, D. Xu, U. Hellsten, G.D. May, Y. Yu, T. Sakurai, T. Umezawa, M.K. Bhattacharyya, D. Sandhu, B. Valliyodan, E. Lindquist, M. Peto, D. Grant, S. Shu, D. Goodstein, K. Barry, M. Futrell-Griggs, B. Abernathy, J. Du, Z. Tian, L. Zhu, N. Gill, T. Joshi, M. Libault, A. Sethurama1, X.-C Zhang, K. Shinozaki, H.T. Nguyen, R. A. Wing, P. Cregan, J. Specht, J. Grimwood, D. Rokhsar, G. Stacey, R.C. Shoemaker and S.A. Jackson. 2010. Genome sequence of the palaeopolyploid soybean. Nature 463:178-183.
- Schnable, P.S., D. Ware, R.S. Fulton, J.C. Stein, F. Wei, S. Pasternak, C. Liang, J. Zhang, L. Fulton, T.A. Graves, P. Minx, A.D. Reily, L. Courtney, S.S. Kruchowski, C. Tomlinson, C. Strong, K. Delehaunty, C. Fronick, Bill Courtney, S.M. Rock, E. Belter, F. Du, K. Kim, R.M. Abbott, M. Cotton, A. Levy, P. Marchetto, K. Ochoa, S.M. Jackson, B. Gillam, W. Chen, L. Yan, J. Higginbotham, M. Cardenas, J. Waligorski, E. Applebaum, L. Phelps, J. Falcone, K. Kanchi, T. Thane, A. Scimone, N. Thane, J. Henke, T. Wang, J. Rupert, N. Shah, K. Rotter, J. Hodges, E. Ingenthron, M. Cordes, S. Kohlberg, J. Sgro, B. Delgado, K. Mead, A. Chinwalla, S. Leonard, K. Crouse, K. Collura, D. Kudrna, J. Currie, R. He, A. Angelova, S. Rajasekar, T. Mueller, R. Lomeli, G. Scara, A. Ko, K. Delaney, M. Wissotski, G. Lopez, D. Campos, M. Braidotti, E. Ashley, W. Golser, HR. Kim, S. Lee, J. Jin, Z. Dujmic, W. Kim, J. Talag, A. Zuccolo, C. Fan, A. Sebastian, M. Kramer, L. Spiegel, L. Nascimiento, T. Zutavern, B. Miller, C. Ambroise, S. Muller, W. Spooner, A. Narehania, L. Ren, S. Wei, S. Kumari, B. Faga, M.J. Levy, L. McMahan, P. Van Buren, M.W. Vaughn, K. Ying, C.-T. Yeh, S.J. Emrich, Y. Jia, A Kalyanaram, A.-P. Hsia, W.B. Barbazuk, R.S. Baucom, T.P. Brutnell, N.C. Carpita, C. Chaparro, J.-M. Chia, J.-M. Deragon, J.C. Estill, Y. Fu, J.A. Jeddeloh, Y. Han, H. Lee, P. Li, D.R. Lisch, S. Liu, Z. Liu, D.H. Nagel, M.C. McCann, P. SanMiguel, A.M. Meyers, D. Nettleton, J. Nguyen, B.W. Penning, L. Ponnala, K.L. Scheider, D.C. Swartz, A. Sharma, C. Soderlund, N.M. Springer, Q. Sun, H. Wang, M. Waterman, R. Westerman, T.K. Wulfgruber, L. Yang, Y. Yu, L. Zhang, S. Zhou, Q. Zhu, J.L. Bennetzen, R.K. Dawe, J. Jiang, N. Jiang, G.G. Presting, S.R. Wessler, S. Aluru, R.A. Martienssen, S.W. Clifton, W.R. McCombie, R.A. Wing, and

- R.K. Wilson. 2009. The B73 maize genome: complexity, diversity and dynamics. *Science* 326:1112-1115.
- Schubert I and MA Lysak. 2011. Interpretation of karyotype evolution should consider chromosome structural constraints. *Trends in Genetics* 27:207-216.
- Schubert I, R Rieger & G Fuchs. 1995. Alteration of the basic chromosome number by fusion-fission cycles. *Genome* 38: 1289-1292.
