

Annex to:

EFSA GMO Panel (EFSA Panel on Genetically Modified Organisms), Mullins E, Bresson J-L, Dalmay T, Dewhurst IC, Epstein MM, Firbank LG, Guerche P, Hejatko J, Moreno FJ, Naegeli H, Nogu_e F, Sanchez Serrano JJ, Savoini G, Veromann E, Veronesi F, Casacuberta, J, Fernandez Dumont A, Gennaro A, Lenzi, P, Lewandowska A, Munoz Guajardo IP, Papadopoulou N and Rostoks N, 2022. Updated scientific opinion on plants developed through cisgenesis and intragenesis. *EFSA Journal* 2022;20(10):7621, 33 pp. <https://doi.org/10.2903/j.efsa.2022.7621>

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Annex A – Outcome of the scientific literature search in support of the updated scientific opinion on plants developed through cisgenesis and intragenesis

A.1. List of all the publications retrieved from the literature search

1. Ako AE, Perroud P-F, Innocent J, Demko V, Olsen O-A and Johansen W, 2017. An intragenic mutagenesis strategy in *Physcomitrella patens* to preserve intron splicing. *Scientific Reports*, 7
2. Albersmeier A, Pfeifer-Sancar K, Rückert C and Kalinowski J, 2017. Genome-wide determination of transcription start sites reveals new insights into promoter structures in the actinomycete *Corynebacterium glutamicum*. *Journal of Biotechnology*, 257:99-109
3. Ali F, Jilani G, Fahim R, Bai L, Wang C, Tian L and Jiang H, 2019. Functional and structural roles of wiry and sturdy rooted emerged macrophytes root functional traits in the abatement of nutrients and metals. *Journal of Environmental Management*, 249
4. Ali MS and Latif Z, 2016. MOLECULAR CHARACTERIZATION OF YEAST STRAINS ISOLATED FROM DIFFERENT SOURCES BY RESTRICTION FRAGMENT LENGTH POLYMORPHISM. *Pakistan Journal of Botany*, 48:363-370
5. Aljawasim B and Vincelli P, 2015. Evaluation of Polymerase Chain Reaction (PCR)-Based Methods for Rapid, Accurate Detection and Monitoring of *Verticillium dahliae* in Woody Hosts by Real-Time PCR (vol 99, pg 866, 2015). *Plant Disease*, 99:1452-1452
6. Almeraya EV and Sanchez-de-Jimenez E, 2016. Intragenic modification of maize. *Journal of Biotechnology*, 238:35-41
7. Altpeter F, Jung JH, Karan R, Zale J, Kim JY, Wu H, Dermawan H, Pathak B, Gretencord R, Lui H, Candreva J and Shanklin J, 2014. Genetic Improvement of the Biofuel Feedstock Sugarcane with Intragenic, Targeted Mutagenesis and Transgenic Biotechnologies. *In Vitro Cellular & Developmental Biology-Animal*, 50:S19-S19
8. Altpeter F and Karan R, 2018. Genetic improvement of sugarcane by transgenic, intragenic and genome editing technologies. *Achieving Sustainable Cultivation of Sugarcane, Vol 2: Breeding, Pests and Diseases*, 38:133-154
9. Amarillo IE, Li WL, Li X, Vilain E and Kantarci S, 2014. De Novo Single Exon Deletion of *AUTS2* in a Patient with Speech and Language Disorder: A Review of Disrupted *AUTS2* and Further Evidence for Its Role in Neurodevelopmental Disorders. *American Journal of Medical Genetics Part A*, 164:958-965
10. Ampuero S, Luchsinger V, Tapia L, Palomino MA and Larrañaga CE, 2011. SP-A1, SP-A2 and SP-D gene polymorphisms in severe acute respiratory syncytial infection in Chilean infants. *Infection, Genetics and Evolution*, 11:1368-1377
11. An C and Mou Z, 2014. Salicylic acid and defense responses in plants. *Phytohormones: A Window to Metabolism, Signaling and Biotechnological Applications*, 9781493904914:191-219
12. An CF, Orbovic V and Mou ZL, 2013. An efficient intragenic vector for generating intragenic and cisgenic plants in citrus. *American Journal of Plant Sciences*, 4:2131-2137
13. Andersen MM, Landes X, Xiang W, Anyshchenko A, Falhof J, Osterberg JT, Olsen LI, Edenbrandt AK, Vedel SE, Thorsen BJ, Sandoe P, Gamborg C, Kappel K and Palmgren MG, 2015. Feasibility of new breeding techniques for organic farming. *Trends in Plant Science*, 20:426-434
14. Andersson HC, Arpaia S, Bartsch D, Casacuberta J, Davies H, u Jardin P, Flachowsky G, Herman L, Jones H, Kaerenlampi S, Kiss J, Kleter G, Kuiper H, Messean A, Nielsen KM, Perry J, Poeting A, Sweet J, Tebbe C, von Wright AJ and Wal J-M, 2012. Scientific opinion addressing the safety assessment of plants developed through cisgenesis and intragenesis EFSA Panel on Genetically Modified Organ. *EFSA Journal*, 10

15. Ao Y, Xu Y, Cui X-f, Wang A, Teng F, Shen L-q and Liu Q-q, 2016. A genetic diversity assessment of starch quality traits in rice landraces from the Taihu basin, China. *Journal of Integrative Agriculture*, 15:493-501
16. Aoi MC and Rourke BC, 2011. Interspecific and Intragenic Differences in Codon Usage Bias Among Vertebrate Myosin Heavy-Chain Genes. *Journal of Molecular Evolution*, 73:74-93
17. Aoi Y, Kawashima SA, Simanis V, Yamamoto M and Sato M, 2014. Optimization of the analogue-sensitive Cdc2/Cdk1 mutant by in vivo selection eliminates physiological limitations to its use in cell cycle analysis. *Open Biology*, 4
18. Ard R and Allshire RC, 2016. Transcription-coupled changes to chromatin underpin gene silencing by transcriptional interference. *Nucleic Acids Research*, 44:10619-10630
19. Arpaia S, Birch ANE, Chesson A, u Jardin P, Gathmann A, Gropp J, Herman L, Hoen-Sorteberg H-G, Jones H, Kiss J, Kleter G, Lagiou P, Lovik M, Messean A, Naegeli H, Nielsen KM, Ovesna J, Perry J, Rostoks N and Tebbe C, 2012. Scientific opinion addressing the safety assessment of plants developed using Zinc Finger Nuclease 3 and other Site-Directed Nucleases with similar function. *EFSA Journal*, 10
20. Arribere JA and Gilbert WV, 2013. Roles for transcript leaders in translation and mRNA decay revealed by transcript leader sequencing. *Genome Research*, 23:977-987
21. Atanassova A and Keiper F, 2018. Plant breeding innovation: A global regulatory perspective. *Cereal Chemistry*, 95:8-16
22. Awad AM, Nag A, Pham NVB, Bradley MC, Jabassini N, Nathaniel J and Clarke CF, 2020. Intragenic suppressor mutations of the COQ8 protein kinase homolog restore coenzyme Q biosynthesis and function in *Saccharomyces cerevisiae*. *PLoS ONE*, 15
23. Bandara NL, Cova V, Tartarini S, Gessler C, Patocchi A, Cestaro A, Troggio M, Velasco R and Komjanc M, 2013. Isolation of Rvi5 (Vm) Locus from *Malus x domestica* 'Murray'. 3rd International Symposium on Molecular Markers in Horticulture, 1100:21-24
24. Bank C, Hietpas RT, Jensen JD and Bolon DNA, 2015. A Systematic Survey of an Intragenic Epistatic Landscape. *Molecular Biology and Evolution*, 32:229-238
25. Bank C, Matuszewski S, Hietpas RT and Jensen JD, 2016. On the (un) predictability of a large intragenic fitness landscape. *Proceedings of the National Academy of Sciences of the United States of America*, 113:14085-14090
26. Bao F, Huang X, Zhu C, Zhang X, Li X and Yang S, 2014. Arabidopsis HSP90 protein modulates RPP4-mediated temperature-dependent cell death and defense responses. *New Phytologist*, 202:1320-1334
27. Baron JA, Chen JS and Culotta VC, 2015. Cu/Zn superoxide dismutase and the proton ATPase Pma1p of *Saccharomyces cerevisiae*. *Biochemical and Biophysical Research Communications*, 462:251-256
28. Barre BP, Hallin J, Yue J-X, Persson K, Mikhalev E, Irizar A, Holt S, Thompson D, Molin M, Warringer J and Liti G, 2020. Intragenic repeat expansion in the cell wall protein gene HPF1 controls yeast chronological aging. *Genome Research*, 30:697-710
29. Barrell PJ, Latimer JM, Baldwin SJ, Thompson ML, Jacobs JME and Conner AJ, 2017. Somatic cell selection for chlorsulfuron-resistant mutants in potato: identification of point mutations in the acetohydroxyacid synthase gene. *BMC Biotechnology*, 17
30. Basso MF, Gomes Ferreira PC, Kobayashi AK, Harmon FG, Nepomuceno AL, Correa Molinari HB and Grossi-de-Sa MF, 2019. MicroRNAs and new biotechnological tools for its modulation and improving stress tolerance in plants. *Plant Biotechnology Journal*, 17:1482-1500
31. Bastos Andrade AC, Soriano Viana JM, Pereira HD, Pinto VB and Fonseca e Silva F, 2019. Linkage disequilibrium and haplotype block patterns in popcorn populations. *PLoS ONE*, 14
32. Bavaresco L, 2019. Impact of grapevine breeding for disease resistance on the global wine industry. *Acta Horticulturae*:7-14
33. Bergamini C, Cardone MF, Anaclerio A, Perniola R, Pichierri A, Genghi R, Alba V, Forleo LR, Caputo AR, Montemurro C, Blanco A and Antonacci D, 2013. Validation Assay of p3_VvAGL11 Marker in a Wide Range of Genetic Background for Early Selection of Stenospermocarpy in *Vitis vinifera* L. *Molecular Biotechnology*, 54:1021-1030
34. Bhargava A and Carmona FF, 2012. Cisgenesis and intragenesis. *Biotechnology: New Ideas, New Developments (A Textbook of Modern Technology)*:137-151

35. Bhat W, Boutin G, Rufiange A and Nourani A, 2013. Casein Kinase 2 Associates with the Yeast Chromatin Reassembly Factor Spt2/Sin1 To Regulate Its Function in the Repression of Spurious Transcription. *Molecular and Cellular Biology*, 33:4198-4211
36. Borg S, Brinch-Pedersen H, Tauris B, Madsen LH, Darbani B, Noeparvar S and Holm PB, 2012. Wheat ferritins: Improving the iron content of the wheat grain. *Journal of Cereal Science*, 56:204-213
37. Botticella E, Sestili F and Lafiandra D, 2012. Characterization of SBEl1a homoeologous genes in bread wheat. *Molecular Genetics and Genomics*, 287:515-524
38. Bradshaw JE, 2017. Plant breeding: past, present and future. *Euphytica*, 213
39. Brand GD, Magalhães MTQ, Tinoco MLP, Aragão FJL, Nicoli J, Kelly SM, Cooper A and Bloch C, 2012. Probing Protein Sequences as Sources for Encrypted Antimicrobial Peptides. *PLoS ONE*, 7
40. Brand GD, Ramada MHS, Manickchand JR, Correa R, Ribeiro DJS, Santos MA, Vasconcelos AG, Abrao FY, Prates MV, Murad AM, Cardozo Fh JL, Leite JRSA, Magalhaes KG, Oliveira AL and Bloch Jr C, 2019. Intragenic antimicrobial peptides (IAPs) from human proteins with potent antimicrobial and anti-inflammatory activity. *PLoS ONE*, 14
41. Brenet F, Moh M, Funk P, Feierstein E, Viale AJ, Socci ND and Scandura JM, 2011. DNA Methylation of the First Exon Is Tightly Linked to Transcriptional Silencing. *PLoS ONE*, 6
42. Brinch-Pedersen H, Madsen CK, Holme IB and Dionisio G, 2014. Increased understanding of the cereal phytase complement for better mineral bio-availability and resource management. *Journal of Cereal Science*, 59:373-381
43. Broggin GAL, Durel CE, Vergne E, Chevreau E, Fahrentrapp J, Vanblaere T, Peil A, Flachowsky H, Hanke MV, Krens FA, Schouten HJ and Gessler C, 2011. Cisgenic Approach for Improved Disease Resistance in Apple. 2nd Genetically Modified Organisms in Horticulture Symposium, 974:117-121
44. Broggin GAL, Kost T, Fahrentrapp J, Patocchi A, Wöhner T, Flachowsky H, Peil A, Hanke MV and Gessler C, 2014. FB-MR5 is an apple gene providing resistance to fire blight. *Acta Horticulturae*, 1056:273-276
45. Broggin GAL, Schlatholter I, Studer B and Patocchi A, 2018. Development of cisgenic lines of apple to enhance resistance to fire blight. *Phytopathology*, 108
46. Brothers M and Rine J, 2019. Mutations in the PCNA DNA Polymerase Clamp of *Saccharomyces cerevisiae* Reveal Complexities of the Cell Cycle and Ploidy on Heterochromatin Assembly. *Genetics*, 213:449-463
47. Brown SD, Audouy C and Lorenz A, 2020. Intragenic meiotic recombination in *Schizosaccharomyces pombe* is sensitive to environmental temperature changes. *Chromosome Research*, 28:195-207
48. Brown SD, Mpaulo SJ, Asogwa MN, Jezequel M, Whitby MC and Lorenz A, 2019. DNA sequence differences are determinants of meiotic recombination outcome. *Scientific Reports*, 9
49. Bruening G, 2011. Not As They Seem. *Annual Review of Phytopathology*, Vol 49, 49:1-16
50. Brunner PC and McDonald BA, 2018. Evolutionary analyses of the avirulence effector AvrStb6 in global populations of *Zyoseptoria tritici* identify candidate amino acids involved in recognition. *Molecular Plant Pathology*, 19:1836-1846
51. Brunner PC, Stefansson TS, Fountaine J, Richina V and McDonald BA, 2016. A Global Analysis of CYP51 Diversity and Azole Sensitivity in *Rhynchosporium commune*. *Phytopathology*, 106:355-361
52. Brunner S, Vetterli C, Krebs H, Hebeisen T, Romeis J and Winzeler M, 2017. GM potato plants are resistant to late blight. *Agrarforschung Schweiz*, 8:208-215
53. Budak H and Akpinar BA, 2015. Plant miRNAs: biogenesis, organization and origins. *Functional & Integrative Genomics*, 15:523-531
54. Busconi M, Marudelli M and Fogher C, 2015. Non-food interventions: Exploring plant biotechnology applications to therapeutic protein production. *Applied Plant Genomics and Biotechnology*:55-71
55. Cafa G, Baroncelli R, Ellison CA and Kurose D, 2020. *Impatiens glandulifera* (Himalayan balsam) chloroplast genome sequence as a promising target for populations studies. *Peerj*, 8
56. Camiolo S, Toome-Heller M, Aime MC, Haridas S, Grigoriev IV, Porceddu A and Mannazzu I, 2019. An analysis of codon bias in six red yeast species. *Yeast*, 36:53-64
57. Cao J and Li X, 2015. Identification and phylogenetic analysis of late embryogenesis abundant proteins family in tomato (*Solanum lycopersicum*). *Planta*, 241:757-772
58. Cao J and Lv Y, 2016. Evolutionary analysis of the jacalin-related lectin family genes in 11 fishes. *Fish & Shellfish Immunology*, 56:543-553

59. Cao Z, Ding W, Wang J and Bing X, 2016. Study on intragenic methylation of the aromatase P450 gene from different rice field eel tissues. *Bulgarian Chemical Communications*, 48:244-250
60. Cardi T, 2016. Cisgenesis and genome editing: combining concepts and efforts for a smarter use of genetic resources in crop breeding. *Plant Breeding*, 135:139-147
61. Carrasco B, Gonzalez M, Gebauer M, Garcia-Gonzalez R, Maldonado J and Silva H, 2018. Construction of a highly saturated linkage map in Japanese plum (*Prunus salicina* L.) using GBS for SNP marker calling. *PLoS ONE*, 13
62. Carvalho RF and Folta KM, 2017. Assessment of promoters and a selectable marker for development of strawberry intragenic vectors. *Plant Cell Tissue and Organ Culture*, 128:259-271
63. Cascone P, Radkova M, Arpaia S, Errico S, Lotz LAP, Magarelli RA, Djilianov D and Guerrieri E, 2018. Unintended effects of a Phytophthora-resistant cisgenic potato clone on the potato aphid *Macrosiphum euphorbiae* and its parasitoid *Aphidius ervi*. *Journal of Pest Science*, 91:565-574
64. Castano VM, 2014. What I cannot create, I do not understand Comment on "Physical methods for genetic transformation of fungi and yeast" by Ana Leonor Rivera, Denis Magana-Ortiz, Miguel Gomez-Lim, Francisco Fernandez and Achim M. Loske. *Physics of Life Reviews*, 11:208-209
65. Castonguay Y, Dube M-P, Cloutier J, Bertrand A, Michaud R and Laberge S, 2013. Molecular physiology and breeding at the crossroads of cold hardiness improvement. *Physiologia Plantarum*, 147:64-74
66. Castro Neto AL, Brito ANALM, Rezende AM, Magalhaes FB and e Melo Neto OP, 2019. In silico characterization of multiple genes encoding the GP63 virulence protein from *Leishmania braziliensis*: identification of sources of variation and putative roles in immune evasion. *Bmc Genomics*, 20
67. Cavatorta J, Perez KW, Gray SM, Van Eck J, Yeam I and Jahn M, 2011. Engineering virus resistance using a modified potato gene. *Plant Biotechnology Journal*, 9:1014-1021
68. Cecchetto G, Richero M, Oestreicher N, Muro-Pastor MI, Pantano S and Scazzocchio C, 2012. Mutations in the basic loop of the Zn binuclear cluster of the UaY transcriptional activator suppress mutations in the dimerisation domain. *Fungal Genetics and Biology*, 49:731-743
69. Chabbert CD, Adjalley SH, Klaus B, Fritsch ES, Gupta I, Pelechano V and Steinmetz LM, 2015. A high-throughput ChIP-Seq for large-scale chromatin studies. *Molecular Systems Biology*, 11
70. Chaudhary N, Kumari I, Sandhu P, Ahmed M and Akhter Y, 2016. Proteome scale census of major facilitator superfamily transporters in *Trichoderma reesei* using protein sequence and structure based classification enhanced ranking. *Gene*, 585:166-176
71. Chavan S, Gray J and Smith SM, 2015. Diversity and evolution of Rp1 rust resistance genes in four maize lines. *Theoretical and Applied Genetics*, 128:985-998
72. Chawla HS, Lee H, Gabur I, Vollrath P, Tamilselvan-Nattar-Amutha S, Obermeier C, Schiessl SV, Song J-M, Liu K, Guo L, Parkin IAP and Snowdon RJ, 2021. Long-read sequencing reveals widespread intragenic structural variants in a recent allopolyploid crop plant. *Plant Biotechnology Journal*, 19:240-250
73. Chawla R, Shakya R and Rommens CM, 2012. Tuber-specific silencing of asparagine synthetase-1 reduces the acrylamide-forming potential of potatoes grown in the field without affecting tuber shape and yield. *Plant Biotechnology Journal*, 10:913-924
74. Cheang S, Meddaugh H, Samples S, Brumund M, Zambrano R and Kimball T, 2021. A NOVEL DLL4 INTRAGENIC DELETION IN AN INFANT WITH ADAMS-OLIVER SYNDROME AND PERSISTENT TRUNCUS ARTERIOSUS WITH CROSSED PULMONARY ARTERIES. *Journal of Investigative Medicine*, 69:503-503
75. Chen C, D'Alessandro E, Murani E, Zheng Y, Giosa D, Yang N, Wang X, Gao B, Li K, Wimmers K and Song C, 2021. SINE jumping contributes to large-scale polymorphisms in the pig genomes. *Mobile DNA*, 12
76. Chen J-Y, Huang J-Q, Li N-Y, Ma X-F, Wang J-L, Liu C, Liu Y-F, Liang Y, Bao Y-M and Dai X-F, 2015. Genome-wide analysis of the gene families of resistance gene analogues in cotton and their response to *Verticillium* wilt. *BMC Plant Biology*, 15
77. Cheng W, Munkvold KR, Gao H, Mathieu J, Schwizer S, Wang S, Yan Y-b, Wang J, Martin GB and Chai J, 2011. Structural Analysis of *Pseudomonas syringae* AvrPtoB Bound to Host BAK1 Reveals Two Similar Kinase-Interacting Domains in a Type III Effector. *Cell Host & Microbe*, 10:616-626
78. Chia M, Tresenrider A, Chen J, Spedale G, Jorgensen V, Unal E and van Werven FJ, 2017. Transcription of a 5' extended mRNA isoform directs dynamic chromatin changes and interference of a downstream promoter. *Elife*, 6

79. Chizzali C, Gusberti M, Schouten HJ, Gessler C and Broggini GAL, 2016. Cisgenic Rvi6 scab-resistant apple lines show no differences in Rvi6 transcription when compared with conventionally bred cultivars. *Planta*, 243:635-644
80. Cho KS and Park TH, 2016. Complete chloroplast genome sequence of *Solanum nigrum* and development of markers for the discrimination of *S. nigrum*. *Horticulture Environment and Biotechnology*, 57:69-78
81. Choi J, Lyons DB, Kim MY, Moore JD and Zilberman D, 2020. DNA Methylation and Histone H1 Jointly Repress Transposable Elements and Aberrant Intragenic Transcripts. *Molecular Cell*, 77:310-+
82. Choi K, Reinhard C, Serra H, Ziolkowski PA, Underwood CJ, Zhao X, Hardcastle TJ, Yelina NE, Griffin C, Jackson M, Mezard C, McVean G, Copenhaver GP and Henderson IR, 2016. Recombination Rate Heterogeneity within *Arabidopsis* Disease Resistance Genes. *Plos Genetics*, 12
83. Chutrakul C, Panchanawaporn S, Jeennor S, Anantayanon J, Vorapreeda T, Vichai V and Laoteng K, 2019. Functional Characterization of Novel U6 RNA Polymerase III Promoters: Their Implication for CRISPR-Cas9-Mediated Gene Editing in *Aspergillus oryzae*. *Current Microbiology*, 76:1443-1451
84. Colaiacovo M, Lamontanara A, Bernardo L, Alberici R, Crosatti C, Giusti L, Cattivelli L and Faccioli P, 2012. On the complexity of miRNA-mediated regulation in plants: novel insights into the genomic organization of plant miRNAs. *Biology Direct*, 7
85. Collinge DB, 2018. Transgenic crops and beyond: how can biotechnology contribute to the sustainable control of plant diseases? *Biotechnology for plant disease control: GMOs and beyond*. *European Journal of Plant Pathology*, 152:977-986
86. Colson G and Huffman WE, 2011. CONSUMERS' WILLINGNESS TO PAY FOR GENETICALLY MODIFIED FOODS WITH PRODUCT-ENHANCING NUTRITIONAL ATTRIBUTES. *American Journal of Agricultural Economics*, 93:358-363
87. Colson GJ, Huffman WE and Rousu MC, 2011. Improving the Nutrient Content of Food through Genetic Modification: Evidence from Experimental Auctions on Consumer Acceptance. *Journal of Agricultural and Resource Economics*, 36:343-364
88. Confalonieri M and Sparvoli F, 2019. Recent advances in *Medicago* spp. Genetic engineering strategies. *The Model Legume *Medicago truncatula**:1149-1161
89. Corredoira E, San Jose MC, Vieitez AM, Allona I, Aragoncillo C and Ballester A, 2016. Agrobacterium-mediated transformation of European chestnut somatic embryos with a *Castanea sativa* (Mill.) endochitinase gene. *New Forests*, 47:669-684
90. Corredoira E, Valladares S, Allona I, Aragoncillo C, Vieitez AM and Ballester A, 2012. Genetic transformation of European chestnut somatic embryos with a native thaumatin-like protein (CsTL1) gene isolated from *Castanea sativa* seeds. *Tree Physiology*, 32:1389-1402
91. Costa LD, Malnoy M and Gribaudo I, 2017. Breeding next generation tree fruits: technical and legal challenges. *Horticulture Research*, 4
92. Cseh A, Soos V, Rakszegi M, Tuerkoesi E, Balazs E and Molnar-Lang M, 2013. Expression of HvCslF9 and HvCslF6 barley genes in the genetic background of wheat and their influence on the wheat beta-glucan content. *Annals of Applied Biology*, 163:142-150
93. Csorba T, Questa JI, Sun Q and Dean C, 2014. Antisense COOLAIR mediates the coordinated switching of chromatin states at FLC during vernalization. *Proceedings of the National Academy of Sciences of the United States of America*, 111:16160-16165
94. Cui F, Cole HA, Clark DJ and Zhurkin VB, 2012. Transcriptional activation of yeast genes disrupts intragenic nucleosome phasing. *Nucleic Acids Research*, 40:10753-10764
95. Cui P, Jin H, Vutukuru MR and Kaplan CD, 2016. Relationships Between RNA Polymerase II Activity and Spt Elongation Factors to Spt-Phenotype and Growth in *Saccharomyces cerevisiae*. *G3-Genes Genomes Genetics*, 6:2489-2504
96. Dale J, Paul J-Y, Dugdale B and Harding R, 2017. Modifying Bananas: From Transgenics to Organics? *Sustainability*, 9
97. Dalla Costa L, Bozzoli M, Pompili V, Piazza S, Broggini GAL, Patocchi A and Malnoy M, 2019. Development of a Taqman real-time PCR method to quantify nptII in apple lines obtained with "established" or "new breeding" techniques of genetic modification. *European Food Research and Technology*, 245:643-652

98. Dalla Costa L, Piazza S, Campa M, Flachowsky H, Hanke M-V and Malnoy M, 2016. Efficient heat-shock removal of the selectable marker gene in genetically modified grapevine. *Plant Cell Tissue and Organ Culture*, 124:471-481
99. De Marchi E, Cavaliere A, Bacenetti J, Milani F, Pigliafreddo S and Banterle A, 2019. Can consumer food choices contribute to reduce environmental impact? The case of cisgenic apples. *Science of the Total Environment*, 681:155-162
100. De Marchi E, Cavaliere A and Banterle A, 2021. Consumers' Choice Behavior for Cisgenic Food: Exploring the Role of Time Preferences. *Applied Economic Perspectives and Policy*, 43:866-891
101. Debat HJ, 2017. New Breeding Techniques. *Plant-Based Genetic Tools for Biofuels Production*:61-82
102. DeGennaro CM, Alver BH, Marguerat S, Stepanova E, Davis CP, Baehler J, Park PJ and Winston F, 2013. Spt6 Regulates Intragenic and Antisense Transcription, Nucleosome Positioning, and Histone Modifications Genome-Wide in Fission Yeast. *Molecular and Cellular Biology*, 33:4779-4792
103. Delwaide AC, Nalley LL, Dixon BL, Danforth DM, Nayga RM, Jr E and J. van Ioo V, 2015. Revisiting GMOs: are there differences in European consumers' acceptance and valuation for cisgenically vs transgenically bred rice? *PLoS ONE*, 10:e0126060 [0126016pp.]-e0126060 [0126016pp.]
104. Deng S and Chua N-H, 2015. Inverted-Repeat RNAs Targeting FT Intronic Regions Promote FT Expression in Arabidopsis. *Plant and Cell Physiology*, 56:1667-1678
105. Derkx AP, Harding CA, Miraghazadeh A and Chandler PM, 2017. Overgrowth (Della) mutants of wheat: development, growth and yield of intragenic suppressors of the Rht-B1c dwarfing gene. *Functional Plant Biology*, 44:525-537
106. Dermawan H, Jung J and Altpeter F, 2014. Developing Intragenic Biotechnology for Sugarcane. *In Vitro Cellular & Developmental Biology-Animal*, 50:S54-S55
107. Dermawan H, Karan R, Jung JH, Zhao Y, Parajuli S, Sanahuja G and Altpeter F, 2016. Development of an intragenic gene transfer and selection protocol for sugarcane resulting in resistance to acetolactate synthase-inhibiting herbicide. *Plant Cell Tissue and Organ Culture*, 126:459-468
108. Dhakshinamoorthy R and Singh SP, 2021. Evolution of Reproductive Division of Labor - Lessons Learned From the Social Amoeba *Dictyostelium discoideum* During Its Multicellular Development. *Frontiers in Cell and Developmental Biology*, 9
109. Dhekney SA, Li ZT and Gray DJ, 2011. Grapevines engineered to express cisgenic *Vitis vinifera* thaumatin-like protein exhibit fungal disease resistance. *In Vitro Cellular & Developmental Biology-Plant*, 47:458-466
110. Diez CM, Roessler K and Gaut BS, 2014. Epigenetics and plant genome evolution. *Current Opinion in Plant Biology*, 18:1-8
111. Ding X-L, Zhang Y-K, Rong X, Zhang K-J, Zhao D-X and Hong X-Y, 2013. Diversity and recombination of *Wolbachia* strains in spider mites based on analysis of the *wsp* gene. *Chinese Journal of Applied Entomology*, 50:354-361
112. Dlodlu MN, Chimphango SBM, Stirton CH and Muasya AM, 2018. Differential Preference of *Burkholderia* and *Mesorhizobium* to pH and Soil Types in the Core Cape Subregion, South Africa. *Genes*, 9
113. Dobon A, Wulff BBH, Vicente Canet J, Fort P and Tornero P, 2013. An Allele of Arabidopsis *COI1* with Hypo- and Hypermorphic Phenotypes in Plant Growth, Defence and Fertility. *PLoS ONE*, 8
114. Dong H, Lei J, Ding L, Wen Y, Ju H and Zhang X, 2013. MicroRNA: Function, detection, and bioanalysis. *Chemical Reviews*, 113:6207-6233
115. Donia A, Ghada B, Hend BT, Sana BM and Amel SH, 2016. Identification, Evolutionary Patterns and Intragenic Recombination of the Gametophytic Self Incompatibility Pollen Gene (SFB) in Tunisian *Prunus* Species (Rosaceae). *Plant Molecular Biology Reporter*, 34:339-352
116. Dooner HK and He L, 2014. Polarized gene conversion at the *bz* locus of maize. *Proceedings of the National Academy of Sciences of the United States of America*, 111:13918-13923
117. Doris SM, Chuang J, Viktorovskaya O, Murawska M, Spatt D, Churchman LS and Winston F, 2018. Spt6 Is Required for the Fidelity of Promoter Selection. *Molecular Cell*, 72:687-+
118. Dorone Y, Boeynaems S, Flores E, Jin B, Hateley S, Bossi F, Lazarus E, Pennington JG, Michiels E, De Decker M, Vints K, Baatsen P, Bassel GW, Otegui MS, Holehouse AS, Exposito-Alonso M, Sukenik S, Gitler AD and Rhee SY, 2021. A prion-like protein regulator of seed germination undergoes hydration-dependent phase separation. *Cell*, 184:4284-+

119. Du H, Liang Z, Zhao S, Nan M-G, Tran L-SP, Lu K, Huang Y-B and Li J-N, 2015. The Evolutionary History of R2R3-MYB Proteins Across 50 Eukaryotes: New Insights Into Subfamily Classification and Expansion. *Scientific Reports*, 5
120. Duan H, Richael C and Rommens CM, 2012. Overexpression of the wild potato eIF4E-1 variant Eva1 elicits Potato virus Y resistance in plants silenced for native eIF4E-1. *Transgenic Research*, 21:929-938
121. Dubina EV, Mukhina ZM, Kharitonov EM, Shilovskiy VN, Kharchenko ES, Esaulova LV, Korkina NN, Maximenko EP and Nikitina IB, 2015a. Creation of Blast Disease-Resistant Rice Sorts with Modern DNA-Markers. *Genetika*, 51:881-886
122. Dubina EV, Mukhina ZM, Kharitonov EM, Shilovskiy VN, Kharchenko ES, Esaulova LV, Korkina NN, Maximenko EP and Nikitina IB, 2015b. Creation of blast disease-resistant rice varieties with modern DNA-markers. *Russian Journal of Genetics*, 51:752-756
123. Duc C, Sherstnev A, Cole C, Barton GJ and Simpson GG, 2013. Transcription Termination and Chimeric RNA Formation Controlled by *Arabidopsis thaliana* FPA. *Plos Genetics*, 9
124. Dudas B, Jenes B, Kiss GB and Maliga P, 2012. Spectinomycin resistance mutations in the *rrn16* gene are new plastid markers in *Medicago sativa*. *Theoretical and Applied Genetics*, 125:1517-1523
125. Durham T, Doucet J and Snyder LU, 2011. Risk of regulation or regulation of risk? A De Minimus framework for genetically modified crops. *AgBioForum*, 14:61-70
126. Dutt M and Grosser J, 2014. An Intragenic Approach for the Genetic Improvement of Citrus. *In Vitro Cellular & Developmental Biology-Animal*, 50:S38-S38
127. Dutt M, Soriano L and Grosser JW, 2014. Intragenic mediated genetic improvement of citrus: What have we learnt? 3rd International Symposium on Citrus Biotechnology, 1135:85-96
128. Dwyer K, Agarwal N, Pile L and Ansari A, 2021. Gene Architecture Facilitates Intron-Mediated Enhancement of Transcription. *Frontiers in Molecular Biosciences*, 8
129. Eckerstorfer MF, Heissenberger A, Reichenbecher W, Steinbrecher RA and Wassmann F, 2019. An EU Perspective on Biosafety Considerations for Plants Developed by Genome Editing and Other New Genetic Modification Techniques (nGMs). *Frontiers in Bioengineering and Biotechnology*, 7
130. Edenbrandt AK, 2018. Demand for pesticide-free, cisgenic food? Exploring differences between consumers of organic and conventional food. *British Food Journal*, 120:1666-1679
131. Edenbrandt AK, Gamborg C and Thorsen BJ, 2018a. Consumers' Preferences for Bread: Transgenic, Cisgenic, Organic or Pesticide-free? *Journal of Agricultural Economics*, 69:121-141
132. Edenbrandt AK, House LA, Gao Z, Olmstead M and Gray D, 2018b. Consumer acceptance of cisgenic food and the impact of information and status quo. *Food Quality and Preference*, 69:44-52
133. Efsa Panel on Genetically Modified O, 2012. Scientific opinion addressing the safety assessment of plants developed through cisgenesis and intragenesis. *EFSA Journal*, 10:2561 [2533pp.]-2561 [2533pp.]
134. Elam CA, Wirschell M, Yamamoto R, Fox LA, York K, Kamiya R, Dutcher SK and Sale WS, 2011. An Axonemal PP2A B-Subunit is Required for PP2A Localization and Flagellar Motility. *Cytoskeleton*, 68:363-372
135. en Nijs T, Schouten H and Krens F, 2011. Cisgenesis Fits in the Toolkit of a Modern Fruit Breeder. 13th Eucarpia Symposium on Fruit Breeding and Genetics, 976:435-438
136. Enfissi EMA, Drapal M, Perez-Fons L, Nogueira M, Berry HM, Almeida J and Fraser PD, 2021. New plant breeding techniques and their regulatory implications: An opportunity to advance metabolomics approaches. *Journal of Plant Physiology*, 258
137. Entrambasaguas L, Ruocco M, Verhoeven KJF, Procaccini G and Marin-Guirao L, 2021. Gene body DNA methylation in seagrasses: inter- and intraspecific differences and interaction with transcriptome plasticity under heat stress. *Scientific Reports*, 11
138. Eraso P, Portillo F and Mazon MJ, 2013. Characterization of Two Second-Site Mutations Preventing Wild Type Protein Aggregation Caused by a Dominant Negative PMA1 Mutant. *PLoS ONE*, 8
139. Eriksson D, 2018. Recovering the Original Intentions of Risk Assessment and Management of Genetically Modified Organisms in the European Union. *Frontiers in Bioengineering and Biotechnology*, 6
140. Eriksson D, Harwood W, Hofvander P, Jones H, Rogowsky P, Stoeger E and Visser RGF, 2018. A Welcome Proposal to Amend the GMO Legislation of the EU. *Trends in Biotechnology*, 36:1100-1103
141. Eriksson D, Stymne S and Schjoerring JK, 2014. The slippery slope of cisgenesis. *Nature Biotechnology*, 32:727-727

142. Erpen L, Tavano ECR, Harakava R, Dutt M, Grosser JW, Piedade SMS, Mendes BMJ and Mourao Filho FAA, 2018. Isolation, characterization, and evaluation of three *Citrus sinensis*-derived constitutive gene promoters. *Plant Cell Reports*, 37:1113-1125
143. Eshaghi M, Zhu L, Chu Z, Li J, Chan CS, Shahab A, Karuturi RKM and Liu J, 2011. Deconvolution of Chromatin Immunoprecipitation-Microarray (ChIP-chip) Analysis of MBF Occupancies Reveals the Temporal Recruitment of Rep2 at the MBF Target Genes. *Eukaryotic Cell*, 10:130-141
144. Espinas NA, Tu LN, Furci L, Shimajiri Y, Harukawa Y, Miura S, Takuno S and Saze H, 2020. Transcriptional regulation of genes bearing intronic heterochromatin in the rice genome. *Plos Genetics*, 16
145. Espinoza C, Schlechter R, Herrera D, Torres E, Serrano A, Medina C and Arce-Johnson P, 2013. Cisgenesis and Intragenesis: New tools For Improving Crops. *Biological Research*, 46:323-331
146. Estep LK, Torriani SFF, Zala M, Anderson NP, Flowers MD, McDonald BA, Mundt CC and Brunner PC, 2015. Emergence and early evolution of fungicide resistance in North American populations of *Zyloseptoria tritici*. *Plant Pathology*, 64:961-971
147. Fan J, Li P, Song R and Wang F, 2012. Generation of insertional mutation library in maize based on activator tightly-linked with *su1*. *Journal of Maize Sciences*, 20:1-8
148. Flachowsky H and Hanke M-V, 2011. Transgenic Fruit Crops in Europe. *Transgenic Horticultural Crops: Challenges and Opportunities*:125-145
149. Fonsahi EG and Awondo SN, 2016. Cost estimates and investment analysis for muscadine grapes production in Georgia. *Journal of Food Distribution Research*, 47:1-5
150. Frascella A, Bettini PP, Kolarik M, Comparini C, Pazzagli L, Luti S, Scala F and Scala A, 2014. Interspecific variability of class II hydrophobin GEO1 in the genus *Geosmithia*. *Fungal Biology*, 118:862-871
151. Fu P-C, Zhang Y-Z, Geng H-M and Chen S-L, 2016. The complete chloroplast genome sequence of *Gentiana lawrencei* var. *farreri* (Gentianaceae) and comparative analysis with its congeneric species. *Peerj*, 4
152. Gagliardi D, Cambiagno DA, Arce AL, Tomassi AH, Giacomelli JI, Ariel FD and Manavella PA, 2019. Dynamic regulation of chromatin topology and transcription by inverted repeat-derived small RNAs in sunflower. *Proceedings of the National Academy of Sciences of the United States of America*, 116:17578-17583
153. Gaiero P, Speranza P and e Jong H, 2018. Introgressive Hybridization in Potato Revealed by Novel Cytogenetic and Genomic Technologies. *American Journal of Potato Research*, 95:607-621
154. Gal C, Murton HE, Subramanian L, Whale AJ, Moore KM, Paszkiewicz K, Codlin S, Baehler J, Creamer KM, Partridge JF, Allshire RC, Kent NA and Whitehall SK, 2016. Abo1, a conserved bromodomain AAA-ATPase, maintains global nucleosome occupancy and organisation. *Embo Reports*, 17:79-93
155. Galarza JI, Delgado N and Henriquez V, 2016. Cisgenesis and intragenesis in microalgae: promising advancements towards sustainable metabolites production. *Applied Microbiology and Biotechnology*, 100:10225-10235
156. Gao L, Wang B, Wang Z-W, Zhou Y, Su Y-J and Wang T, 2013. Plastome Sequences of *Lygodium japonicum* and *Marsilea crenata* Reveal the Genome Organization Transformation from Basal Ferns to Core Leptosporangiates. *Genome Biology and Evolution*, 5:1403-1407
157. Gao Y, e Bang TC and Schjoerring JK, 2019. Cisgenic overexpression of cytosolic glutamine synthetase improves nitrogen utilization efficiency in barley and prevents grain protein decline under elevated CO₂. *Plant Biotechnology Journal*, 17:1209-1221
158. Garcia B, Stollar EJ and Davidson AR, 2012. The Importance of Conserved Features of Yeast Actin-Binding Protein 1 (Abp1p): The Conditional Nature of Essentiality. *Genetics*, 191:1199-U1226
159. Gardiner SE, 2014. II International Symposium on Biotechnology of Fruit Species, Nelson, New Zealand. *Acta Horticulturae*:228 pp.-228 pp.
160. Gaspero Gd and Morgante M, 2016. New genetic technologies for viticulture. *Informatore Agrario*, 72:55-57
161. Gatzmann F, Falckenhayn C, Gutekunst J, Hanna K, Raddatz G, Carneiro VC and Lyko F, 2018. The methylome of the marbled crayfish links gene body methylation to stable expression of poorly accessible genes. *Epigenetics & Chromatin*, 11
162. Gaur R, Verma S, Pradhan S, Ambreen H and Bhatia S, 2020. A high-density SNP-based linkage map using genotyping-by-sequencing and its utilization for improved genome assembly of chickpea (*Cicer arietinum* L.). *Functional & Integrative Genomics*, 20:763-773