- Schubert, I. and J.L. Oud. 1997. There is an upper limit of chromosome size for normal development of an organism. *Cell*, 88:515-520. (QH573.C380
- Schubert, I., R. Rieger, and J. Fuchs. 1995. Alteration of basic chromosome number by fusion-fission cycles. *Genome*, 38:1289-1292. (QH431.C21)
- Shams I & O Raskina. 2020. Supernumerary B chromosomes and plant genome changes: A snapshot of wild populations of *Aegilops speltoides* Tausch (Poaceae, Triticeae). *Int. J. Mol. Sci.* 21: 3768
- Sheppard AE, MA Ayliffe, L Blatch, A Day, SK Delaney, N Khairul-Fahmy, Y Li, P Madesis, AJ Pryor and JN Timmis. 2008. Transfer of plastic DNA to the nucleus is elevated during male gametogenesis in tobacco. *Plant Physiol.* 148(1): 328-336.
- Shirasu, K., A.H. Schulman, T. Lahaye, and P. Shulze-Lefert. 2000. A contiguous 66-kb barley DNA sequence provides evidence for reversible genome expansion. *Genome Res.* 10:908-915.
- Sijen, T., and R. H. Plasterk. 2003. Transposon silencing in the *Caenorhabditis elegans* germ line by natural RNAi. *Nature*. 426:310-314.
- Shulaev, V. D.J. Sargent, R.N. Crowhurst, T.C. Mockler, O. Folkerts, A.L Delcher, P. Jaiswal, K. Mockaitis, A. Liston, S.P. Mane, P. Burns, T.M. Davis, J.P. Slovin, N. Bassil, R.P. Hellens, C. Evans, T. Harkins, C. Kodira, B. Desany, O.R. Crasta, R.V. Jensen, A.C. Allan, T.P. Michael, J.C. Setubal, J.-M. Celton, D.J.G. Rees, K.P. Williams, S.H. Holt, J.J. Ruiz Rojas, M. Chatterjee, B. Liu, H. Silva, L. Meisel, A. Adato, S.A. Filichkin, M. Troggio, R. Viola, T.-L. Ashman, H. Wang, P. Dharmawardhana, J. Elser, R. Raja, H.D. Priest, D.W. Bryant Jr, S.E. Fox, S.A. Givan, L.J. Wilhelm, S. Naithani, A. Christoffels, D.Y Salama, J. Carter, E. Lopez Girona, A. Zdepski, W. Wang, R. A Kerstetter, W. Schwab, S.S Korban, J. Davik, A. Monfort, B. Denoyes-Rothan, P. Arus, R. Mittler, B. Flinn, A. Aharoni, J.L. Bennetzen, S.L. Salzberg, A.W. Dickerman, R. Velasco, M. Borodovsky, R.E. Veilleux and K.M Folta. 2011. The genome of woodland strawberry (*Fragaria vesca*). *Nature Genetics* 43: 109–116.
- Simonin KA & AB Roddy. 2018. Genome downsizing, physiological novelty, and the global dominance of flowering plants. *PLOS Biology*. 16(1): e2003706
- Skalická, K., K.Y. Lim, R. Matyášek, B. Koukalová, A.R. Leitch, A. Kovařík. 2003. Rapid evolution of parental rDNA in a synthetic tobacco allotetraploid line. *American Journal of Botany* 90: 988-996.
- Skalická, K., K.Y. Lim, R. Matyášek, M. Matzke, A.R. Leitch, and A. Kovárik. 2005. Preferential elimination of repeated DNA sequences from the paternal, *Nicotiana tomentosiformis* genome donor of a synthetic, allotetraploid tobacco. *New Phytologist* 166: 291-303.
- Šmarda P, P Bures, L Horová and O rotreklová. 2008. Intrapopulation genome size dynamics in *Festuca pallens*. *Ann Bot* 102:599-607.
- Soltis, D.E., P.S. Soltis, and J.A. Tate. 2003. Advances in the study of polyploidy since plant speciation. *New Phytologist* 161: 173-191.
- Song,K., P.Lu, K.Tang, and T.C.Osborn. 1995. Rapid genome change in synthetic polyploids of *Brassica* and its implications for polyploid evolution. *Proc. Natl. Acad. Sci. USA* 92:7719-7723.