163. Geijer C, Ahmadpour D, Palmgren M, Filipsson C, Klein DM, Tamas MJ, Hohmann S and Lindkvist-Petersson K, 2012. Yeast Aquaglyceroporins Use the Transmembrane Core to Restrict Glycerol Transport. *Journal of Biological Chemistry*, 287:23562-23570
164. Genereaux J, Kvas S, Dobransky D, Karagiannis J, Gloor GB and Brandl CJ, 2012. Genetic Evidence Links the ASTRA Protein Chaperone Component Tti2 to the SAGA Transcription Factor Tra1. *Genetics*, 191:765-U190
165. Gentile A, Urbinati G and Caboni E, 2021. Adventitious shoot regeneration from leaves of peach cultivars growing in vitro: The effect of cytokinins. *Acta Horticulturae*, 1307:285-289
166. Gessler C, 2011. Cisgenic disease resistant apples: a product with benefits for the environment, producer and consumer. *Outlooks on Pest Management*, 22:216-219
167. Gessler C, 2017. Biotechnology for a pesticide free orchard: a promise or an utopia? *Acta Horticulturae*:1-6
168. Gessler C and Broggin GAL, 2013. An orchard without fungicides: a promise or utopia of biotechnology? *IOBC/WPRS Bulletin*, 91:3-10
169. Gessler C, Vanblaere T, Parravicini G and Broggin GAL, 2012. Cisgenic 'Gala' Containing the Scab Resistance Gene from *Malus floribunda* 821 and the Fire Blight Resistance Genes from M. 'Evereste'. 2nd International Symposium on Biotechnology of Fruit Species, 1048:43-49
170. Gheysen G and Custers R, 2017. Why Organic Farming Should Embrace Co-Existence with Cisgenic Late Blight-Resistant Potato. *Sustainability*, 9
171. Gheysen G, Heremans B, Van Droogenbroeck B, Custers R, Vossen JH, Visser RGF, Jacobsen E, Hutten R and Haverkort AJ, 2013. Durable Cisgenic Resistance to *Phytophthora infestans* in Potato, and Perspectives for Applications in Africa. 9th Triennial African Potato Association Conference:122-127
172. Girijarani M, Satyanarayana PV, Suryanarayana Y, Rao PVR, Neerajakshi C, Chamundeswari N, Ravikumar BNSVR, Pavani SL, Kondayya K, Ratnasree P, Vishnuvardhan KM, Sivaramprasad K and Reddy AV, 2015. ENHANCEMENT OF FLOOD TOLERANCE IN A HIGH YIELDING RICE VARIETY 'AMARA' BY MARKER ASSISTED SELECTION. *Sabrao Journal of Breeding and Genetics*, 47:439-447
173. Giudice G, Moffa L, Varotto S, Cardone MF, Bergamini C, De Lorenzis G, Velasco R, Nerva L and Chitarra W, 2021. Novel and emerging biotechnological crop protection approaches. *Plant Biotechnology Journal*, 19:1495-1510
174. Glastad KM, Gokhale K, Liebig J and Goodisman MAD, 2016. The caste- and sex-specific DNA methylome of the termite *Zootermopsis nevadensis*. *Scientific Reports*, 6
175. Glastad KM, Hunt BG, Yi SV and Goodisman MAD, 2014. Epigenetic inheritance and genome regulation: is DNA methylation linked to ploidy in haplodiploid insects? *Proceedings of the Royal Society B-Biological Sciences*, 281
176. Golshani F, Fakheri BA, Solouki M, Mahdinezhad N and Feriz MRK, 2020. EVOLUTIONARY AND PHYLOGENIC RELATIONSHIPS OF WILD AND CROP SPECIES OF IRANIAN SAFFRON BY DNA BARCODING. *Bangladesh Journal of Botany*, 49:287-296
177. Gomez-Navarro N, Jordan-Pla A, Estruch F and Perez-Ortin JE, 2016. Defects in the NC2 repressor affect both canonical and non-coding RNA polymerase II transcription initiation in yeast. *Bmc Genomics*, 17
178. Gomolinska AM, Szczecinska M, Sawicki J, Krawczyk K and Szkudlarz P, 2017. Phylogenetic analysis of selected representatives of the genus *Erica* based on the genes encoding the DNA-dependent RNA polymerase I. *Biodiversity: Research and Conservation*, 46:1-18
179. Gonneau C, Noret N, Gode C, Kitt J, Sirguy C, Sterckeman T, Koch MA and Pauwels M, 2017. Design and validation of sixteen single nucleotide polymorphism to investigate plastid DNA sequence variation in *Noccaea caerulescens* (Brassicaceae). *Conservation Genetics Resources*, 9:67-71
180. Gonthier P and Garbelotto M, 2011. Amplified fragment length polymorphism and sequence analyses reveal massive gene introgression from the European fungal pathogen *Heterobasidion annosum* into its introduced congener *H. irregulare*. *Molecular Ecology*, 20:2756-2770
181. Gonzalez-Arenzana L, Perez-Martin F, Llanos Palop M, Sesena S, Santamaria P, Lopez R and Lopez-Alfaro I, 2015. Genomic diversity of *Oenococcus oeni* populations from Castilla La Mancha and La Rioja Tempranillo red wines. *Food Microbiology*, 49:82-94
182. Gonzalez S, Villa E, Rodriguez M, Ramirez M, Zavala J, Armas R, Dassori A, Contreras J, Raventos H, Flores D, Jerez A, Ontiveros A, Nicolini H and Escamilla M, 2019. Fine-mapping scan of bipolar disorder susceptibility loci in Latino pedigrees. *American Journal of Medical Genetics Part B-Neuropsychiatric Genetics*, 180:213-222

183. Goryacheva II, Gorelova TV and Andrianov BV, 2015. *Drosophila melanogaster* cell culture as an experimental model to study recombination in *Wolbachia pipientis*. *Russian Journal of Genetics*, 51:1159-1164
184. Gouot E, Bhat W, Rufiange A, Fournier E, Paquet E and Nourani A, 2018. Casein kinase 2 mediated phosphorylation of Spt6 modulates histone dynamics and regulates spurious transcription. *Nucleic Acids Research*, 46:7612-7630
185. Goutam U, Thakur K, Salaria N and Kukreja S, 2018. Recent Approaches for Late Blight Disease Management of Potato Caused by *Phytophthora infestans*. *Fungi and Their Role in Sustainable Development: Current Perspectives*:311-325
186. Grasser KD, 2020. The FACT Histone Chaperone: Tuning Gene Transcription in the Chromatin Context to Modulate Plant Growth and Development. *Frontiers in Plant Science*, 11
187. Grasso FM, Marini M, Vitale A, Firrao G and Granata G, 2012. Canker and dieback on *Platanus x acerifolia* caused by *Diaporthe scabra*. *Forest Pathology*, 42:510-513
188. Gray DJ, Li ZT and Dhekney SA, 2012. Progress in the Development of Intragenic Grapevine. *In Vitro Cellular & Developmental Biology-Animal*, 48:18-18
189. Gray DJ, Li ZT and Dhekney SA, 2014. Precision breeding of grapevine (*Vitis vinifera* L.) for improved traits. *Plant Science*, 228:3-10
190. Gray DJ, Li ZT, Kim K-H and Silva DD, 2013. The Development of Cisgenic Grapevines. *Hortscience*, 48:S172-S172
191. Grosse-Holz FM and van der Hoorn RAL, 2016. Juggling jobs: roles and mechanisms of multifunctional protease inhibitors in plants. *New Phytologist*, 210:794-807
192. Gu X-Y, Foley ME, Horvath DP, Anderson JV, Feng J, Zhang L, Mowry CR, Ye H, Suttle JC, Kadowaki K-i and Chen Z, 2011. Association Between Seed Dormancy and Pericarp Color Is Controlled by a Pleiotropic Gene That Regulates Abscisic Acid and Flavonoid Synthesis in Weedy Red Rice. *Genetics*, 189:1515-+
193. Guo J, Sun W, Liu H, Chi J, Odiba AS, Li G, Jin L and Xin C, 2020. Aldehyde dehydrogenase plays crucial roles in response to lower temperature stress in *Solanum tuberosum* and *Nicotiana benthamiana*. *Plant Science*, 297
194. Guo Y, Wang S, Vogl C and Ehrendorfer F, 2012. Nuclear and plastid haplotypes suggest rapid diploid and polyploid speciation in the N Hemisphere *Achillea millefolium* complex (Asteraceae). *BMC Evolutionary Biology*, 12:(3 January 2012)-(2013 January 2012)
195. Hadjilouka A, Paramithiotis S and Drosinos EH, 2018. Genetic Analysis of the *Listeria* Pathogenicity Island 1 of *Listeria monocytogenes* 1/2a and 4b Isolates. *Current Microbiology*, 75:857-865
196. Haesaert G, Vossen JH, Custers R, De Loose M, Haverkort A, Heremans B, Hutten R, Kessel G, Landschoot S, Van Droogenbroeck B, Visser RGF and Gheysen G, 2015. Transformation of the potato variety Desiree with single or multiple resistance genes increases resistance to late blight under field conditions. *Crop Protection*, 77:163-175
197. Hainer SJ and Martens JA, 2011. Identification of Histone Mutants That Are Defective for Transcription-Coupled Nucleosome Occupancy. *Molecular and Cellular Biology*, 31:3557-3568
198. Han KM, Dharmawardhana P, Arias RS, Ma C, Busov V and Strauss SH, 2011. Gibberellin-associated cisgenes modify growth, stature and wood properties in *Populus*. *Plant Biotechnology Journal*, 9:162-178
199. Hang R, Wang Z, Yang C, Luo L, Mo B, Chen X, Sun J, Liu C and Cao X, 2021. Protein arginine methyltransferase 3 fine-tunes the assembly/disassembly of pre-ribosomes to repress nucleolar stress by interacting with RPS2B in *Arabidopsis*. *Molecular Plant*, 14:223-236
200. Hanke MV, Flachowsky H, Patocchi A and Gessler C, 2013. New Breeding Technologies Through Genetic Engineering in Apple (*Malus x domestica*). *In Vitro Cellular & Developmental Biology-Animal*, 49:S18-S18
201. Hasani A and Hasani M, 2017. Method of identifying genetic characteristics of fungal disease-inhibiting enzyme in beans. *Journal of Balkan Ecology*, 20:157-162
202. Haverkort AJ, Boonekamp PM, Hutten R, Jacobsen E, Lotz LAP, Kessel GJT, Vossen JH and Visser RGF, 2016. Durable Late Blight Resistance in Potato Through Dynamic Varieties Obtained by Cisgenesis: Scientific and Societal Advances in the DuRPh Project. *Potato Research*, 59:35-66
203. Haverkort AJ and Kempenaar C, 2016. Recent advances in biotechnology and information technology in the potato industry. *The Dundee Conference: Crop Protection in Northern Britain 2016*, 23-24 February 2016, Dundee, UK:183-190
204. Hayano S, Okuno Y, Tsutsumi M, Inagaki H, Fukasawa Y, Kurahashi H, Kojima S, Takahashi Y and Kato T, 2019. Corrigendum to "Frequent intragenic microdeletions of elastin in familial supravalvular aortic stenosis." [Int.

- J. *Cardiol.*, 274 (2019) 290–295](S0167527318323283)(10.1016/j.ijcard.2018.09.032). *International Journal of Cardiology*, 292:283
205. Hayashi M and Umezu K, 2017. Homologous recombination is required for recovery from oxidative DNA damage. *Genes & Genetic Systems*, 92:73-80
206. He L-Y, Zhao X-Q, Ge X-M and Bai F-W, 2012. Identification and functional study of a new FLO10-derivative gene from the industrial flocculating yeast SPSC01. *Journal of Industrial Microbiology & Biotechnology*, 39:1135-1140
207. Heckmann S, Lermontova I, Berckmans B, De Veylder L, Baeumlein H and Schubert I, 2011. The E2F transcription factor family regulates CENH3 expression in *Arabidopsis thaliana*. *Plant Journal*, 68:646-656
208. Herdt RW and Nelson R, 2011. *Biotechnology and Agriculture: Current and Emerging Applications*. *Genetically Modified Food and Global Welfare*, 10:1-27
209. Hervas-Aguilar MA, Bichsel KJ and Oakley BR, 2014. Intragenic complementation reveals that gamma-tubulin has at least three functions important for growth of *Aspergillus nidulans*. *Molecular Biology of the Cell*, 25
210. Hewezi T, 2020. Epigenetic Mechanisms in Nematode-Plant Interactions. *Annual Review of Phytopathology*, Vol 58, 58:119-138
211. Higuera-Sobrino JJ, Blanco-Portales R, Moyano E, Rodríguez-Franco A, Muñoz-Blanco J and Caballero JL, 2021. Silencing of strawberry pathogen defence related candidate genes by using specific strawberry fruit ripening-related promoters: An intragenic approach to improve fruit quality and resistance. *Acta Horticulturae*, 1309:83-91
212. Holme IB, 2014. Targeted mutagenesis using TALENs as means to improve cereal grain quality. *Cereal Foods World*, 59:A8-A9
213. Holme IB, Dionisio G and Brinch-Pedersen H, 2021. A Roadmap to Modulated Anthocyanin Compositions in Carrots. *Plants-Basel*, 10
214. Holme IB, Dionisio G, Brinch-Pedersen H, Wendt T, Madsen CK, Vincze E and Holm PB, 2012. Cisgenic barley with improved phytase activity. *Plant Biotechnology Journal*, 10:237-247
215. Holme IB, Madsen CK, Wendt T and Brinch-Pedersen H, 2020. Horizontal Stacking of PAPHy_a Cisgenes in Barley Is a Potent Strategy for Increasing Mature Grain Phytase Activity. *Frontiers in Plant Science*, 11
216. Holme IB, Wendt T and Holm PB, 2013. Intragenesis and cisgenesis as alternatives to transgenic crop development. *Plant Biotechnology Journal*, 11:395-407
217. Horizon MI, Michael W, Antonius S and Iman R, 2021. Dominant Enterobacteriaceae in tempeh were primarily originated from soybean. *Food Science and Biotechnology*, 30:861-868
218. Hou H, Atlihan N and Lu Z-X, 2014. New biotechnology enhances the application of cisgenesis in plant breeding. *Frontiers in Plant Science*, 5:389-389
219. Hou Z and Cao J, 2016. Comparative study of the P2X gene family in animals and plants. *Purinergic Signalling*, 12:269-281
220. Hu L, Li H, Qin R, Xu R, Li J, Li L, Wei P and Yang J, 2016. Plant phosphomannose isomerase as a selectable marker for rice transformation. *Scientific Reports*, 6
221. Hu W, Zhou T, Wang P, Wang B, Song J, Han Z, Chen L, Liu K and Xing Y, 2019. Development of whole-genome agarose-resolvable LInDel markers in rice. *Rice*, 13:(06 January 2020)-(2006 January 2020)
222. Huang H-Y, Jiang W-B, Hu Y-W, Wu P, Zhu J-Y, Liang W-Q, Wang Z-Y and Lin W-H, 2013. BR Signal Influences *Arabidopsis* Ovule and Seed Number through Regulating Related Genes Expression by BZR1. *Molecular Plant*, 6:456-469
223. Hudson J, 2017. Genetically modified products and GMO foods: A game of chance. *Developing New Functional Food and Nutraceutical Products*:481-494
224. Hudson J, Caplanova A and Novak M, 2015. Public attitudes to GM foods. The balancing of risks and gains. *Appetite*, 92:303-313
225. Ilardi V and Tavazza M, 2015. Biotechnological strategies and tools for Plum pox virus resistance: trans-, intra-, cis-genesis, and beyond. *Frontiers in Plant Science*, 6
226. Islam MS, Roni MZK, Mondal R and Shimasaki K, 2020. Cis vs. trans: is cisgenesis an attractive alternative for transgenesis to make genetic modification acceptable to the public? *Acta Horticulturae*:423-431
227. Ismagul A, Maltseva E, Iskakova G, Yang N, Lopato S, Eliby S and Langridge P, 2014. Gene Stacking in Cisgenic Wheat. *In Vitro Cellular & Developmental Biology-Plant*, 50:515-516

228. Jacobsen E, 2013. Cisgenesis: a modern way of domesticating traits of the breeders' gene pool. *CAB Reviews*, 8:1-10
229. Jaensch M, Paris R, Amoako-Andoh F, Keulemans W, Davey MW, Pagliarani G, Tartarini S and Patocchi A, 2014. A Phenotypic, Molecular and Biochemical Characterization of the First Cisgenic Scab-Resistant Apple Variety 'Gala'. *Plant Molecular Biology Reporter*, 32:679-690
230. Jafari G, Wasko BM, Tonge A, Schurman N, Dong C, Li Z, Peters R, Kayser E-B, Pitt JN, Morgan PG, Sedensky MM, Crofts AR and Kaeberlein M, 2015. Tether mutations that restore function and suppress pleiotropic phenotypes of the *C. elegans* isp-1(qm150) Rieske iron-sulfur protein. *Proceedings of the National Academy of Sciences of the United States of America*, 112:E6148-E6157
231. Jai G, 2013. Impact of GMO's on environment and human health. *Recent Research in Science and Technology*, 5:26-29
232. Janevska D, Din E, Tobar-Rubin R, Alvarez R and Chaudhry F, 2012. Finding novel intragenic suppressors of a constitutively active allele of Gs alpha. *Faseb Journal*, 26
233. Jeong KS, Shin JK, Maki M and Pak J-H, 2016. PHYLOGENY OF GALIUM L. (RUBIACEAE) FROM KOREA AND JAPAN BASED ON CHLOROPLAST DNA SEQUENCE. *Bangladesh Journal of Plant Taxonomy*, 23:237-246
234. Ji X, Yu L, Tang M, Tian D, Yang S, Zhang X and Traw MB, 2020. Pleiotropic changes revealed by in situ recovery of the semi-dwarf gene sd1 in rice. *Journal of Plant Physiology*, 248
235. Jia S, 2018. Risk assessment and regulation of genetically engineered crops: history and reformation. *Scientia Agricultura Sinica*, 51:601-612
236. Jiu S, Zhu X, Wang J, Zhang C, Mu Q, Wang C and Fang J, 2015. Genome-Wide Mapping and Analysis of Grapevine MicroRNAs and Their Potential Target Genes. *Plant Genome*, 8
237. Jo K, 2013. Unveiling and deploying durability of late blight resistance in potato: from natural stacking to cisgenic stacking. *Unveiling and deploying durability of late blight resistance in potato: from natural stacking to cisgenic stacking*:168 pp.-168 pp.
238. Jo K, Kim C, Kim S, Kim T, Bergervoet M, Jongsma MA, Visser RGF, Jacobsen E and Vossen JH, 2014. Development of late blight resistant potatoes by cisgene stacking. *BMC Biotechnology*, 14:(29 May 2014)-(2029 May 2014)
239. Jo KR, Zhu S, Bai Y, Hutten RCB, Kessel GJT, Vleeshouwers VGAA, Jacobsen E, Visser RGF and Vossen JH, 2016. Problematic Crops: 1. Potatoes: Towards Sustainable Potato Late Blight Resistance by Cisgenic R Gene Pyramiding. *Plant Pathogen Resistance Biotechnology*:171-191
240. Johnson CE, Premasathan A, Trask JS and Kanthaswamy S, 2013. Species Identification of *Cannabis sativa* Using Real-Time Quantitative PCR (qPCR). *Journal of Forensic Sciences*, 58:486-490
241. Johnson P, Mitchell V, McClure K, Kellems M, Marshall S, Allison MK, Lindley H, Nguyen H-TT, Tackett JE and Duina AA, 2015. A Systematic Mutational Analysis of a Histone H3 Residue in Budding Yeast Provides Insights into Chromatin Dynamics. *G3-Genes Genomes Genetics*, 5:741-749
242. Joshi SG, Schaart JG, Groenwold R, Jacobsen E, Schouten HJ and Krens FA, 2011. Functional analysis and expression profiling of HcrVf1 and HcrVf2 for development of scab resistant cisgenic and intragenic apples. *Plant Molecular Biology*, 75:579-591
243. Jung J, Dermawan H and Altpeter F, 2014. Suppression of Lignin Biosynthesis in Sugarcane Following Intragenic Precision Breeding. *In Vitro Cellular & Developmental Biology-Plant*, 50:508-509
244. Jung JH, Kannan B, Dermawan H, Moxley GW and Altpeter F, 2016. Precision breeding for RNAi suppression of a major 4-coumarate:coenzyme A ligase gene improves cell wall saccharification from field grown sugarcane. *Plant Molecular Biology*, 92:505-517
245. Kamrani M, Kohnhrouz BB and Gholizadeh A, 2011. Cisgenic inhibition of the potato cold induced phosphorylase L gene expression and decrease in sugar contents. *African Journal of Biotechnology*, 10:10076-10082
246. Kamthan A, Chaudhuri A, Kamthan M and Datta A, 2016. Genetically modified (GM) crops: milestones and new advances in crop improvement. *Theoretical and Applied Genetics*, 129:1639-1655
247. Kandel R, Dutt M, Grosser JW, Gray DJ, Li ZT, Sittler V, Bergey DR and Dhekney SA, 2014. Evaluation of plant-based reporter systems for improvement of cold-hardy grape cultivars. 29th International Horticultural Congress on Horticulture - Sustaining Lives, Livelihoods and Landscapes (IHC) / 4th International Symposium on Tropical Wines / International Symposium on Grape and Wine Production in Diverse Regions, 1115:57-61

248. Kaplan-Levy RN, Alster-Gloukhovski A, Benyamini Y and Zohary T, 2016. Lake Kinneret phytoplankton: integrating classical and molecular taxonomy. *Hydrobiologia*, 764:283-302
249. Karas BJ, Ross L, Novero M, Amyot L, Shrestha A, Inada S, Nakano M, Sakai T, Bonetta D, Sato S, Murray JD, Bonfante P and Szczyglowski K, 2021. Intragenic complementation at the *Lotus japonicus* CELLULOSE SYNTHASE-LIKE D1 locus rescues root hair defects. *Plant Physiology*, 186:2037-2050
250. Karasev ES, Andronov EE, Aksenova TS, Chizhevskaya EP, Tupikin AE and Provorov NA, 2019. Evolution of Goat's Rue Rhizobia (*Neorhizobium galegae*): Analysis of Polymorphism of the Nitrogen Fixation and Nodule Formation Genes. *Russian Journal of Genetics*, 55:263-266
251. Kaur N, Pandey A and Tiwari S, 2016. Provitamin a enrichment for tackling malnutrition. *Banana: Genomics and Transgenic Approaches for Genetic Improvement*:277-299
252. Kearns P, Nikaido T, Dagallier B and Hosokawa M, 2014. Biotechnology and biosafety activities at OECD - a policy development perspective. 29th International Horticultural Congress on Horticulture - Sustaining Lives, Livelihoods and Landscapes (IHC) / 3rd International Genetically Modified Organisms in Horticulture Symposium - Past, Present and Future, 1124:63-67
253. Kessel GJT, Mullins E, Evenhuis A, Stellingwerf J, Cortes VO, Phelan S, van den Bosch T, Forch MG, Goedhart P, van der Voet H and Lotz LAP, 2018. Development and validation of IPM strategies for the cultivation of cisgenically modified late blight resistant potato. *European Journal of Agronomy*, 96:146-155
254. Khan SA, Chibon P-Y, e Vos RCH, Schipper BA, Walraven E, Beekwilder J, van Dijk T, Finkers R, Visser RGF, van de Weg EW, Bovy A, Cestaro A, Velasco R, Jacobsen E and Schouten HJ, 2012a. Genetic analysis of metabolites in apple fruits indicates an mQTL hotspot for phenolic compounds on linkage group 16. *Journal of Experimental Botany*, 63:2895-2908
255. Khan SA, Schaart JG, Beekwilder J, Allan AC, Tikunov YM, Jacobsen E and Schouten HJ, 2012b. The mQTL hotspot on linkage group 16 for phenolic compounds in apple fruits is probably the result of a leucoanthocyanidin reductase gene at that locus. *BMC research notes*, 5:618-618
256. Khuman A, Arora S, Makkar H, Patel A and Chaudhary B, 2020. Extensive intragenic divergences amongst ancient WRKY transcription factor gene family is largely associated with their functional diversity in plants. *Plant Gene*, 22
257. Kim D-H and Sung S, 2017. Vernalization-Triggered Intragenic Chromatin Loop Formation by Long Noncoding RNAs. *Developmental Cell*, 40:302-312
258. Kim JY, Kwon YJ, Kim S-I, Kim D, Song JT and Seo HS, 2016. Ammonium Inhibits Chromomethylase 3-Mediated Methylation of the Arabidopsis Nitrate Reductase Gene NIA2. *Frontiers in Plant Science*, 6
259. Kindgren P, Ivanov M and Marquardt S, 2020. Native elongation transcript sequencing reveals temperature dependent dynamics of nascent RNAPII transcription in Arabidopsis. *Nucleic Acids Research*, 48:2332-2347
260. Kirdök E, Ekinci H and Çiftçi YÖ, 2015. Cryopreservation of somatic embryos of ornamental plants. *Somatic Embryogenesis in Ornamentals and Its Applications*:121-139
261. Konagaya K-i, Tsuda M, Okuzaki A, Ando S and Tabei Y, 2013. Application of the acetolactate synthase gene as a cisgenic selectable marker for *Agrobacterium*-mediated transformation in Chinese cabbage (*Brassica rapa* ssp *pekinensis*). *Plant Biotechnology*, 30:125-U125
262. Kondo K and Nakamura K, 2014. Scientific Review on Novel Genome Editing Techniques. *Food Hygiene and Safety Science*, 55:231-246
263. Kost TD, Gessler C, Jaensch M, Flachowsky H, Patocchi A and Broggini GAL, 2015. Development of the First Cisgenic Apple with Increased Resistance to Fire Blight. *PLoS ONE*, 10
264. Kost TD, Jansch M, Gessler C, Flachowsky H, Patocchi A and Broggini GAL, 2017. Generation of a cisgenic apple line of cultivar 'Gala' with increased fire blight resistance. *Acta Horticulturae*, 1172:79-84
265. Kostal T, 2017. Offline Induction Machine Parameters Identification Suitable for Self-commissioning. *International Conference on Applied Electronics (AE)*:79-82
266. Koster MJE, Yildirim AD, Weil PA, Holstege FCP and Timmers HTM, 2014. Suppression of intragenic transcription requires the MOT1 and NC2 regulators of TATA-binding protein. *Nucleic Acids Research*, 42:4220-4229
267. Kozminska A, Wiszniewska A, Hanus-Fajerska E and Muszynska E, 2018. Recent strategies of increasing metal tolerance and phytoremediation potential using genetic transformation of plants. *Plant Biotechnology Reports*, 12:1-14

268. Krause SMB, Naether A, Ortiz Cortes V, Mullins E, Kessel GJT, Lotz LAP and Tebbe CC, 2020. No Tangible Effects of Field-Grown Cisgenic Potatoes on Soil Microbial Communities. *Frontiers in Bioengineering and Biotechnology*, 8
269. Krawczyk K and Sawicki J, 2013. The Uneven Rate of the Molecular Evolution of Gene Sequences of DNA-Dependent RNA Polymerase I of the Genus *Lamium* L. *International Journal of Molecular Sciences*, 14:11376-11391
270. Krens FA and Kamo K, 2011. Genomic Tools and Prospects for New Breeding Techniques in Flower Bulb Crops. 2nd Genetically Modified Organisms in Horticulture Symposium, 974:139-147
271. Krens FA, Salentijn EMJ, Schaart JG, Schouten HJ and Jacobsen E, 2012. Current Progress in Trans- and Cisgenic Apple and Strawberry Breeding. 1st International Symposium on Genetic Modifications - Challenges and Opportunities for Horticulture in the World, 941:37-48
272. Krens FA, Schaart JG, van der Burgh AM, Tinnenbroek-Capel IEM, Groenwold R, Kodde LP, Broggini GAL, Gessler C and Schouten HJ, 2015. Cisgenic apple trees; development, characterization, and performance. *Frontiers in Plant Science*, 6
273. Kronberger N, Wagner W and Nagata M, 2014. How Natural Is "More Natural"? The Role of Method, Type of Transfer, and Familiarity for Public Perceptions of Cisgenic and Transgenic Modification. *Science Communication*, 36:106-130
274. Kucharczyk R, Dautant A, Godard F, Tribouillard-Tanvier D and i Rago J-P, 2019. Functional investigation of an universally conserved leucine residue in subunit a of ATP synthase targeted by the pathogenic m.9176 T > G mutation. *Biochimica Et Biophysica Acta-Bioenergetics*, 1860:52-59
275. Kuligowska K, Lutken H, Hegelund JN and Muller R, 2013. Future Perspectives of In Vitro Culture and Plant Breeding. 8th International Symposium on In Vitro Culture and Horticultural Breeding, 1083:27-33
276. Kumar GS, Chang W, Xie T, Patel A, Zhang Y, Wang GG, David G and Radhakrishnan I, 2012. Sequence Requirements for Combinatorial Recognition of Histone H3 by the MRG15 and Pf1 Subunits of the Rpd3S/Sin3S Corepressor Complex. *Journal of Molecular Biology*, 422:519-531
277. Kumar GS, Xie T, Zhang Y and Radhakrishnan I, 2011. Solution Structure of the mSin3A PAH2-Pf1 SID1 Complex: A Mad1/Mxd1-Like Interaction Disrupted by MRG15 in the Rpd3S/Sin3S Complex. *Journal of Molecular Biology*, 408:987-1000
278. Kumar J and Pratap A, 2014. Alien gene transfer: Challenges and opportunities. *Alien Gene Transfer in Crop Plants*, 1:289-307
279. Kumar K, Arora PK and Gill MIS, 2017. Breeding avenues in fruit crops for imparting resistance against insect pests. *Breeding Insect Resistant Crops for Sustainable Agriculture*:289-322
280. Kumar K, Gambhir G, Dass A, Tripathi AK, Singh A, Jha AK, Yadava P, Choudhary M and Rakshit S, 2020. Genetically modified crops: current status and future prospects. *Planta*, 251
281. Kumari M, Devanna BN, Singh PK, Rajashekara H, Sharma V and Sharma TR, 2017. Stacking of blast resistance orthologue genes in susceptible indica rice line improves resistance against *Magnaporthe oryzae*. *3 Biotech*, 8
282. Kuo HY and Chang YW, 2012. The role of MUC1 in initial biofilm formation of clinical isolates of *Saccharomyces cerevisiae*. *Mycoses*, 55:133-133
283. Kurepa J and Smalle J, 2013. Reversion of the *Arabidopsis* rpn12a-1 exon-trap mutation by an intragenic suppressor that weakens the chimeric 5' splice site. *F1000Research*, 2:60-60
284. Kushalappa AC, Yogendra KN, Sarkar K, Kage U and Karre S, 2016. Gene discovery and genome editing to develop cisgenic crops with improved resistance against pathogen infection. *Canadian Journal of Plant Pathology*, 38:279-295
285. Kuzma J, Kokotovich A and Kuzhabekova A, 2016. Attitudes towards Governance of Gene Editing. *Asian Biotechnology and Development Review*, 18:69-92
286. Lam M, Wolff K, Griffiths H and Carmichael A, 2014. Correction: An Aqueous Extract of *Fagonia cretica* Induces DNA Damage, Cell Cycle Arrest and Apoptosis in Breast Cancer Cells via FOXO3a and p53 Expression (vol 9, e102655, 2014). *PLoS ONE*, 9
287. Lambie EJ, Bruce RD, Iii Z and Jeffrey Y, 2015. Novel Alleles of gon-2, a *C. elegans* Ortholog of Mammalian TRPM6 and TRPM7, Obtained by Genetic Reversion Screens. *PLoS ONE*, 10

288. Larson JR, Facemyer EM, Shen K-F, Ukil L and Osmani SA, 2014. Insights into Dynamic Mitotic Chromatin Organization Through the NIMA Kinase Suppressor SonC, a Chromatin-Associated Protein Involved in the DNA Damage Response. *Genetics*, 196:177-+
289. Lasin P, Weise A, Reinders A and Ward JM, 2020. Arabidopsis Sucrose Transporter AtSuc1 introns act as strong enhancers of expression. *Plant and Cell Physiology*, 61:1054-1063
290. Layeghifard M, Peres Neto PR and Makarenkov V, 2013. Inferring explicit weighted consensus networks to represent alternative evolutionary histories. *BMC Evolutionary Biology*, 13:(23 December 2013)-(2023 December 2013)
291. Lazebnik J, Dicke M, ter Braak CJF and van Loon JJA, 2017. Biodiversity analyses for risk assessment of genetically modified potato. *Agriculture Ecosystems & Environment*, 249:196-205
292. Le TN, Miyazaki Y and Saze H, 2014. Epigenetic regulation of intragenic transposon in Arabidopsis. *Genes & Genetic Systems*, 89:275-275
293. Le TN, Miyazaki Y, Takuno S and Saze H, 2015. Epigenetic regulation of intragenic transposable elements impacts gene transcription in Arabidopsis thaliana. *Nucleic Acids Research*, 43:3911-3921
294. Le TN, Osabe K, Miyazaki Y and Saze H, 2016. Epigenetic regulation of intragenic repeats in plant genomes. *Genes & Genetic Systems*, 91:317-317
295. Lebeda A and Cohen Y, 2011. Cucurbit downy mildew (*Pseudoperonospora cubensis*)-biology, ecology, epidemiology, host-pathogen interaction and control. *European Journal of Plant Pathology*, 129:157-192
296. Lenglet A, Jaslan D, Toyota M, Mueller M, Mueller T, Schonknecht G, Marten I, Gilroy S, Hedrich R and Farmer EE, 2017. Control of basal jasmonate signalling and defence through modulation of intracellular cation flux capacity. *New Phytologist*, 216:1161-1169
297. Li E, Yue F, Chang Q, Guo X, He X and Zhang B, 2013a. Deletion of Intragenic Tandem Repeats in Unit C of FLO1 of *Saccharomyces cerevisiae* Increases the Conformational Stability of Flocculin under Acidic and Alkaline Conditions. *PLoS ONE*, 8
298. Li Q, Guo J, Lin X, Yang X, Ma Y, Fan G-C and Chang J, 2013b. An Intragenic SRF-Dependent Regulatory Motif Directs Cardiac-Specific microRNA-1-1/133a-2 Expression. *PLoS ONE*, 8
299. Li Q, Li J, Sun J-L, Ma X-F, Wang T-T, Berkey R, Yang H, Niu Y-Z, Fan J, Li Y, Xiao S and Wang W-M, 2016a. Multiple Evolutionary Events Involved in Maintaining Homologs of Resistance to Powdery Mildew 8 in *Brassica napus*. *Frontiers in Plant Science*, 7
300. Li R, Quan S, Yan X, Biswas S, Zhang D and Shi J, 2017. Molecular characterization of genetically-modified crops: Challenges and strategies. *Biotechnology Advances*, 35:302-309
301. Li W, Yang Z, Yao J, Li J, Song W and Yang X, 2018. Cellulose synthase-like D1 controls organ size in maize. *BMC Plant Biology*, 18
302. Li Y, 2012. Multiplex SSR analysis of *Phytophthora infestans* in different countries and the importance for potato breeding. Multiplex SSR analysis of *Phytophthora infestans* in different countries and the importance for potato breeding:206 pp.-206 pp.
303. Li Y, Muthuramalingam M and Mahalingam R, 2016b. Plant responses to tropospheric ozone. *Genetic Manipulation in Plants for Mitigation of Climate Change*:1-241
304. Li Y, Xia Z, Peng J, Zhou T and Fan Z, 2013c. Evidence of recombination and genetic diversity in southern rice black-streaked dwarf virus. *Archives of Virology*, 158:2147-2151
305. Li ZT, Kim K-H, Jasinski JR, Creech MR and Gray DJ, 2012. Large-scale characterization of promoters from grapevine (*Vitis* spp.) using quantitative anthocyanin and GUS assay systems. *Plant Science*, 196:132-142
306. Lim M, Woo H, Shin K, Ryu T, Yeo Y, Kweon S and Park S, 2014. Novel plant breeding techniques and risk assessment. *Korean Journal of Breeding Science*, 46:333-341
307. Limeria C, Sabbadini S, Sweet JB and Mezzetti B, 2017. New Biotechnological Tools for the Genetic Improvement of Major Woody Fruit Species. *Frontiers in Plant Science*, 8
308. Lin C-H and Workman JL, 2011. Suppression of cryptic intragenic transcripts is required for embryonic stem cell self-renewal. *Embo Journal*, 30:1420-1421
309. Lin X, Zhang Y, Kuang H and Chen J, 2013. Frequent loss of lineages and deficient duplications accounted for low copy number of disease resistance genes in Cucurbitaceae. *Bmc Genomics*, 14
310. Liu H, Fu Y, Xie J, Cheng J, Ghabrial SA, Li G, Peng Y, Yi X and Jiang D, 2012. Evolutionary genomics of mycovirus-related dsRNA viruses reveals cross-family horizontal gene transfer and evolution of diverse viral lineages. *BMC Evolutionary Biology*, 12

311. Liu J-J, Sniezko RA and Ekramoddoullah AKM, 2011. Association of a Novel *Pinus monticola* Chitinase Gene (PmCh4B) with Quantitative Resistance to *Cronartium ribicola*. *Phytopathology*, 101:904-911
312. Liu K and Sun Q, 2021. Intragenic tRNA-promoted R-loops orchestrate transcription interference for plant oxidative stress responses. *The Plant cell*,
313. Liu S, Schnable JC, Ott A, Yeh C-TE, Springer NM, Yu J, Muehlbauer G, Timmermans MCP, Scanlon MJ and Schnable PS, 2018. Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. *Molecular Biology and Evolution*, 35:2762-2772
314. Liu S, Wang Z, Wang H, Su Y and Wang T, 2020. Patterns and Rates of Plastid *rps12* Gene Evolution Inferred in a Phylogenetic Context using Plastomic Data of Ferns. *Scientific Reports*, 10
315. Lombardo L and Zelasco S, 2016. Biotech Approaches to Overcome the Limitations of Using Transgenic Plants in Organic Farming. *Sustainability*, 8
316. Lotz LAP, van de Wiel CCM and Smulders MJM, 2020. Genetic engineering at the heart of agroecology. *Outlook on Agriculture*, 49:21-28
317. Louwaars N and Jochemsen H, 2021. An Ethical and Societal Analysis for Biotechnological Methods in Plant Breeding. *Agronomy-Basel*, 11
318. Lu H, Viswanath V, Ma C, Etherington E, Dharmawardhana P, Shevchenko O, Strauss SH, Pearce DW, Rood SB and Busov V, 2015. Recombinant DNA modification of gibberellin metabolism alters growth rate and biomass allocation in *Populus*. *Tree Genetics & Genomes*, 11
319. Luque A, Sebai SC, Santiago-Schuebel B, Le Coz Y, Jenot D, Ramaen O, Sauveplane V and Pandjaitan R, 2014a. In vivo evolution of metabolic pathways by homeologous recombination in mitotic cells. *Metabolic Engineering*, 23:123-135
320. Luque A, Sebai SC, Sauveplane V, Ramaen O and Pandjaitan R, 2014b. In vivo evolution of metabolic pathways Assembling old parts to build novel and functional structures. *Bioengineered*, 5:347-356
321. Lusser M and Davies HV, 2013. Comparative regulatory approaches for groups of new plant breeding techniques. *New Biotechnology*, 30:437-446
322. Lutken H, Kodahl N and Mueller R, 2014. New developments in GMO science - from gene function to application. 29th International Horticultural Congress on Horticulture - Sustaining Lives, Livelihoods and Landscapes (IHC) / 3rd International Genetically Modified Organisms in Horticulture Symposium - Past, Present and Future, 1124:41-48
323. Lutken H, Laura M, Borghi C, Orgaard M, Allavena A and Rasmussen SK, 2011. Expression of *KxhKN4* and *KxhKN5* genes in *KalanchoA* << *blossfeldiana* 'Molly' results in novel compact plant phenotypes: towards a cisgenesis alternative to growth retardants. *Plant Cell Reports*, 30:2267-2279
324. MacDiarmid CW, Taggart J, Jeong J, Kerdsoomboon K and Eide DJ, 2016. Activation of the Yeast UBI4 Polyubiquitin Gene by Zap1 Transcription Factor via an Intragenic Promoter Is Critical for Zinc-deficient Growth. *Journal of Biological Chemistry*, 291:18880-18896
325. Mainak B, Kumar SS, Ashutosh K and Rabiya P, 2021. Cisgenics as New Horizon in Crop Improvement. *Research Journal of Biotechnology*, 16:193-201
326. Maltseva E, Iskakova G, Ismagul A, Chirkin A, Naizabayeva D, Ismagulova G, Malakhova N, Aitkhozhina N, Eliby S and Skiba Y, 2021. A cisgenic approach in the transformation of bread wheat cv. saratovskaya 29 with class I chitinase gene. *Open Biotechnology Journal*, 15:29-35
327. Maltseva E, Ismagul A, Iskakova G, Chirkin A, Skiba Y, Ismagulova G, Eliby S and Aitkhozhina N, 2014. Wheat cisgenic transformation with class I chitinase gene. *Journal of Biotechnology*, 185:S116-S117
328. Maltseva ER, Iskakova GA, Rsaliev AS, Skiba YA, Naizabaeva DA, Ismagulova GA, Ismagul A and Eliby S, 2018. Assessment of cisgenic bread wheat lines carrying class I chitinase gene to leaf rust. *Journal of Biotechnology*, 280:S80-S81
329. Maltseva ER, Ismagul AZ, Iskakova GA, Chirkin AP, Skiba YA, Ismagulova GA, Eliby S and Aitkhozhina NA, 2016. WHEAT CISGENIC TRANSFORMATION WITH CLASS I CHITINASE. *Bulletin of the National Academy of Sciences of the Republic of Kazakhstan*:98-105
330. Manan S, 2020. Current status of crops genetic transformation. *Minerva Biotechnologica*, 32:128-138
331. Mandel JR, McAssey EV, Roland KM and McCauley DE, 2012. Mitochondrial Gene Diversity Associated with the *atp9* Stop Codon in Natural Populations of Wild Carrot (*Daucus carota* ssp *carota*). *Journal of Heredity*, 103:418-425