- Springer NM, SN Anderson, CM Andorf, KR Ahren, F Bai, O Barad, WB Barbazuk, HW Bass, K Baruch, G Ben-Zvi, ES Buckler, R Bukowski, MS Campbell, EKS Cannon, P Chomet, RK Dawe, R Davenport, HK Dooner, LH Du, C Du, KA Easterling, C Gault, J-C Guan, CT Hunter, G Jander, Y Jiao, KE Koch, G Kol, TG Köllner, T Kudo, Q Li, F Lu, D Mayfield-Jones, W Mei, DR McCarty, JN Noshay, JL Portwood II, G Rnen,

- AM Settles, D Shem-Tov, J Shi, I Soifer, JC Stein, MC Stitzer, M Suzuki, DL Vera, E Vollbrecht, JT Vrebalov, D Ware, S Wei, K Wimalanathan, MR Woodhouse, W Xiong and TP Brutnell. 2018. The maize W22 genome provides a foundation for functional genomics and transposon biology. *Nature Genetics* 50: 1282–1288.
- Springer, N.M., K. Ying, Y. Fu, T. Ji, C.T. Yeh, Y. Jia, W. Wu, T. Richmond, J. Kitzman, H. Rosenbaum, A.L. Iniguez, W.B. Barbazuk, J.A. Jeddeloh, D. Nettleton and P.S. Schnable. 2009. Maize inbreds exhibit high levels of copy number variation (CNV) and presence/absence variation (PAV) in genome content. *PLoS Genetics*. 5: e1000734.
- Staginnus C, W Gregor, MF Mette, CH Teo, EG Borroto-Fernández, M Laimer da Câmara Machado, M Matze & T Schwarzacher. 2007. Endogenous pararetroviral sequences in tomato (*Solanum lycopersicum*) and related species *BMC Plant Biology* 7:24
- Staginnus C and KR Richert-Pöggeler. 2006. Endogenous pararetroviruses: two-faced travelers in the plant genome. *Trends Plant Sci* 11:485-491.
- Stavnstrup SS, Molina JP, Lütken H, R Müller & JN Hegelund. 2020. Ancient horizontal gene transfer from *Rhizobium rhizogenes* to European genera of the Figwort family (Scrophulariaceae). *Euphytica* 216, 186
- Stebbins, G. L. 1950. Variation and Evolution in Plants. Columbia University Press.
- Strand, M., T.A. Prolla, R.M. Liskay, and T.D. Petes. 1993. Destabilization of tracts of simple repetitive DNA in yeast by mutations affecting DNA mismatch repair. *Nature* 365:274-276. (Q1.N285)
- Stucky J & RC Jackson. 1975. DNA content of seven species of Astereae and its significance to theories of chromosome evolution in the tribe. *American Journal of Botany*, 62(5): 509-518.
- Suda J, LA Meyerson, IJ Leitch & P Pysek. 2014. The hidden side of plant invasions: the role of genome size. *New Phytologist*, 205: 994-1007
- Swanson-Wagner RA, Eichten SR, Kumari S, Tiffin P, Stein JC, Ware D, Springer NM. 2010. Pervasive gene content variation and copy number variation in maize and its undomesticated progenitor. *Genome Research* 20: 1689–1699.
- Taketa, S., H. Ando, K. Takeda, M. Ichii, and R. von Bothmer. 2005. Ancestry of American polyploid *Hordeum* species with I genome inferred from 5S and 18S-25S rDNA. *Ann. Bot.* 96:21-33.
- Tang H, JE Bowers, X Wang, R Ming, M Alam & AH Paterson. 2008. Synteny and collinearity in plant genomes. *Science* 320: 486-488.
- Tanksley, S.D., R. Bernatzky, N.L. Lapitan, and J.P. Prince. 1988. Conservation of gene repertoire but not gene order in pepper and tomato. *Proc. Natl. Acad. Sci. USA* 85:6419-6423. (Q11.N276)
- Tao Y, X Zhao, E Mace, R Henry & D Jordan. 2019. Exploring and exploiting pan-genomics for crop improvement. *Molecular Plant* 12: 156-169.
- Tian et al. 2012. Nonreference TE insertions identified in the 31 wild and cultivated soybean genomes. *Plant Cell* 24:4422-4436
- Town CD, F Cheung, R Maiti, J Crabtree, BJ Haas, JR Wortman, EE Hine, R Althoff, TS Arbogast, LJ Tallon, M Vigouroux, M Trick, and I Bancroft. 2006. Comparative genomics of *Brassica oleracea* and *Arabidopsis thaliana* reveal gene loss, fragmentation and dispersal after polyploidy. *Plant Cell* 18:1348-1359.