332. Maniga A, Ghisaura S, Perrotta L, Marche MG, Cella R and Albani D, 2017. Distinctive features and differential regulation of the DRTS genes of *Arabidopsis thaliana*. *PLoS ONE*, 12
333. Marinova IN, Engelbrecht J, Ewald A, Langholm LL, Holmberg C, Kragelund BB, Gordon C, Nielsen O and Hartmann-Petersen R, 2015. Single Site Suppressors of a Fission Yeast Temperature-Sensitive Mutant in *cdc48* Identified by Whole Genome Sequencing. *PLoS ONE*, 10
334. Marquardt S, Raitskin O, Wu Z, Liu F, Sun Q and Dean C, 2014. Functional Consequences of Splicing of the Antisense Transcript COOLAIR on FLC Transcription. *Molecular Cell*, 54:156-165
335. Martelli GP and Rubino L, 2016. Transgenic resistance induced by pathogens: use of a small biotech application. *Georgofili*, 12:81-90
336. Martinez-Alarcon D, Mora-Aviles A, Espinoza-Nunez A, Serrano Jamaica LM, Cruz-Hernandez A, Rodriguez-Torres A, Castro-Guillen JL, Blanco-Labra A and Garcia-Gasca T, 2019. Rhizosecretion of a cisgenic lectin by genetic manipulation of Tepary bean plants (*Phaseolus acutifolius*). *Journal of Biotechnology*, 306
337. Maruyama S, Shoguchi E, Satoh N and Minagawa J, 2015. Diversification of the Light-Harvesting Complex Gene Family via Intra- and Intergenic Duplications in the Coral Symbiotic Alga *Symbiodinium*. *PLoS ONE*, 10
338. McKnight K, Liu H and Wang Y, 2011. Intragenic Transcription and the Regulation of Protein Function. *Molecular Biology of the Cell*, 22
339. McKnight K, Liu H and Wang Y, 2014. Replicative Stress Induces Intragenic Transcription of the ASE1 Gene that Negatively Regulates Ase1 Activity. *Current Biology*, 24:1101-1106
340. Meena RP, Prabha K and Baranwal VK, 2019. Genome characterization of citrus yellow vein-clearing virus: limited heterogeneity of viral genomes in Mandarivirus-infecting different citrus species. *3 Biotech*, 9
341. Mejia N, Soto B, Guerrero M, Casanueva X, Houel C, Angeles-Miccono Mdl, Ramos R, Cunff LI, Boursiquot JM, Hinrichsen P and Adam-Blondon AF, 2011. Molecular, genetic and transcriptional evidence for a role of VvAGL11 in stenospermocarpic seedlessness in grapevine. *BMC Plant Biology*, 11:18pp.-18pp.
342. Merritt BA, Zhang X, Triplett EW, Mou Z and Orbovic V, 2021. Selection of transgenic citrus plants based on glyphosate tolerance conferred by a citrus 5-enolpyruvylshikimate-3-phosphate synthase variant. *Plant Cell Reports*,
343. Mertens S, Gallone B, Steensels J, Herrera-Malaver B, Cortebeek J, Nolmans R, Saels V, Vyas VK and Verstrepen KJ, 2019. Reducing phenolic off-flavors through CRISPR-based gene editing of the FDC1 gene in *Saccharomyces cerevisiae* x *Saccharomyces eubayanus* hybrid lager beer yeasts. *PLoS ONE*, 14
344. Meslet-Cladiere L and Vallon O, 2012. A new method to identify flanking sequence tags in *chlamydomonas* using 3'-RACE. *Plant Methods*, 8:(26 June 2012)-(2026 June 2012)
345. Micol-Ponce R, Aguilera V and Ponce MR, 2014. A genetic screen for suppressors of a hypomorphic allele of *Arabidopsis* ARGONAUTE1. *Scientific Reports*, 4
346. Mielby H, Sandoe P and Lassen J, 2013a. Multiple aspects of unnaturalness: are cisgenic crops perceived as being more natural and more acceptable than transgenic crops? *Agriculture and Human Values*, 30:471-480
347. Mielby H, Sandoe P and Lassen J, 2013b. The role of scientific knowledge in shaping public attitudes to GM technologies. *Public Understanding of Science*, 22:155-168
348. Minnis CJ, Townsend S, Petschnigg J, Tinelli E, Bahler J, Russell C and Mole SE, 2021. Global network analysis in *Schizosaccharomyces pombe* reveals three distinct consequences of the common 1-kb deletion causing juvenile CLN3 disease. *Scientific Reports*, 11
349. Miroshnichenko I, Timerbaev V, Okuneva A, Klementyeva A, Sidorova T, Pushin A and Dolgov S, 2020. Enhancement of resistance to PVY in intragenic marker-free potato plants by RNAi-mediated silencing of eIF4E translation initiation factors. *Plant Cell Tissue and Organ Culture*, 140:691-705
350. Mirzaie Fouladvand Z, Pourjam E, Castillo P and Pedram M, 2019. Genetic diversity, and description of a new dagger nematode, *Xiphinema afratakhtehnsis* sp. nov., (Dorylaimida: Longidoridae) in natural forests of southeastern Gorgan, northern Iran. *PLoS ONE*, 14
351. Mishra M, Verma RK and Gaur RK, 2020. Identification of Chilli leaf curl virus and associated betasatellite infecting *Osteospermum fruticosum* in Rajasthan, India. *3 Biotech*, 10
352. Mishra S, Alavilli H, Lee B-h, Panda SK and Sahoo L, 2015. Cloning and characterization of a novel vacuolar Na⁺/H⁺ antiporter gene (*VuNHX1*) from drought hardy legume, cowpea for salt tolerance. *Plant Cell Tissue and Organ Culture*, 120:19-33
353. Mitchell NM, Sherrard AL, Dasari S, Magee DM, Gryns TE and Lake DF, 2018. Proteogenomic Re-Annotation of *Coccidioides posadasii* Strain Silveira. *Proteomics*, 18

354. Mlalazi B, Welsch R, Namanya P, Khanna H, Geijskes RJ, Harrison MD, Harding R, Dale JL and Bateson M, 2012. Isolation and functional characterisation of banana phytoene synthase genes as potential cisgenes. *Planta*, 236:1585-1598
355. Mohanta TK, Bashir T, Hashem A, Abd Allah EF and Bae H, 2017. Genome Editing Tools in Plants. *Genes*, 8
356. Molesini B, Pii Y and Pandolfini T, 2012. Fruit improvement using intragenesis and artificial microRNA. *Trends in Biotechnology*, 30:80-88
357. Mondal S, Rutkoski JE, Velu G, Singh PK, Crespo-Herrera LA, Guzman C, Bhavani S, Lan C, He X and Singh RP, 2016. Harnessing Diversity in Wheat to Enhance Grain Yield, Climate Resilience, Disease and Insect Pest Resistance and Nutrition Through Conventional and Modern Breeding Approaches. *Frontiers in Plant Science*, 7
358. Morgan JK, Lijuan Z, Wenbin L, Shatters RG, Manjunath K and Yong-Ping D, 2012. Improved real-time PCR detection of "Candidatus Liberibacter asiaticus" from citrus and psyllid hosts by targeting the intragenic tandem-repeats of its prophage genes. *Molecular and Cellular Probes*, 26:90-98
359. Moriwaki T, Miyazawa Y, Fujii N and Takahashi H, 2014. GNOM regulates root hydrotropism and phototropism independently of PIN-mediated auxin transport. *Plant Science*, 215:141-149
360. Mottola A and Morschhaeuser J, 2019. An Intragenic Recombination Event Generates a Snf4-Independent Form of the Essential Protein Kinase Snf1 in *Candida albicans*. *MSphere*, 4
361. Mouton L, Thierry M, Henri H, Baudin R, Gnankine O, Reynaud B, Zchori-Fein E, Becker N, Fleury F and Delatte H, 2012. Evidence of diversity and recombination in *Arsenophonus* symbionts of the *Bemisia tabaci* species complex. *Bmc Microbiology*, 12
362. Moyle R, Pretorius L-S, Mojtahedi N, Nowak E and Schenk P, 2018. INTtrait - Intragenic New Breeding Technology for the Introduction of Production and Consumer Traits. *In Vitro Cellular & Developmental Biology-Plant*, 54:S93-S93
363. Mullins E, 2019. Communicating the risks of genetically modified organisms: lessons learnt from an Irish field of cisgenic potatoes. *Journal of Experimental Botany*, 70:3699-3703
364. Murat C, Riccioni C, Belfiori B, Cichocki N, Labbe J, Morin E, Tisserant E, Paolucci F, Rubini A and Martin F, 2011. Distribution and localization of microsatellites in the Perigord black truffle genome and identification of new molecular markers. *Fungal Genetics and Biology*, 48:592-601
365. Muratova OA, Beketova MP, Kuznetsova MA, Rogozina EV and Khavkin EE, 2020. South American species *Solanum alandiae* Card. and *S. Okadae* Hawkes et Hjerting as potential sources of genes for potato late blight resistance. *Proceedings on Applied Botany, Genetics and Breeding*, 181:73-83
366. Muringai V, Fan X and Goddard E, 2020. Canadian consumer acceptance of gene-edited versus genetically modified potatoes: A choice experiment approach. *Canadian Journal of Agricultural Economics-Revue Canadienne D Agroeconomie*, 68:47-63
367. Muthusamy M, Uma S, Suthanthiram B, Saraswathi MS and Chandrasekar A, 2019. Genome-wide identification of novel, long non-coding RNAs responsive to *Mycosphaerella eumusae* and *Pratylenchus coffeae* infections and their differential expression patterns in disease-resistant and sensitive banana cultivars. *Plant Biotechnology Reports*, 13:73-83
368. Muyle A, Ross-Ibarra J, Seymour DK and Gaut BS, 2021. Gene body methylation is under selection in *Arabidopsis thaliana*. *Genetics*, 218
369. Myers CN, Berner GB, Holthoff JH, Martinez-Fonts K, Harper JA, Alford S, Taylor MN and Duina AA, 2011. Mutant Versions of the *S. cerevisiae* Transcription Elongation Factor Spt16 Define Regions of Spt16 That Functionally Interact with Histone H3. *PLoS ONE*, 6
370. Nakayama A, Fukushima S, Goto S, Matsushita A, Shimono M, Sugano S, Jiang C, Akagi A, Yamazaki M, Inoue H and Takatsuji H, 2013. Genome-wide identification of WRKY45-regulated genes that mediate benzothiadiazole-induced defense responses in rice. *BMC Plant Biology*, 13:(4 October 2013)-(2014 October 2013)
371. Nalley L, Tsiboe F, Durand-Morat A, Shew A and Thoma G, 2016. Economic and Environmental Impact of Rice Blast Pathogen (*Magnaporthe oryzae*) Alleviation in the United States. *PLoS ONE*, 11
372. Namous H, Penagaricano F, Del Corvo M, Capra E, Thomas DL, Stella A, Williams JL, Marsan PA and Khatib H, 2018. Integrative analysis of methylomic and transcriptomic data in fetal sheep muscle tissues in response to maternal diet during pregnancy. *Bmc Genomics*, 19

373. Nanayakkara D, Edirisingha I, Dissanayake L, Weerasinghe D, Suriyagoda L, Herath V, Perera C and Jayatilake D, 2020. A novel intragenic marker targeting the ectodomain of bacterial blight-resistance gene Xa21 for marker-assisted selection in rice. *Journal of Crop Improvement*, 34:824-841
374. Natalini A, Acciarri N and Cardi T, 2021. Breeding for Nutritional and Organoleptic Quality in Vegetable Crops: The Case of Tomato and Cauliflower. *Agriculture-Basel*, 11
375. Nelson CD, Powell WA, Merkle SA, Carlson JE, Hebard FV, Islam-Faridi N, Staton ME and Georgi L, 2014. Biotechnology of Trees: Chestnut. *Tree Biotechnology*:3-35
376. Newman TE, Lee J, Williams SJ, Choi S, Halane MK, Zhou J, Solomon P, Kobe B, Jones JDG, Segonzac C and Sohn KH, 2019. Autoimmunity and effector recognition in *Arabidopsis thaliana* can be uncoupled by mutations in the RRS1-R immune receptor. *New Phytologist*, 222:954-965
377. Ni J, Zhu Z, Wang G, Shen Y, Zhang Y and Wu P, 2014. Intragenic Suppressor of Osiaa23 Revealed a Conserved Tryptophan Residue Crucial for Protein-Protein Interactions. *PLoS ONE*, 9
378. Ni L, Zhao Z, Xu H, Chen S and Dorje G, 2016. The complete chloroplast genome of *Gentiana straminea* (Gentianaceae), an endemic species to the Sino-Himalayan subregion. *Gene*, 577:281-288
379. Nielsen M, Ard R, Leng X, Ivanov M, Kindgren P, Pelechano V and Marquardt S, 2019. Transcription-driven chromatin repression of Intragenic transcription start sites. *Plos Genetics*, 15
380. Nietsch J, Brueggemann T, Becker D and Fladung M, 2017. Old methods rediscovered: application and improvement of two direct transformation methods to hybrid poplar (*Populus tremula* x *P-alba*). *Plant Cell Tissue and Organ Culture*, 130:183-196
381. Niu J-Y, Li L, Shi S, Li H, Wang X-R, Liu Y-Y, Niu Y-L and Zhao J-C, 2018. Phylogenetic Analysis of the Genus *Pohlia* (Bryophyta, Bryaceae) Using Chloroplast and Nuclear Ribosomal DNA. *Phytotaxa*, 351:141-153
382. Noda-Garcia L, Juarez-Vazquez AL, Avila-Arcos MC, Verduzco-Castro EA, Montero-Moran G, Gaytan P, Carrillo-Tripp M and Barona-Gomez F, 2015. Insights into the evolution of enzyme substrate promiscuity after the discovery of (beta alpha)(8) isomerase evolutionary intermediates from a diverse metagenome. *BMC Evolutionary Biology*, 15
383. Norouzitallab P, Baruah K, Bossier P and Vanrompay D, 2019a. Nonmammalian model organisms in epigenetic research: an overview. *Transgenerational Epigenetics*, 2nd Edition, 13:251-261
384. Norouzitallab P, Baruah K, Vanrompay D and Bossier P, 2019b. Can epigenetics translate environmental cues into phenotypes? *Science of the Total Environment*, 647:1281-1293
385. Nwugo CC, Doud MS, Duan Y and Lin H, 2016. Proteomics analysis reveals novel host molecular mechanisms associated with thermotherapy of 'Ca. *Liberibacter asiaticus*'-infected citrus plants. *BMC Plant Biology*, 16:(14 November 2016)-(2014 November 2016)
386. Ocares N, Jimenez N, Nunez R, Perniola R, Marsico AD, Cardone MF, Bergamini C and Mejia N, 2020. Unraveling the Deep Genetic Architecture for Seedlessness in Grapevine and the Development and Validation of a New Set of Markers for VviAGL11-Based Gene-Assisted Selection. *Genes*, 11
387. Okagaki RJ, Dukowic-Schulze S, Eggleston WB and Muehlbauer GJ, 2018. A Critical Assessment of 60 Years of Maize Intragenic Recombination. *Frontiers in Plant Science*, 9
388. Olsen RH, Schønheyder HC, Christensen H and Bisgaard M, 2012. *Enterococcus faecalis* of Human and Poultry Origin Share Virulence Genes Supporting the Zoonotic Potential of *E. faecalis*. *Zoonoses and Public Health*, 59:256-263
389. Ortega E, Martinez-Garcia PJ and Dicenta F, 2011. The Study of Self-(in)Compatibility in CEBAS-CSIC Almond Breeding Programme. 1st Workshop on Floral Biology and S-Incompatibility in Fruit Species, 967:171-180
390. Ortega JL, Rajapakse W, Bagga S, Apodaca K, Lucero Y and Sengupta-Gopalan C, 2018. An intragenic approach to confer glyphosate resistance in chile (*Capsicum annuum*) by introducing an in vitro mutagenized chile EPSPS gene encoding for a glyphosate resistant EPSPS protein. *PLoS ONE*, 13
391. Ortiz V, Phelan S and Mullins E, 2016. A temporal assessment of nematode community structure and diversity in the rhizosphere of cisgenic *Phytophthora infestans*-resistant potatoes. *BMC Ecology*, 16:(1 December 2016)-(2011 December 2016)
392. Pace CD, 2015. Genomic tools and plant genes to mitigate impacts of climate change and extreme environments. *CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources*, 10
393. Pacifico D and Paris R, 2016. Effect of Organic Potato Farming on Human and Environmental Health and Benefits from New Plant Breeding Techniques. Is It Only a Matter of Public Acceptance? *Sustainability*, 8

394. Paez-Valencia J, Sanchez-Lares J, Marsh E, Dorneles LT, Santos MP, Sanchez D, Winter A, Murphy S, Cox J, Trzaska M, Metler J, Kozic A, Facanha AR, Schachtman D, Sanchez CA and Gaxiola RA, 2013. Enhanced Proton Translocating Pyrophosphatase Activity Improves Nitrogen Use Efficiency in Romaine Lettuce. *Plant Physiology*, 161:1557-1569
395. Palani S, Srinivasan R, Zambon P, Kamnev A, Gayathri P and Balasubramanian MK, 2018. Steric hindrance in the upper 50 kDa domain of the motor Myo2p leads to cytokinesis defects in fission yeast. *Journal of Cell Science*, 131
396. Palmgren MG, Edenbrandt AK, Vedel SE, Andersen MM, Landes X, Osterberg JT, Falhof J, Olsen LI, Christensen SB, Sandoe P, Gamborg C, Kappel K, Thorsen BJ and Pagh P, 2015. Are we ready for back-to-nature crop breeding? *Trends in Plant Science*, 20:155-164
397. Palomo-Rios E, Quesada MA, Matas AJ, Pliego-Alfaro F and Mercado JA, 2018. The History and Current Status of Genetic Transformation in Berry Crops. *Genomes of Rosaceous Berries and Their Wild Relatives*:139-160
398. Pals-Rylandsdam R, Turcic K, Carroll J, Tobar-Rubin R, Janevska D, Din E, Alvarez R and Choudhry F, 2013. Constitutive activity of Gs alpha R201H is suppressed by disruption of either of two hydrophobic pockets within the protein. *Faseb Journal*, 27
399. Pan Q, Li L, Yang X, Tong H, Xu S, Li Z, Li W, Muehlbauer GJ, Li J and Yan J, 2016. Genome-wide recombination dynamics are associated with phenotypic variation in maize. *New Phytologist*, 210:1083-1094
400. Pandolfi V, Costa Ferreira Neto JR, Silva MD, Barbosa Amorim LL, Wanderley-Nogueira AC, e Oliveira Silva RL, Kido EA, Crovella S and Benko Iseppon AM, 2017. Resistance (R) Genes: Applications and Prospects for Plant Biotechnology and Breeding. *Current Protein & Peptide Science*, 18:323-334
401. Panter S, Mouradov A, Badenhorst P, Martelotto L, Griffith M, Smith KF and Spangenberg G, 2017. Re-Programming Photosynthetic Cells of Perennial Ryegrass (*Lolium perenne* L) for Fructan Biosynthesis through Transgenic Expression of Fructan Biosynthetic Genes under the Control of Photosynthetic Promoters. *Agronomy-Basel*, 7
402. Paraskevopoulos K, Federici S and European Food Safety Authority EFS, 2021. Overview of EFSA and European national authorities' scientific opinions on the risk assessment of plants developed through New Genomic Techniques. *EFSA Journal*, 19
403. Park K-T, Villar MT, Artigues A and Lutkenhaus J, 2017. MinE conformational dynamics regulate membrane binding, MinD interaction, and Min oscillation. *Proceedings of the National Academy of Sciences of the United States of America*, 114:7497-7504
404. Parvaiz A, Mustafa G and Joyia FA, 2018. Understanding invasive plant mycoparasites and their remedy through advanced molecular approaches. *Pakistan Journal of Phytopathology*, 30:213-227
405. Paul S, Ali N, Gayen D, Datta SK and Datta K, 2012. Molecular breeding of Osfer 2 gene to increase iron nutrition in rice grain. *GM crops & food*, 3:310-316
406. Pavone V and Martinelli L, 2015. Cisgenics as emerging bio-objects: bio-objectification and bio-identification in agrobiotech innovation. *New Genetics and Society*, 34:52-71
407. Pearce S, Saville R, Vaughan SP, Chandler PM, Wilhelm EP, Sparks CA, Al-Kaff N, Korolev A, Boulton MI, Phillips AL, Hedden P, Nicholson P and Thomas SG, 2011. Molecular Characterization of Rht-1 Dwarfing Genes in Hexaploid Wheat. *Plant Physiology*, 157:1820-1831
408. Pereira J, Silva K, Garald M, Jeffrey J and Mou Z, 2016. Characterization of Arabidopsis Defense-related Gene Homologues in Tomato and Strawberry. *Phytopathology*, 106:13-13
409. Perkins-Veazie P, Gunter C and Trandel M, 2020. Postharvest handling of organically produced specialty crops. *Advances in Postharvest Management of Horticultural Produce*, 66:391-408
410. Perozeni F, Cazzaniga S, Baier T, Zanoni F, Zoccatelli G, Lauersen KJ, Wobbe L and Ballottari M, 2020. Turning a green alga red: engineering astaxanthin biosynthesis by intragenic pseudogene revival in *Chlamydomonas reinhardtii*. *Plant Biotechnology Journal*, 18:2053-2067
411. Peterson PA, 2015. Mechanisms contributing to genetic diversity in maize populations. *The Genetics and Exploitation of Heterosis in Crops*:149-161
412. Pimpinelli S and Piacentini L, 2020. Environmental change and the evolution of genomes: Transposable elements as translators of phenotypic plasticity into genotypic variability. *Functional Ecology*, 34:428-441
413. Pirscher F, Bartkowski B, Theesfeld I and Timaeus J, 2018. Nature-identical outcomes, artificial processes: governance of CRISPR/cas genome editing as an ethical challenge. *Ethical tensions from new technology: the case of agricultural biotechnology*:137-150

414. Pirscher F and Theesfeld I, 2018. The ethical dilemma with governing CRISPR/Cas genome editing. 14th Congress of the European Society for Agricultural and Food Ethics - Professionals in Food Chains: Ethics, Roles and Responsibilities:419-423
415. Platt JL, Kent NA, Kimmel AR and Harwood AJ, 2017. Regulation of nucleosome positioning by a CHD Type III chromatin remodeler and its relationship to developmental gene expression in *Dictyostelium*. *Genome Research*, 27:591-600
416. Poltronieri P, 2016. GMO Acceptance in the World and Issues for the Overcoming of Restrictions: Cisgenesis, RNA Transfer, Rootstock to Shoot Delivery, Novel Methods of Transformation. *Biotransformation of Agricultural Waste and By-Products: The Food, Feed, Fibre, Fuel (4F) Economy*:309-341
417. Poltronieri P and Hong Y, 2015. Applied Plant Genomics and Biotechnology. *Applied Plant Genomics and Biotechnology*:1-315
418. Poltronieri P and Reza IB, 2015. Transgenic, cisgenic and novel plant products: Challenges in regulation and safety assessment. *Applied Plant Genomics and Biotechnology*:1-16
419. Poplawski LE, Gray DJ and Trigiano RN, 2014. Assessment of Extracellular Enzymes Produced by Fungi Isolated from Muscadine Grapes. *Hortscience*, 49:S125-S125
420. Porceddu A, Zenoni S and Camiolo S, 2013. The Signatures of Selection for Translational Accuracy in Plant Genes. *Genome Biology and Evolution*, 5:1117-1126
421. Powell W, Newhouse A, Baier K, McGuigan L, Oakes A, Stewart K, Tschaplinski T and Maynard C, 2014. Can Genetic Engineering Help Save the American Chestnut? *In Vitro Cellular & Developmental Biology-Animal*, 50:S23-S24
422. Prasad GS, Raju B and Kumar KR, 2013. CISGENESIS - an alternate approach for development of genetically modified crops. *Annals of Biological Research*, 4:109-115
423. Pratap A, Das A, Kumar S and Gupta S, 2021. Current Perspectives on Introgression Breeding in Food Legumes. *Frontiers in Plant Science*, 11
424. Pratap A and Kumar J, 2014. Alien gene transfer in crop plants: An introduction. *Alien Gene Transfer in Crop Plants*, 1:1-23
425. Pratelli R, Guerra DD, Yu S, Wogulis M, Kraft E, Frommer WB, Callis J and Pilot G, 2012. The Ubiquitin E3 Ligase LOSS OF GDU2 Is Required for GLUTAMINE DUMPER1-Induced Amino Acid Secretion in *Arabidopsis*. *Plant Physiology*, 158:1628-1642
426. Preston C and Antonsen T, 2021. Integrity and Agency: Negotiating New Forms of Human-Nature Relations in Biotechnology. *Environmental Ethics*, 43:21-41
427. Prezotto LF, Perondini ALP, Hernandez-Ortiz V, Marino CL and Selivon D, 2017. *Wolbachia* strains in cryptic species of the *Anastrepha fraterculus* complex (Diptera, Tephritidae) along the Neotropical Region. *Systematic and Applied Microbiology*, 40:59-67
428. Puchta O, Cseke B, Czaja H, Tollervy D, Sanguinetti G and Kudla G, 2016. Network of epistatic interactions within a yeast snoRNA. *Science*, 352:840-844
429. Pushpa D, Yogendra KN, Gunnaiah R, Kushalappa AC and Murphy A, 2014. Identification of Late Blight Resistance-Related Metabolites and Genes in Potato through Nontargeted Metabolomics. *Plant Molecular Biology Reporter*, 32:584-595
430. Pysh LD, 2015. Two alleles of the *AtCesA3* gene in *Arabidopsis thaliana* display intragenic complementation. *American Journal of Botany*, 102:1434-1441
431. Qi H-D, Lin Y, Ren Q-P, Wang Y-Y, Xiong F and Wang X-L, 2019. RNA Splicing of *FLC* Modulates the Transition to Flowering. *Frontiers in Plant Science*, 10
432. Qi M, Li Z, Liu C, Hu W, Ye L, Xie Y, Zhuang Y, Zhao F, Teng W, Zheng Q, Fan Z, Xu L, Lang Z, Tong Y and Zhang Y, 2018. CGT-seq: epigenome-guided de novo assembly of the core genome for divergent populations with large genome. *Nucleic Acids Research*, 46
433. Qi W-H, Yan C-c, Li W-J, Jiang X-M, Li G-Z, Zhang X-Y, Hu T-Z, Li J and Yue B-S, 2016. Distinct patterns of simple sequence repeats and GC distribution in intragenic and intergenic regions of primate genomes. *Aging-Us*, 8:2635-2654
434. Qing-Qing Y, Chang-Quan Z, Man-Ling C, Dong-Sheng Z, Jin-Zhu C, Qing W, Qian-Feng L, Heng-Xiu Y, Ming-Hong G, Samuel Sai-Ming S and Qiao-Quan L, 2016. Biofortification of rice with the essential amino acid lysine: molecular characterization, nutritional evaluation, and field performance. *Journal of Experimental Botany*, 67:4285-4296

435. Qu D, Song Y, Li WM, Pei XW, Wang ZX, Jia SR and Zhang YQ, 2011. Isolation and characterization of the organ-specific and light-inducible promoter of the gene encoding rubisco activase in potato (*Solanum tuberosum*). *Genetics and Molecular Research*, 10:621-631
436. Questa JI, Song J, Geraldo N, An H and Dean C, 2016. Arabidopsis transcriptional repressor VAL1 triggers Polycomb silencing at FLC during vernalization. *Science*, 353:485-488
437. Radkova M, Lyubenova A, Slavov S, Batchvarova R, Kalushkov P and Djilianov D, 2017. FEEDING COLORADO POTATO BEETLE ON LATE BLIGHT RESISTANT CISGENIC POTATO LINES HAS NO EFFECT ON THE INSECT AS A NON TARGET ORGANISM. *Comptes Rendus De L Academie Bulgare Des Sciences*, 70:895-902
438. Rai MK and Shekhawat NS, 2014. Recent advances in genetic engineering for improvement of fruit crops. *Plant Cell Tissue and Organ Culture*, 116:1-15
439. Raj RS, Singh C, Modi A and Subhash N, 2015. Genetic transformation of lowland rice variety GR11 for drought tolerance and its ratification for upland paddy cultivation. *Indian Journal of Genetics and Plant Breeding*, 75:30-40
440. Rajkumar MS, Gupta K, Khemka NK, Garg R and Jain M, 2020. DNA methylation reprogramming during seed development and its functional relevance in seed size/weight determination in chickpea. *Communications Biology*, 3
441. Rakosy-Tican E, 2014. Genetic Engineering in Potato Improvement. *Omics Applications in Crop Science*:139-161
442. Ramada MHS, Brand GD, Abrao FY, Oliveira M, Cardozo Filho JL, Galbieri R, Gramacho KP, Prates MV and Bloch C, 2017. Encrypted Antimicrobial Peptides from Plant Proteins. *Scientific Reports*, 7
443. Randise-Hinchliff CE and Brickner JH, 2012. A New Direction for Gene Looping. *Developmental Cell*, 23:919-921
444. Rangani G, Underwood JL and Srivastava V, 2015. Chromatin analysis of an Arabidopsis Phytochrome A allele reveals the correlation of transcriptional repression with recalcitrance to histone acetylation. *Plant Growth Regulation*, 75:179-186
445. Rankinen T, Sung YJ, Sarzynski MA, Rice TK, Rao DC and Bouchard C, 2012. Heritability of submaximal exercise heart rate response to exercise training is accounted for by nine SNPs. *Journal of Applied Physiology*, 112:892-897
446. Rastogi A, Lin X, Lombard B, Loew D and Tirichine L, 2015. Probing the evolutionary history of epigenetic mechanisms: what can we learn from marine diatoms. *Aims Genetics*, 2:173-191
447. Ratnaparkhe MB, Wang X, Li J, Compton RO, Rainville LK, Lemke C, Kim C, Tang H and Paterson AH, 2011. Comparative analysis of peanut NBS-LRR gene clusters suggests evolutionary innovation among duplicated domains and erosion of gene microsynteny. *New Phytologist*, 192:164-178
448. Raveendar S, Lee G, Lee K, Shin M, Kim S, Lee J, Cho G and Hyun D, 2019. DNA barcoding for efficient identification of *Triticum* subspecies: evaluation of four candidate loci on phylogenetic relationships. *Plant Breeding and Biotechnology*, 7:220-228
449. Remington DL, 2015. Alleles versus mutations: Understanding the evolution of genetic architecture requires a molecular perspective on allelic origins. *Evolution*, 69:3025-3038
450. Ren Y, West-Foyle H, Surcel A, Miller C and Robinson DN, 2014. Genetic suppression of a phosphomimic myosin II identifies system-level factors that promote myosin II cleavage furrow accumulation. *Molecular Biology of the Cell*, 25:4150-4165
451. Reyna-Llorens I, Burgess SJ, Reeves G, Singh P, Stevenson SR, Williams BP, Stanley S and Hibberd JM, 2018. Ancient duons may underpin spatial patterning of gene expression in C-4 leaves. *Proceedings of the National Academy of Sciences of the United States of America*, 115:1931-1936
452. Rhee S, Chae H and Kim S, 2015. PlantMirnaT: miRNA and mRNA integrated analysis fully utilizing characteristics of plant sequencing data. *Methods*, 83:80-87
453. Ribarits A, 2015. New techniques for plant breeding and the consequences of their application in practice. 65. Tagung Zukunftiges Saatgut - Produktion, Vermarktung, Nutzung und Konservierung. Future Seed - Production, Marketing, Use and Conservation. 24-26 November, 2014 Raumberg-Gumpenstein, Austria:71-75
454. Ribarits A, Bruller W, Hartmann J, Hochegger R, Mechtler K, Peterseil V, Sollinger J, Stepanek W, Widhalm I, Wogerbauer M and Leonhardt C, 2014. Use of novel techniques in plant breeding and practical consequences concerning detection, traceability, labeling, and risk assessment. *AgBioForum*, 17:183-190

455. Rice BL, Acosta MM, Pacheco MA and Escalante AA, 2013. Merozoite surface protein-3 alpha as a genetic marker for epidemiologic studies in *Plasmodium vivax*: A cautionary note. *Malaria Journal*, 12
456. Richael CM and Rommens CM, 2012. Employment of Cytokinin Vectors for Marker-Free and Backbone-Free Transformation. *Transgenic Plants: Methods and Protocols*, Second Edition, 847:3-10
457. Ricroch A, Harwood W, Svobodova Z, Sagi L, Hundleby P, Badea EM, Rosca I, Cruz G, Salema Fevereiro MP, Marfa Riera V, Jansson S, Morandini P, Bojinov B, Cetiner S, Custers R, Schrader U, Jacobsen H-J, Martin-Laffon J, Boisron A and Kuntz M, 2016. Challenges facing European agriculture and possible biotechnological solutions. *Critical Reviews in Biotechnology*, 36:875-883
458. Ricroch AE and Henard-Damave M-C, 2016. Next biotech plants: new traits, crops, developers and technologies for addressing global challenges. *Critical Reviews in Biotechnology*, 36:675-690
459. Riegler M, Iturbe-Ormaetxe I, Woolfit M, Miller WJ and O'Neill SL, 2012. Tandem repeat markers as novel diagnostic tools for high resolution fingerprinting of *Wolbachia*. *Bmc Microbiology*, 12
460. Righetti L, Djennane S, Berthelot P, Cournol R, Wilmot N, Loridon K, Vergne E and Chevreau E, 2014. Elimination of the nptII marker gene in transgenic apple and pear with a chemically inducible R/Rs recombinase. *Plant Cell Tissue and Organ Culture*, 117:335-348
461. Riviere G, 2014. Epigenetic features in the oyster *Crassostrea gigas* suggestive of functionally relevant promoter DNA methylation in invertebrates. *Frontiers in Physiology*, 5
462. Robinson KL, Tohidi-Esfahani D, Ponton F, Simpson SJ, Sword GA and Lo N, 2016. Alternative migratory locust phenotypes are associated with differences in the expression of genes encoding the methylation machinery. *Insect Molecular Biology*, 25:105-115
463. Robinson LC, Phillips J, Brou L, Boswell EP and Tatchell K, 2012. Suppressors of *ipl1-2* in Components of a Glc7 Phosphatase Complex, Cdc48 AAA ATPase, TORC1, and the Kinetochore. *G3-Genes Genomes Genetics*, 2:1687-1701
464. Roccaro AM, Sacco A, Ma D, Shi J, Mishima Y, Moschetta M, Handin RI and Ghobrial IM, 2015. A New Model for Studying the Dissemination of Myeloma Cells throughout the Bone Marrow Using Embryonic Zebrafish. *Blood*, 126
465. Rocha-Meneses L, Ferreira JA, Mushtaq M, Karimi S, Orupold K and Kikas T, 2020. Genetic modification of cereal plants: A strategy to enhance bioethanol yields from agricultural waste. *Industrial Crops and Products*, 150
466. Rogers DW, McConnell E, Miller EL and Greig D, 2017. Diminishing Returns on Intragenic Repeat Number Expansion in the Production of Signaling Peptides. *Molecular Biology and Evolution*, 34:3176-3185
467. Rohde K, Federbusch M, Horstmann A, Keller M, Villringer A, Stumvoll M, Tonjes A, Kovacs P and Bottcher Y, 2015. Genetic variants in *AKR1B10* associate with human eating behavior. *BMC Genetics*, 16:(25 March 2015)-(2025 March 2015)
468. Rojas M, Tiessen A, Ascencio F, Angulo C and Gomez-Anduro G, 2015. Two Promoters of Beta-Glucosidase Paralogs (*ZmBGlu2* and *ZmBGlu5*) Highly Active in Tropical Young Maize Hybrid Seedlings. *Plant Molecular Biology Reporter*, 33:1666-1674
469. Romero-Romero JL, Inostroza-Blancheteau C, Orellana D, Aquea F, Reyes-Diaz M, Gil PM, Pablo Matte J and Arce-Johnson P, 2018. Stomata regulation by tissue-specific expression of the *Citrus sinensis* MYB61 transcription factor improves water-use efficiency in *Arabidopsis*. *Plant Physiology and Biochemistry*, 130:54-60
470. Rommens C and Stivison A, 2012. Reintroduction of genetically engineered potatoes into the US market. *Phytopathology*, 102:151-151
471. Rommens CM, Conner A, Yan H and Hanley Z, 2011. Intragenic vectors and market-free transformation tools for a greener biotechnology. *Plant Transformation Technologies*:93-107
472. Ron-Parra J, Morales-Rivera MM, Jimenez-Lopez J, Jimenez-Cordero AA, De La Cruz-Larios L and Sanchez-Gonzalez JJ, 2016. Maternal genetic inheritance of red pericarp in the grain of maize. *Maydica*, 61
473. Ronsmans A, Wery M, Szachnowski U, Gautier C, Descrimes M, Dubois E, Morillon A and Georis I, 2019. Transcription-dependent spreading of the *Dal80* yeast GATA factor across the body of highly expressed genes. *Plos Genetics*, 15
474. Rosellini D, 2011. Selectable marker genes from plants: reliability and potential. *In Vitro Cellular & Developmental Biology-Plant*, 47:222-233

475. Rossetto D, Cramet M, Wang AY, Steunou A-L, Lacoste N, Schulze JM, Cote V, Monnet-Saksouk J, Piquet S, Nourani A, Kobor MS and Cote J, 2014. Eaf5/7/3 form a functionally independent NuA4 submodule linked to RNA polymerase II-coupled nucleosome recycling. *Embo Journal*, 33:1397-1415
476. Rottmann T, Zierer W, Subert C, Sauer N and Stadler R, 2016. STP10 encodes a high-affinity monosaccharide transporter and is induced under low-glucose conditions in pollen tubes of *Arabidopsis*. *Journal of Experimental Botany*, 67:2387-2399
477. Rottmann TM, Fritz C, Lauter A, Schneider S, Fischer C, Danzberger N, Dietrich P, Sauer N and Stadler R, 2018. Protoplast-Esculin Assay as a New Method to Assay Plant Sucrose Transporters: Characterization of AtSUC6 and AtSUC7 Sucrose Uptake Activity in *Arabidopsis Col-0* Ecotype. *Frontiers in Plant Science*, 9
478. Rousseliere D and Rousseliere S, 2017. Is biotechnology (more) acceptable when it enables a reduction in phytosanitary treatments? A European comparison of the acceptability of transgenesis and cisgenesis. *PLoS ONE*, 12
479. Ryffel GU, 2012. Organic plants: Gene-manipulated plants compatible with organic farming. *Biotechnology Journal*, 7
480. Ryffel GU, 2014. Transgene flow: facts, speculations and possible countermeasures. *GM crops & food*, 5:249-258
481. Ryffel GU, 2017. I Have a Dream: Organic Movements Include Gene Manipulation to Improve Sustainable Farming. *Sustainability*, 9
482. Sabbadini S, Capriotti L, Limera C, Navacchi O, Tempesta G and Mezzetti B, 2018. A plant regeneration platform to apply new breeding techniques for improving disease resistance in grapevine rootstocks and cultivars. *41st World Congress of Vine and Wine*, 12
483. Saber A, Khosroushahi AY, Faghfoori Z, Seyyedi M and Alipour B, 2019. Molecular identification and probiotic characterization of isolated yeasts from Iranian traditional dairies. *Progress in Nutrition*, 21:445-457
484. Sackman AM and Rokyta DR, 2013. The Adaptive Potential of Hybridization Demonstrated with Bacteriophages. *Journal of Molecular Evolution*, 77:221-230
485. Saied MH, Marzec J, Khalid S, Smith P, Down TA, Rakyan VK, Molloy G, Raghavan M, Debernardi S and Young BD, 2012. Genome wide analysis of acute myeloid leukemia reveal leukemia specific methylome and subtype specific hypomethylation of repeats. *PLoS ONE*, 7
486. Saini AK, Nanda JS, Martin-Marcos P, Dong J, Zhang F, Bhardwaj M, Lorsch JR and Hinnebusch AG, 2014. Eukaryotic translation initiation factor eIF5 promotes the accuracy of start codon recognition by regulating P-i release and conformational transitions of the preinitiation complex. *Nucleic Acids Research*, 42:9623-9640
487. Sallam N and Moussa M, 2021. DNA methylation changes stimulated by drought stress in ABA-deficient maize mutant vp10. *Plant Physiology and Biochemistry*, 160:218-224
488. Salonia F, Ciacciulli A, Poles L, Pappalardo HD, La Malfa S and Licciardello C, 2020. New Plant Breeding Techniques in Citrus for the Improvement of Important Agronomic Traits. A Review. *Frontiers in Plant Science*, 11
489. Samaddar M, Goswami AV, Purushotham J, Hegde P and D'Silva P, 2014. Role of the loop L-4,L-5 in allosteric regulation in mtHsp70s: in vivo significance of domain communication and its implications in protein translocation. *Molecular Biology of the Cell*, 25:2129-2142
490. Sandler G, Wright SI and Agrawal AF, 2021. Patterns and Causes of Signed Linkage Disequilibria in Flies and Plants. *Molecular Biology and Evolution*,
491. Sansavini S and Dondini L, 2016. Innovations in conventional and biotechnological breeding in fruit tree species. *Italus Hortus*, 23:45-62
492. Sanso M, Parua PK, Pinto D, Svensson JP, Pag V, Bitton DA, MacKinnon S, Garcia P, Hidalgo E, Bahler J, Tanny JC and Fisher RP, 2020. Cdk9 and H2Bub1 signal to Clr6-Cll/Rpd3S to suppress aberrant antisense transcription. *Nucleic Acids Research*, 48:7154-7168
493. Santos E, Sanchez E, Hidalgo L, Chavez T, Villao L, Pacheco R, Flores J, Korneva S and Navarrete O, 2014. Advances in banana transformation through *Agrobacterium tumefaciens* in Ecuador: progress, challenges and perspectives. *29th International Horticultural Congress on Horticulture - Sustaining Lives, Livelihoods and Landscapes (IHC) / 9th International Symposium on Banana / ISHS-ProMusa Symposium on Unravelling the Banana's Genomic Potential*, 1114:197-202
494. Sasaki T, Naumann U, Forai P, Matzke AJM and Matzke M, 2012. Unusual Case of Apparent Hypermutation in *Arabidopsis thaliana*. *Genetics*, 192:1271-+