- Tuskan GA, S DiFazio, S Jansson et al. 2006. The genome of cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313: 1596-1604.
- Tuteja JH, SJ Clough, WC Chan and LO Vodkin. 2004. Tissue-specific gene silencing mediated by a naturally occurring chalcone synthase gene cluster in *Glycine max*. *Plant Cell* 16: 819-835
- Van't Hof, J. and A.H. Sparrow. 1963. A relationship between DNA content, nuclear volume, and minimum mitotic cycle time. *Proc. Natl. Acad. Sci.* 49: 897-902.

- Varshney RK, W Chen, Y Li, AK Bharti, RK Saxena, JA Schleuter, MTA Donoghue, S Azam, G Fan, AM Whaley, AD Farmer, J Sheridan, A Iwata, R Tuteja, RV Penmetsa, W Wu, HD Upadhyaya, S-P Yang, T Shah, KB Saxena, T Michael, WR McCombie, B Yang, G Zhang, H Yang, J Wang, C Spillane, DR Cook, GD May, X Xu, and SA Jackson. 2011. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nature Biotech.* DOI:10.1038/nbt.2022.
- Vigouroux Y, Jaqueth JS, Matsuoka Y, Smith OS, Beavis WF, Smith JSC, Doebley J (2002) Rate and pattern of mutation at microsatellite loci in maize. *Mol Biol Evol* 19: 1251-1260
- Vinogradov, A.E. 2003. Selfish DNA is maladaptive: evidence from the plant Red list. *Trends in Genetics* 19:609-614.
- Vision, T. 2005. Gene order in plants: a slow but sure shuffle. *New Phytol.* 168:51-60.
- Vispé S, Satoh MS. 2000. DNA repair patch-mediated double strand DNA break formation in human cells. *J Biol Chem* 275:27386-27392
- Vitte C, Margaux-Alsion F, Alix K, and Tenaillon M. I. 2014. The bright side of transposons in crop evolution. *Briefings in Functional Genomics* vol 13 no 4 276-295
- Vitte C & O Panaud. 2005. LTR retrotransposons and flowering plant genome size: emergence of the increase/decrease model. *Cytogenet Genome Res.* 110: 91-107
- Vollmann J, and P Ruckebauer P. 1997. From Gregor Mendel to molecular plant breeding - a review. *Die Bodenkultur* 48: 53-65
- Walbot V and CA Cullis. 1985. Rapid genomic change in higher plants. *Ann Rev Plant Physiol.* 36:367-396.
- Wang B, X Yang, Y Jia, P Jia, N Dang, S Wang, T Xu, X Zhao, S Gao, Q Dong & K Ye. 2022. High-quality *Arabidopsis thaliana* genome assembly with Nanopore and HiFi Long Reads. *Genomics, Proteomics & Bioinformatics*, 20(1): 4-13.
- Wang G and HK Dooner. 2006. Remarkable variation in maize genome structure inferred from haplotype diversity at the *bz* locus. *PNAS* 103:17644-17649.
- Wang H, S Sun, W Ge, L Zhao, B H, K Wang, Z Lyu, L Chen, S Xu, J Guo, M Li, P Su, X Li, G Wang, C Bo, X Fang, W Zhuang, X Cheng, J Wu, L Dong, W Chen, W Li, G Xiao, J Zhao, Y Hao, Y Xu, Y Gao, W Liu, Y Liu, H Yin, J Li, X Li, Y Zhao, X Wang, F Ni, X Ma, A Li, SS Xu, G Bai, E Nevo, C Gao, H Ohm & L Kong. 2020. *Science*. 368: eaba5435 <https://dx.doi.org/10.1126/science.aba5435>
- Wang, J., L. Tian, A. Madlung, H.-S. Lee, M. Chen, J.J. Lee, B. Watson, T. Kagochi, L. Comai, and Z.J. Chen. 2004. Stochastic and epigenetic changes of gene expression in *Arabidopsis* polyploids. *Genetics* 167: 1961-1973.
- Wang, W., Zheng, H., Fan, C., Li, J., Shi, J., Cai, Z., Zhang, G., Liu, D., Zhang, J., Vang, S., Lu, Z., Wong, G.K., Long, M., and J. Wang. 2006, High rate of chimeric gene origination by retrotransposition in plant genomes. *Plant Cell* 18: 1791-1802.