- 495.Sato M, Shimizu M, Shea DJ, Hoque M, Kawanabe T, Miaji N, Fujimoto R, Fukai E and Okazaki K, 2019. Allele specific DNA marker for fusarium resistance gene FocBo1 in Brassica oleracea. *Breeding Science*, 69:308-315
- 496.Savadi S, Prasad P, Kashyap PL and Bhardwaj SC, 2018. Molecular breeding technologies and strategies for rust resistance in wheat (*Triticum aestivum*) for sustained food security. *Plant Pathology*, 67:771-791
- 497.Savazzini F, Ricci G and Tartarini S, 2015. Apple allergens genomics and biotechnology: Unravelling the determinants of apple allergenicity. *Applied Plant Genomics and Biotechnology*:35-54
- 498.Saze H, 2013. Control of intragenic heterochromatin in *Arabidopsis*. *Genes & Genetic Systems*, 88:336-336
- 499.Saze H, 2018. Epigenetic regulation of intragenic transposable elements: a two-edged sword. *Journal of Biochemistry*, 164:323-328
- 500.Saze H, Kitayama J, Takashima K, Miura S, Harukawa Y, Ito T and Kakutani T, 2013. Mechanism for full-length RNA processing of *Arabidopsis* genes containing intragenic heterochromatin. *Nature Communications*, 4
- 501.Schaart JG, Krens FA, Wolters AMA and Visser RGF, 2011a. Transformation Methods for Obtaining Marker-Free Genetically Modified Plants. *Plant Transformation Technologies*:229-242
- 502.Schaart JG, Tinnenbroek-Capel IEM and Krens FA, 2011b. Isolation and characterization of strong gene regulatory sequences from apple, *Malus x domestica*. *Tree Genetics & Genomes*, 7:135-142
- 503.Schaart JG, van de Wiel CCM, Lotz LAP and Smulders MJM, 2016. Opportunities for Products of New Plant Breeding Techniques. *Trends in Plant Science*, 21:438-449
- 504.Schlathölter I, Broggin GAL, Meissle M, Romeis J, Studer B and Patocchi A, 2021. Multi-level assessment of field-grown cisgenic apple trees. *Acta Horticulturae*, 1307:239-246
- 505.Scholey D, Burton E, Morgan N, Sanni C, Madsen CK, Dionisio G and Brinch-Pedersen H, 2017. P and Ca digestibility is increased in broiler diets supplemented with the high-phytase HIGHPHY wheat. *Animal*, 11:1457-1463
- 506.Schouten H, 2014a. Reply to Cisgenesis as a golden mean. *Nature Biotechnology*, 32:728
- 507.Schouten H, 2014b. The slippery slope of cisgenesis Reply. *Nature Biotechnology*, 32:728-728
- 508.Sharma D, Chhabra R, Muthusamy V, Zunjare RU and Hossain F, 2021. Molecular characterization of elite maize (*Zea mays* L.) inbreds using markers associated with iron and zinc transporter genes. *Genetic Resources and Crop Evolution*, 68:1545-1556
- 509.Shew AM, Nalley LL, Danforth DM, Dixon BL, Nayga RM, Jr D and Anne-Cecile V, 2016. Are all GMOs the same? Consumer acceptance of cisgenic rice in India. *Plant Biotechnology Journal*, 14:4-7
- 510.Shieh GS, Pan C-H, Wu J-H, Sun Y-J, Wang C-C, Hsiao W-C, Lin C-Y, Tung L, Chang T-H, Fleming AB, Hillyer C, Lo Y-C, Berger SL, Osley MA and Kao C-F, 2011. H2B ubiquitylation is part of chromatin architecture that marks exon-intron structure in budding yeast. *Bmc Genomics*, 12
- 511.Shlykov MA, Zheng WH, Chen JS and Saier MH, 2012. Bioinformatic characterization of the 4-Toluene Sulfonate Uptake Permease (TSUP) family of transmembrane proteins. *Biochimica Et Biophysica Acta-Biomembranes*, 1818:703-717
- 512.Silva AC, Xu X, Kim H-S, Fillingham J, Kislinger T, Mennella TA and Keogh M-C, 2012. The Replication-independent Histone H3-H4 Chaperones HIR, ASF1, and RTT106 Co-operate to Maintain Promoter Fidelity. *Journal of Biological Chemistry*, 287:1709-1718
- 513.Silva TN, Oz T and Altpeter F, 2015. Stacking of Intragenic Herbicide Resistant Genes in Sugarcane. *In Vitro Cellular & Developmental Biology-Animal*, 51:S50-S50
- 514.Silva TN, Oz T and Altpeter F, 2016. Stacking of Two Intragenic Herbicide Resistance Genes into Sugarcane for Improved Weed Control. *In Vitro Cellular & Developmental Biology-Animal*, 52:S58-S58
- 515.Silverio ALF and Saier MH, 2011. Bioinformatic Characterization of the Trimeric Intracellular Cation-Specific Channel Protein Family. *Journal of Membrane Biology*, 241:77-101
- 516.Singh A, Joshi M and Devi EL, 2016. Alternative to transgenesis: Cisgenesis and intragenesis. *Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools*, 1:345-367
- 517.Singh AK, 2017. Wild relatives of cultivated plants in India: A reservoir of alternative genetic resources and more. *Wild Relatives of Cultivated Plants in India: A Reservoir of Alternative Genetic Resources and More*:1-310
- 518.Small B, 2012. Genetically engineered forage crops: New Zealand public attitudes. Capturing opportunities and overcoming obstacles in Australian agronomy. *Proceedings of 16th Australian Agronomy Conference 2012, 14-18 October 2012, Armidale, New South Wales, Australia*:12-12

519. Smith MJ, Bryant EE, Joseph FJ and Rothstein R, 2019. DNA damage triggers increased mobility of chromosomes in G1-phase cells. *Molecular Biology of the Cell*, 30:2620-2625
520. Solieri L, Verspohl A, Bonciani T, Caggia C and Giudici P, 2015. Fast method for identifying inter- and intra-species *Saccharomyces* hybrids in extensive genetic improvement programs based on yeast breeding. *Journal of Applied Microbiology*, 119:149-161
521. Song G-Q, 2012. Genetic Transformation: Bridging from Functional Genomics to Specialty Crop Improvement. *In Vitro Cellular & Developmental Biology-Animal*, 48:18-18
522. Song G-Q and Hancock JF, 2012. Recent Advances in Blueberry Transformation. *International Journal of Fruit Science*, 12:316-332
523. Song S, Liu B, Zhai J, Zhang Y, Wang K and Qi T, 2021. The intragenic suppressor mutation *Leu59Phe* compensates for the effect of detrimental mutations in the jasmonate receptor *COI1*. *Plant Journal*,
524. Song X, Wang J, Ma X, Li Y, Lei T, Wang L, Ge W, Guo D, Wang Z, Li C, Zhao J and Wang X, 2016. Origination, Expansion, Evolutionary Trajectory, and Expression Bias of AP2/ERF Superfamily in *Brassica napus*. *Frontiers in Plant Science*, 7
525. Soriano JM, Madduri M, Schaart JG, van der Burgh A, van Kaauwen MPW, Tomic L, Groenwold R, Velasco R, van de Weg E and Schouten HJ, 2014. Fine mapping of the gene *Rvi18 (V25)* for broad-spectrum resistance to apple scab, and development of a linked SSR marker suitable for marker-assisted breeding. *Molecular Breeding*, 34:2021-2032
526. Souza Menezes KA, Costa Escobar IE, Resende Fraiz AC, Vieira Martins LM and Fernandes-Junior PI, 2017. Genetic Variability and Symbiotic Efficiency of *Erythrina velutina* Willd. Root Nodule Bacteria from the Semi-Arid Region in Northeastern Brazil. *Revista Brasileira De Ciencia Do Solo*, 41
527. Srinivas S and Cronan JE, 2017. An Eight-Residue Deletion in *Escherichia coli* *FabG* Causes Temperature-Sensitive Growth and Lipid Synthesis Plus Resistance to the Calmodulin Inhibitor Trifluoperazine. *Journal of Bacteriology*, 199
528. Stefanczyk E, Plich J, Janiszewska M, Smyda-Dajmund P, Sobkowiak S and Sliwka J, 2020. Marker-assisted pyramiding of potato late blight resistance genes *Rpi-rzc1* and *Rpi-phu1* on di- and tetraploid levels. *Molecular Breeding*, 40
529. Stein A, Wittkop B, Liu L, Obermeier C, Friedt W and Snowdon RJ, 2013. Dissection of a major QTL for seed colour and fibre content in *Brassica napus* reveals colocalization with candidate genes for phenylpropanoid biosynthesis and flavonoid deposition. *Plant Breeding*, 132:382-389
530. Stergiopoulos I, Cordovez V, Okmen B, Beenen HG, Kema GHJ and De Wit PJGM, 2014. Positive selection and intragenic recombination contribute to high allelic diversity in effector genes of *Mycosphaerella fijiensis*, causal agent of the black leaf streak disease of banana. *Molecular Plant Pathology*, 15:447-460
531. Stinard PS, 2011. Which seed color gene of *r1* responds to inhibitors (*Inr*) and enhancers (*Enr*) of aleurone color? *Maize Genetics Cooperation Newsletter*:28-28
532. Stover E, Avila Y, Li ZT and Gray D, 2013. Transgenic expression in citrus of *Vitis MybA1* from a bidirectional promoter resulted in variable anthocyanin expression and was not suitable as a screenable marker without antibiotic selection. *Proceedings of the Florida State Horticultural Society*, 126:84-88
533. Stukenbrock EH and Dutheil JY, 2018. Fine-Scale Recombination Maps of Fungal Plant Pathogens Reveal Dynamic Recombination Landscapes and Intragenic Hotspots. *Genetics*, 208:1209-1229
534. Swarupa V, Ravishankar KV and Rekha A, 2014. Plant defense response against *Fusarium oxysporum* and strategies to develop tolerant genotypes in banana. *Planta*, 239:735-751
535. Takita T, Larson HK and Ishimatsu A, 2011. The natural history of mudskippers in northern Australia, with field identification characters. *Beagle*, 27:189-204
536. Takuno S and Gaut BS, 2012. Body-Methylated Genes in *Arabidopsis thaliana* Are Functionally Important and Evolve Slowly. *Molecular Biology and Evolution*, 29:219-227
537. Takuno S and Gaut BS, 2013. Gene body methylation is conserved between plant orthologs and is of evolutionary consequence. *Proceedings of the National Academy of Sciences of the United States of America*, 110:1797-1802
538. Takuno S, Seymour DK and Gaut BS, 2017. The Evolutionary Dynamics of Orthologs That Shift in Gene Body Methylation between *Arabidopsis* Species. *Molecular Biology and Evolution*, 34:1479-1491

539. Tamang TM, Park J, Kakeshpour T, Valent B, Jia Y, Wang G-L and Park S, 2018. Development of Selectable Marker-free Cisgenic Rice Plants Expressing a Blast Resistance Gene Pi9. *In Vitro Cellular & Developmental Biology-Animal*, 54:S44-S44
540. Tanaka T, Eusebio-Cope A, Sun L and Suzuki N, 2012. Mycoreovirus genome alterations: similarities to and differences from rearrangements reported for other reoviruses. *Frontiers in Microbiology*, 3
541. Tanaka T, Sun L, Tsutani K and Suzuki N, 2011. Rearrangements of mycoreovirus 1 S1, S2 and S3 induced by the multifunctional protein p29 encoded by the prototypic hypovirus *Cryphonectria hypovirus 1* strain EP713. *Journal of General Virology*, 92:1949-1959
542. Tang W, Yuan M, Wang R, Yang Y, Wang C, Oses-Prieto JA, Kim T-W, Zhou H-W, Deng Z, Gampala SS, Gendron JM, Jonassen EM, Lillo C, DeLong A, Burlingame AL, Sun Y and Wang Z-Y, 2011. PP2A activates brassinosteroid-responsive gene expression and plant growth by dephosphorylating BZR1. *Nature Cell Biology*, 13:124-U149
543. Taniguchi K, Motohara K, Kusaba M and Nakata M, 2014. Phylogenetic Relationships between *Chrysanthemum seticuspe* f. *seticuspe* and *C. seticuspe* f. *boreale* Based on NCED3a Gene. *Memoirs of the National Museum of Nature and Science*:17-22
544. te Pas MFW, Veldkamp T, e Haas Y, Bannink A and Ellen ED, 2021. Adaptation of Livestock to New Diets Using Feed Components without Competition with Human Edible Protein Sources-A Review of the Possibilities and Recommendations. *Animals*, 11
545. Tekaia F, Dujon B and Richard G-F, 2013. Detection and Characterization of Megasatellites in Orthologous and Nonorthologous Genes of 21 Fungal Genomes. *Eukaryotic Cell*, 12:794-803
546. Telem RS, Wani SH, Singh NB, Nandini R, Sadhukhan R, Bhattacharya S and Mandal N, 2013. Cisgenics - A Sustainable Approach for Crop Improvement. *Current Genomics*, 14:468-476
547. Temel HY, Gol D, Akkale HBK, Kahriman A and Tanyolac MB, 2015. Single nucleotide polymorphism discovery through Illumina-based transcriptome sequencing and mapping in lentil. *Turkish Journal of Agriculture and Forestry*, 39:470-488
548. Thomas QA, Ard R, Liu J, Li B, Wang J, Pelechano V and Marquardt S, 2020. Transcript isoform sequencing reveals widespread promoter-proximal transcriptional termination in *Arabidopsis*. *Nature Communications*, 11
549. Thunstrom S, Sodermark L, Ivarsson L, Samuelsson L and Stefanova M, 2015. UBE2A deficiency syndrome: A report of two unrelated cases with large Xq24 deletions encompassing UBE2A gene. *American Journal of Medical Genetics, Part A*, 167:204-210
550. Tian H, Yang Y, Wang R, Fan Y, Yi H, Jiang B, Wang L, Ren J, Xu L, Zhang Y, Ge J, Liu Y, Wang F and Zhao J, 2021. Screening of 200 Core SNPs and the Construction of a Systematic SNP-DNA Standard Fingerprint Database with More Than 20,000 Maize Varieties. *Agriculture-Basel*, 11
551. Timerbaev VR, Mitiouchkina TY and Dolgov SV, 2019. Production of marker-free cisgenic apple plants using inducible site-specific recombinase and a bifunctional selectable gene. *Acta Horticulturae*, 1261:149-156
552. To TK, Saze H and Kakutani T, 2015. DNA Methylation within Transcribed Regions. *Plant Physiology*, 168:1219-1225
553. Toevs EA, Guenther JF, Johnson AJ, McIntosh CS and Thornton MK, 2011. An industry perspective of all-native and transgenic potatoes. *AgBioForum*, 14:14-19
554. Tokizawa M, Kusunoki K, Koyama H, Kurotani A, Sakurai T, Suzuki Y, Sakamoto T, Kurata T and Yamamoto YY, 2017. Identification of *Arabidopsis* genic and non-genic promoters by paired-end sequencing of TSS tags. *Plant Journal*, 90:587-605
555. Tokmakov SV, Mukhina ZM, Bogomaz DI and Matveeva TV, 2012. Development of a molecular marker for assessment of intraspecific polymorphism by the Rc gene that determines the red color of pericarp in rice *Oryza sativa* L. *Russian Journal of Genetics: Applied Research*, 2:357-366
556. Tolza C, Bejjani F, Evanno E, Mahfoud S, Moquet-Torcy G, Gostan T, Maqbool MA, Kirsh O, Piechaczyk M and Jariel-Encontre I, 2019. AP-1 Signaling by Fra-1 Directly Regulates HMGA1 Oncogene Transcription in Triple-Negative Breast Cancers. *Molecular Cancer Research*, 17:1999-2014
557. Tomaru Y, Osabe K, Okazaki K and Fujimoto R, 2013. Transcriptional regulation of key gene of vernalization, FLOWERING LOCUS C. *Bulletin of the Faculty of Agriculture, Niigata University*, 66:105-110
558. Tong Y-a, Peng H, Zhan C, Fan L, Ai T and Wang S, 2013. Genome-Wide Analysis Reveals Diversity of Rice Intronic miRNAs in Sequence Structure, Biogenesis and Function. *PLoS ONE*, 8

559. Touat-Todeschini L, Hiriart E and Verdel A, 2012. Nucleosome positioning and transcription: fission yeast CHD remodellers make their move. *Embo Journal*, 31:4371-4372
560. Tran PT, Sharifi MN, Poddar S, Dent RM and Niyogi KK, 2012. Intragenic Enhancers and Suppressors of Phytoene Desaturase Mutations in *Chlamydomonas reinhardtii*. *PLoS ONE*, 7
561. Tulbure MG, Ghioca-Robrecht DM, Johnston CA and Whigham DF, 2012. Inventory and Ventilation Efficiency of Nonnative and Native *Phragmites australis* (Common Reed) in Tidal Wetlands of the Chesapeake Bay. *Estuaries and Coasts*, 35:1353-1359
562. Turcic K, Tobar-Rubin R, Janevska D, Carroll J, Din E, Alvarez R, Haick J and Pals-Rylaarsdam R, 2014. Three intragenic suppressors of a GTPase-deficient allele of *GNAS* associated with McCune-Albright syndrome. *Journal of Molecular Endocrinology*, 52:321-331
563. Turgeon MO, Silander TL, Doycheva D, Liao XH, Rigden M, Ongaro L, Zhou X, Joustra SD, Wit JM, Wade MG, Heuer H, Refetoff S and Bernard DJ, 2017. TRH action is impaired in pituitaries of male *IGSF1*-deficient mice. *Endocrinology*, 158:815-830
564. Turner M, Yu O and Subramanian S, 2012. Genome organization and characteristics of soybean microRNAs. *Bmc Genomics*, 13
565. Usharani TR, Sowmya HD, Sunisha C and Mohandas S, 2016. Engineering resistance to *Fusarium* wilt. *Banana: Genomics and Transgenic Approaches for Genetic Improvement*:211-226
566. Uthup TK, Rajamani A, Ravindran M and Saha T, 2016. Molecular evolution and functional characterisation of haplotypes of an important rubber biosynthesis gene in *Hevea brasiliensis*. *Plant Biology*, 18:720-728
567. Uthup TK, Saha T, Ravindran M and Bini K, 2013. Impact of an intragenic retrotransposon on the structural integrity and evolution of a major isoprenoid biosynthesis pathway gene in *Hevea brasiliensis*. *Plant Physiology and Biochemistry*, 73:176-188
568. Uwimana N, Collin P, Jeronimo C, Haibe-Kains B and Robert F, 2017. Bidirectional terminators in *Saccharomyces cerevisiae* prevent cryptic transcription from invading neighboring genes. *Nucleic Acids Research*, 45:6417-6426
569. Van de Velde K, Chandler PM, Van Der Straeten D and Rohde A, 2017. Differential coupling of gibberellin responses by *Rht-B1c* suppressor alleles and *Rht-B1b* in wheat highlights a unique role for the DELLA N-terminus in dormancy. *Journal of Experimental Botany*, 68:443-455
570. van Hove L and Gillund F, 2017. Is it only the regulatory status? Broadening the debate on cisgenic plants. *Environmental Sciences Europe*, 29
571. Vanblaere T, Flachowsky H, Gessler C and Broggin GAL, 2014. Molecular characterization of cisgenic lines of apple 'Gala' carrying the *Rvi6* scab resistance gene. *Plant Biotechnology Journal*, 12:2-9
572. Vanblaere T, Szankowski I, Schaart J, Schouten H, Flachowsky H, Broggin GAL and Gessler C, 2011. The development of a cisgenic apple plant. *Journal of Biotechnology*, 154:304-311
573. Vanittanakom N, Szekely J, Khanthawong S, Sawutdechakul P, Vanittanakom P and Fisher MC, 2014. Molecular detection of *Pythium insidiosum* from soil in Thai agricultural areas. *International Journal of Medical Microbiology*, 304:321-326
574. Vargas WA, Sanz-Martin JM, Rech GE, Armijos-Jaramillo VD, Rivera LP, Mercedes Echeverria M, Diaz-Minguez JM, Thon MR and Sukno SA, 2016. A Fungal Effector With Host Nuclear Localization and DNA-Binding Properties Is Required for Maize Anthracnose Development. *Molecular Plant-Microbe Interactions*, 29:83-95
575. Vazquez-Lobo A, Roujol D, Zuniga-Sanchez E, Albenne C, Pinero D, Gamboa de Buen A and Jamet E, 2012. The highly conserved spermatophyte cell wall DUF642 protein family: Phylogeny and first evidence of interaction with cell wall polysaccharides in vitro. *Molecular Phylogenetics and Evolution*, 63:510-520
576. Veilleux RE, Oosumi T, Wadl PA, Baxter AJ, Holt SH, Ruiz-Rojas JJ, Pattison J, Flinn B, Dan Y, Nessler C and Shulaev V, 2012. Insertional Mutagenesis in the Diploid Strawberry (*Fragaria vesca*). 1st International Symposium on Genetic Modifications - Challenges and Opportunities for Horticulture in the World, 941:49-54
577. Verzaux E, van Arkel G, Vleeshouwers VGAA, van der Vossen EAG, Niks RE, Jacobsen E, Vossen J and Visser RGF, 2012. High-Resolution Mapping of Two Broad-Spectrum Late Blight Resistance Genes from Two Wild Species of the *Solanum circaeifolium* Group. *Potato Research*, 55:109-123
578. Vila M, Diaz-Santos E, e la Vega M, Rodriguez H, Vargas A and Leon R, 2012. Promoter Trapping in Microalgae Using the Antibiotic Paromomycin as Selective Agent. *Marine Drugs*, 10:2749-2765