- Wang W, L Chen, K Fengler, J Bolar, V Llaca, X Wang, CB Clark, TJ Fleury, J Myrvold, D Oneal, MM van Dyk, A Hudson, J Munkvold, A Bumgarten, J Thompson, G Cai, O Crasta, R Aggarwal & J Ma. 2021. A giant NLR gene confers broad-spectrum resistance to *Phytophthora sojae* in soybean. *Nature Communications*, 12: 6263
- Wendel JF. 2015. The wondrous cycles of polyploidy in plants. *American Journal of Botany*. 102: 1753 – 1756.
- Wendel JF, RC Cronn, JS Johnson, and HJ Price. 2002. Feast and famine in plant genomes. *Genetics* 115:37-47.
- Wendel, J.F., A. Schnabel, And T. Seelanan. 1995. Bidirectional interlocus concerted evolution following allopolyploid speciation in cotton (*Gossypium*). *Proceedings of the National Academy of Sciences U.S.A.* 92: 280-284.

- Wendel JF, D Lisch, G H & AS Mason. 2018. The long and short of doubling down: polyploidy, epigenetics, and the temporal dynamics of genome fractionation. *Current Opinion in Genetics & Development* 49: 1-7
- Wenke T, T Döbel, TR Sørensen, H Junghans, B Weisshaar & T Schmidt. 2011. Targeted identification of short interspersed nuclear element families shows their widespread existence and extreme heterogeneity in plant cells. *Plant Cell*, 23: 3117–3128
- Wessler, S.R., T.E. Bureau, and S.E. White. 1995. LTR-retrotransposons and MITEs - important players in the evolution of plant genomes. *Curr. Opinion Genet. Dev.* 5:814-821. (QH426.C88)
- Wicker T, JP Buchmann and B Keller. 2010. Patching gaps in plant genomes results in gene movement and erosion of colinearity. *Genome Research* 20:1229-1237.
- Wicker T, KFX Mayer, H Gunlach, M Martis, B Steuernagel, U Scholz, H Simková, M Kubaláková, F Choulet, S Taudien, M Platzer, C Feuillet, T Fahima, H Budak, J Dolezel, B Keller, and N Stein. 2011. Frequent gene movement and pseudogene evolution is common to the large and complex genomes of wheat, barley, and their relatives. *Plant Cell*, 23:1706-1718.
- Woodhouse, M.R., J.C. Schable, B.S. Pedersen, E. Lyons, E. Lisch, S. Subramaniam, and M. Freeling. 2010. Following tetraploidy in maize, a short deletion mechanism removed genes preferentially from one of the two homeologs. *PLOS Biology* 8:31000409
- Wu, K. S. and S. D. Tanksley. 1993. Abundance, polymorphism and genetic mapping of microsatellites in rice. *Mol. Gen. Genet.* 241:225-235.
- Xiao, H., N. Jiang, E. Schaffner, E.J. Stockinger, and E. van der Knaap. 2008. A retrotransposon-mediated gene duplication underlies morphological variation of tomato fruit. *Science* 319: 1527-1530.
- Yandeu-Nelson MD, XJ Xia, J Li, MG Neuffer and PG Schnable PS .2006. Unequal sister chromatid and homolog recombination at a tandem duplication of the A1 locus in maize. *Genetics* 173: 2211-2226
- Zabala, G. and L.O. Vodkin. 2005. The *wp* mutation of *Glycine max* carries a gene-fragment-rich transposon of the CACTA superfamily. *Plant Cell* 17:2619-2632.
- Zabala G and L Vodkin L. 2007. Novel exon combinations generated by alternative splicing of gene fragments mobilized by a CACTA transposon in *Glycine max*. *BMC Plant Biol* 7: 38
- Zietkiewicz, E., Rafalski, A., and D. Labuda. 1993. Genome fingerprinting by simple sequence repeat (SSR)-Anchored polymerase chain reaction amplification. *Genomics*. 20:176-183.
- Zhang, J. and T. Peterson. 1999. Genome rearrangements by nonlinear transposons in maize. *Genetics* 153: 1403-1410
- Zhang L, J Hu, X Han, et al. 2019. A high-quality apple genome assembly reveals the association of a retrotransposon and red fruit colour. *Nature Communications* 10: 1494