579. Vincelli P, 2016. Genetic Engineering and Sustainable Crop Disease Management: Opportunities for Case-by-Case Decision-Making. *Sustainability*, 8
580. Viswanath V, Albrechtsen BR and Strauss SH, 2012. Global regulatory burden for field testing of genetically modified trees. *Tree Genetics & Genomes*, 8:221-226
581. Vossen JH, van Arkel G, Bergervoet M, Jo K-R, Jacobsen E and Visser RGF, 2016. The *Solanum demissum* R8 late blight resistance gene is an Sw-5 homologue that has been deployed worldwide in late blight resistant varieties. *Theoretical and Applied Genetics*, 129:1785-1796
582. Wang C, Wang Q, Zhu X, Cui M, Jia H, Zhang W, Tang W, Leng X and Shen W, 2019a. Characterization on the conservation and diversification of miRNA156 gene family from lower to higher plant species based on phylogenetic analysis at the whole genomic level. *Functional & Integrative Genomics*, 19:933-952
583. Wang D and Peterson T, 2013. Isolation of Sequences Flanking Ac Insertion Sites by Ac Casting. *Plant Transposable Elements: Methods and Protocols*, 1057:117-122
584. Wang G-F and Balint-Kurti PJ, 2015. Cytoplasmic and Nuclear Localizations Are Important for the Hypersensitive Response Conferred by Maize Autoactive Rp1-D21 Protein. *Molecular Plant-Microbe Interactions*, 28:1023-1031
585. Wang G-F and Balint-Kurti PJ, 2016. Maize Homologs of CCoAOMT and HCT, Two Key Enzymes in Lignin Biosynthesis, Form Complexes with the NLR Rp1 Protein to Modulate the Defense Response. *Plant Physiology*, 171:2166-2177
586. Wang G-F, He Y, Strauch R, Olukolu BA, Nielsen D, Li X and Balint-Kurti PJ, 2015. Maize Homologs of Hydroxycinnamoyltransferase, a Key Enzyme in Lignin Biosynthesis, Bind the Nucleotide Binding Leucine-Rich Repeat Rp1 Proteins to Modulate the Defense Response. *Plant Physiology*, 169:2230-2243
587. Wang H-LV and Chekanova JA, 2019. Novel mRNAs 3' end-associated cis-regulatory elements with epigenomic signatures of mammalian enhancers in the Arabidopsis genome. *Rna*, 25:1242-1258
588. Wang H, Chung PJ, Liu J, Jang I-C, Kean MJ, Xu J and Chua N-H, 2014a. Genome-wide identification of long noncoding natural antisense transcripts and their responses to light in Arabidopsis. *Genome Research*, 24:444-453
589. Wang H, Kan G, Li S, Ma X, Jia S and Liu Y, 2011. Breeding of high efficient nitrogen utilization transgenic rice through intragenesis technology. *Acta Agriculturae Zhejiangensis*, 23:862-869
590. Wang J-Z, Lei Y, Xiao Y, He X, Liang J, Jiang J, Dong S, Ke H, Leon P, Zerbe P, Xiao Y and Dehesh K, 2020a. Uncovering the functional residues of Arabidopsis isoprenoid biosynthesis enzyme HDS. *Proceedings of the National Academy of Sciences of the United States of America*, 117:355-361
591. Wang J, Zeng H, Gong Z, Liang Y, Ai X, Guo J, Mo M, Li X and Zheng J, 2019b. Comprehensive assessment of complex salt-alkali tolerance of the upland cotton varieties resources. *Journal of Agricultural Science and Technology (Beijing)*, 21:1-11
592. Wang M and Ibeagha-Awemu EM, 2021. Impacts of Epigenetic Processes on the Health and Productivity of Livestock. *Frontiers in Genetics*, 11
593. Wang X, Zhang Y, Yang N, Cheng H and Min Y, 2020b. DNMT3a mediates paclitaxel-induced abnormal expression of LINE-1 by increasing the intragenic methylation. *Yichuan*, 42:100-111
594. Wang Y-P, Xie J-H, Wu EJ, Yahuza L, Duan G-H, Shen L-L, Liu H, Zhou S-H, Nkurikiyimfura O, Andersson B, Yang L-N, Shang L-P, Zhu W and Zhan J, 2020c. Lack of gene flow between *Phytophthora infestans* populations of two neighboring countries with the largest potato production. *Evolutionary Applications*, 13:318-329
595. Wang Y, Chen M, Wang H, Wang J-F and Bao D, 2014b. Microsatellites in the Genome of the Edible Mushroom, *Volvariella volvacea*. *Biomed Research International*, 2014
596. Watthanasiri P, Geadkaew-Krenc A, Smooker PM and Grams R, 2021. *Fischoederius elongatus* (Poirier, 1883) Stiles & Goldberger, 1910, a cryptic species of pouched amphistome (Gastrothylacidae)? *Molecular and biochemical parasitology*, 245:111405-111405
597. Whelan AI and Lema MA, 2015. Regulatory framework for gene editing and other new breeding techniques (NBTs) in Argentina. *Gm Crops & Food-Biotechnology in Agriculture and the Food Chain*, 6:253-265
598. Wiest A, Barchers D, Eaton M, Henderson R, Schnittker R and McCluskey K, 2013. Molecular analysis of intragenic recombination at the tryptophan synthetase locus in *Neurospora crassa*. *Journal of Genetics*, 92:523-528

599. Willems S, Fraiture M-A, Deforce D, De Keersmaecker SCJ, De Loose M, Ruttink T, Herman P, Van Nieuwerburgh F and Roosens N, 2016. Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. *Food Chemistry*, 192:788-798
600. Win KT, Yamagata Y, Doi K, Uyama K, Nagai Y, Toda Y, Kani T, Ashikari M, Yasui H and Yoshimura A, 2017. A single base change explains the independent origin of and selection for the nonshattering gene in African rice domestication. *New Phytologist*, 213:1925-1935
601. Woegerbauer M, Kuffner M, Domingues S and Nielsen KM, 2015. Involvement of aph(3')-IIa in the formation of mosaic aminoglycoside resistance genes in natural environments. *Frontiers in Microbiology*, 6
602. Woody JL and Shoemaker RC, 2011. Gene expression: sizing it all up. *Frontiers in Genetics*, 2:70-Article No.: 70
603. Wu B, Hu W, Ayaad M, Liu H and Xing Y, 2017a. Intragenic recombination between two non-functional semi-dwarf 1 alleles produced a functional SD1 allele in a tall recombinant inbred line in rice. *PLoS ONE*, 12
604. Wu D, Bi C, Wang X, Xu Y, Ye Q and Ye N, 2017b. The complete chloroplast genome sequence of an economic plant *Coffea canephora*. *Mitochondrial DNA Part B-Resources*, 2:483-485
605. Wuerdig J, Flachowsky H and Hanke M-V, 2013. Studies on heat shock induction and transgene expression in order to optimize the Flp/FRT recombinase system in apple (*Malus x domestica* Borkh.). *Plant Cell Tissue and Organ Culture*, 115:457-467
606. Wuerdig J, Flachowsky H, Sass A, Peil A and Hanke M-V, 2015. Improving resistance of different apple cultivars using the Rvi6 scab resistance gene in a cisgenic approach based on the Flp/FRT recombinase system. *Molecular Breeding*, 35
607. Wuerschum T, Maurer HP, Dreyer F and Reif JC, 2013. Effect of inter- and intragenic epistasis on the heritability of oil content in rapeseed (*Brassica napus* L.). *Theoretical and Applied Genetics*, 126:435-441
608. Würdig J, Flachowsky H and Hanke MV, 2013. Studies on heat shock induction and transgene expression in order to optimize the Flp/FRT recombinase system in apple (*Malus x domestica* Borkh.). *Plant Cell, Tissue and Organ Culture*, 115:457-467
609. Würdig J, Flachowsky H, Peil A and Hanke MV, 2012. Cisgenic generation of apple trees (*Malus x domestica*) with resistance to *Venturia inaequalis*. *Julius-Kuhn-Archiv*:408-409
610. Xiang B, Li X, Qian J, Wang L, Ma L, Tian X and Wang Y, 2016. The Complete Chloroplast Genome Sequence of the Medicinal Plant *Swertia mussotii* Using the PacBio RS II Platform. *Molecules*, 21
611. Xie Y, Ravet K and Pearce S, 2021. Extensive structural variation in the Bowman-Birk inhibitor family in common wheat (*Triticum aestivum* L.). *Bmc Genomics*, 22
612. Xin C, Li N and Guo J, 2012. Potato Late Blight Control Using R-Gene Polyculture by GMO. *International Conference on Future Energy, Environment, and Materials (FEEM)*, 16:1925-1929
613. Xu G, Zhang J, Lyu H, Song Q, Feng Q, Xiang H and Zheng S, 2018a. DNA methylation mediates BmDeaf1-regulated tissue- and stage-specific expression of BmCHSA-2b in the silkworm, *Bombyx mori*. *Epigenetics & Chromatin*, 11
614. Xu X, Kanai R, Nakazawa N, Wang L, Toyoshima C and Yanagida M, 2018b. Suppressor mutation analysis combined with 3D modeling explains cohesin's capacity to hold and release DNA. *Proceedings of the National Academy of Sciences of the United States of America*, 115:E4833-E4842
615. Xu Y, Gan E-S, Zhou J, Wee W-Y, Zhang X and Ito T, 2014. Arabidopsis MRG domain proteins bridge two histone modifications to elevate expression of flowering genes. *Nucleic Acids Research*, 42:10960-10974
616. Yadav NS, Khadka J, Domb K, Zemach A and Grafi G, 2018. CMT3 and SUVH4/KYP silence the exonic Eukniveel retroelement to allow for reconstitution of CMT1 mRNA. *Epigenetics & Chromatin*, 11
617. Yan F, Di S, Murai Y, Iwashina T, Anai T and Takahashi R, 2016. New Allelic Variant Discovered at Soybean Flower Color Locus W1 Encoding Flavonoid 3 ' 5 '-hydroxylase. *Crop Science*, 56:1506-1513
618. Yang L-N, Liu H, Duan G-H, Huang Y-M, Liu S, Fang Z-G, Wu EJ, Shang L and Zhan J, 2020a. The *Phytophthora infestans* AVR2 Effector Escapes R2 Recognition Through Effector Disordering. *Molecular Plant-Microbe Interactions*, 33:921-931
619. Yang L, Ouyang H-B, Fang Z-G, Zhu W, Wu EJ, Luo G-H, Shang L-P and Zhan J, 2018. Evidence for intragenic recombination and selective sweep in an effector gene of *Phytophthora infestans*. *Evolutionary Applications*, 11:1342-1353

620. Yang X, Yan J, Zhang Z, Lin T, Xin T, Wang B, Wang S, Zhao J, Zhang Z, Lucas WJ, Li G and Huang S, 2020b. Regulation of plant architecture by a new histone acetyltransferase targeting gene bodies. *Nature Plants*, 6:809-+
621. Yao JL, Karunairetnam S, Tomes S and Gleave AP, 2011. Developing Apple Intragenic Transformation Systems. 2nd Genetically Modified Organisms in Horticulture Symposium, 974:109-115
622. Yee DC, Shlykov MA, Västermark A, Reddy VS, Arora S, Sun EI and Saier Jr MH, 2013. The transporter-opsin-G protein-coupled receptor (TOG) superfamily. *FEBS Journal*, 280:5780-5800
623. Yi-Wen H, Yue Yang M, Echeveste CE, Kiyoko O, Jianying Z, Martha Y, Chien-Wei L, Jianhua Y, Pengyuan L, Ming D, Chongde S, Jianbo X and Li-Shu W, 2020. Black raspberries attenuate colonic adenoma development in ApcMin mice: relationship to hypomethylation of promoters and gene bodies. *Food Frontiers*, 1:234-242
624. Ying X, Redfern B, Gmitter FG and Jr D, 2020. Heterologous Expression of the Constitutive Disease Resistance 2 and 8 Genes from Poncirus trifoliata Restored the Hypersensitive Response and Resistance of Arabidopsis cdr1 Mutant to Bacterial Pathogen Pseudomonas syringae. *Plants-Basel*, 9
625. You L-Y, Lin J, Xu H-W, Chen C-X, Chen J-Y, Zhang J, Zhang J, Li Y-X, Ye C, Zhang H, Jiang J, Zhu J-K, Li QQ and Duan C-G, 2021. Intragenic heterochromatin-mediated alternative polyadenylation modulates miRNA and pollen development in rice. *New Phytologist*,
626. Young MW, Mullins E and Squire GR, 2017. Environmental risk assessment of blight-resistant potato: use of a crop model to quantify nitrogen cycling at scales of the field and cropping system. *Environmental Science and Pollution Research*, 24:21434-21444
627. Yu D, Ma X, Zuo Z, Shao W, Wang H and Meng Y, 2017. Bioinformatics resources for deciphering the biogenesis and action pathways of plant small RNAs. *Rice*, 10:(7 August 2017)-(2017 August 2017)
628. Yu D, Shi K, Wen X, Xie F, Wang T, Liu S and He L, 2018. Evidence of the genetic diversity and clonal population structure of Oenococcus oeni strains isolated from different wine-making regions of China. *Journal of Microbiology*, 56:556-564
629. Zhan J, Thrall PH, Papaix J, Xie L and Burdon JJ, 2015. Playing on a Pathogen's Weakness: Using Evolution to Guide Sustainable Plant Disease Control Strategies. *Annual Review of Phytopathology*, Vol 53, 53:19-43
630. Zhan X-Y and Zhu Q-Y, 2018. Molecular typing of Legionella pneumophila isolates from environmental water samples and clinical samples using a five-gene sequence typing and standard Sequence-Based Typing. *PLoS ONE*, 13
631. Zhang G, Lukoszek R, Mueller-Roeber B and Ignatova Z, 2011. Different sequence signatures in the upstream regions of plant and animal tRNA genes shape distinct modes of regulation. *Nucleic Acids Research*, 39:3331-3339
632. Zhang H, Ali A, Hou F, Wu T, Guo D, Zeng X, Wang F, Zhao H, Chen X, Xu P and Wu X, 2018. Effects of ploidy variation on promoter DNA methylation and gene expression in rice (*Oryza sativa* L.). *BMC Plant Biology*, 18
633. Zhang H, Tan K, Li S, Ma H and Zheng H, 2020a. DNA methylation in molluscs growth and development: An overview. *Aquaculture Research*,
634. Zhang K-J, Han X and Hong X-Y, 2013. Various infection status and molecular evidence for horizontal transmission and recombination of Wolbachia and Cardinium among rice planthoppers and related species. *Insect Science*, 20:329-344
635. Zhang W, Liu W, Song Y, Xu H, Menghe B, Zhang H and Sun Z, 2015. Multilocus sequence typing of a dairy-associated *Leuconostoc mesenteroides* population reveals clonal structure with intragenic homologous recombination. *Journal of Dairy Science*, 98:2284-2293
636. Zhang Z, Gou X, Xun H, Bian Y, Ma X, Li J, Li N, Gong L, Feldman M, Liu B and Levy AA, 2020b. Homoeologous exchanges occur through intragenic recombination generating novel transcripts and proteins in wheat and other polyploids. *Proceedings of the National Academy of Sciences of the United States of America*, 117:14561-14571
637. Zhang Z, Li N, Hou C, Gao K, Tang X and Guo X, 2020c. Analysis of reassortant and intragenic recombination in Cypovirus. *Virology Journal*, 17
638. Zhao Z, Guo C, Sutharzan S, Li P, Echt CS, Zhang J and Liang C, 2014. Genome-Wide Analysis of Tandem Repeats in Plants and Green Algae. *G3-Genes Genomes Genetics*, 4:67-78
639. Zhao Z, Li C and Li Y, 2018. The characteristics and distribution of tandem repeats in *Sorghum bicolor* genome. *Journal of Henan Agricultural Sciences*, 47:33-42

640. Zhao Z and Zhang M, 2018. Characteristics of tandem repeats in Citrus clementina genome. *Southwest China Journal of Agricultural Sciences*, 31:1571-1577
641. Zheng S, Crickard JB, Srikanth A and Reese JC, 2014. A Highly Conserved Region within H2B Is Important for FACT To Act on Nucleosomes. *Molecular and Cellular Biology*, 34:303-314
642. Zhou H, Xia D, Zhao D, Li Y, Li P, Wu B, Gao G, Zhang Q, Wang G, Xiao J, Li X, Yu S, Lian X and He Y, 2021. The origin of Wx(la) provides new insights into the improvement of grain quality in rice. *Journal of Integrative Plant Biology*, 63:878-888
643. Zhou L, Powell CA, Hoffman MT, Li W, Fan G, Liu B, Lin H and Duan Y, 2011a. Diversity and Plasticity of the Intracellular Plant Pathogen and Insect Symbiont "Candidatus Liberibacter asiaticus" as Revealed by Hypervariable Prophage Genes with Intragenic Tandem Repeats. *Applied and Environmental Microbiology*, 77:6663-6673
644. Zhou M, Sun J, Wang Q-H, Song L-Q, Zhao G, Wang H-Z, Yang H-X and Li X, 2011b. Genome-wide analysis of clustering patterns and flanking characteristics for plant microRNA genes. *FEBS Journal*, 278:929-940
645. Zhou MB, Liu XM and Tang DQ, 2011c. Transposable elements in Phyllostachys pubescens (Poaceae) genome survey sequences and the full-length cDNA sequences, and their association with simple-sequence repeats. *Genetics and Molecular Research*, 10:3026-3037
646. Zhu D, Rosa S and Dean C, 2015. Nuclear Organization Changes and the Epigenetic Silencing of FLC during Vernalization. *Journal of Molecular Biology*, 427:659-669
647. Zhu Q, Bennetzen JL and Smith SM, 2013. Isolation and Diversity Analysis of Resistance Gene Homologues from Switchgrass. *G3-Genes Genomes Genetics*, 3:1031-1042
648. Zhu S, 2014. R gene stacking by trans- and cisgenesis to achieve durable late blight resistance in potato. R gene stacking by trans- and cisgenesis to achieve durable late blight resistance in potato:164 pp.-164 pp.
649. Zhuo Y, Gao G, Shi Ja, Zhou X and Wang X, 2013. miRNAs: Biogenesis, Origin and Evolution, Functions on Virus-Host Interaction. *Cellular Physiology and Biochemistry*, 32:499-510
650. Zuber J, Danial SA, Connelly SM, Naider F and Dumont ME, 2015. Identification of Destabilizing and Stabilizing Mutations of Ste2p, a G Protein-Coupled Receptor in Saccharomyces cerevisiae. *Biochemistry*, 54:1787-1806

A.2. List of selected publications retrieved from the literature search

1. Almeraya EV and Sanchez-de-Jimenez E, 2016. Intragenic modification of maize. *Journal of Biotechnology*, 238:35-41
2. An CF, Orbovic V and Mou ZL, 2013. An efficient intragenic vector for generating intragenic and cisgenic plants in citrus. *American Journal of Plant Sciences*, 4:2131-2137
3. Bandara NL, Cova V, Tartarini S, Gessler C, Patocchi A, Cestaro A, Troglio M, Velasco R and Komjanc M, 2013. Isolation of Rvi5 (V_m) Locus from Malus x domestica 'Murray'. *3rd International Symposium on Molecular Markers in Horticulture*, 1100:21-24
4. Barrell PJ, Latimer JM, Baldwin SJ, Thompson ML, Jacobs JME and Conner AJ, 2017. Somatic cell selection for chlorsulfuron-resistant mutants in potato: identification of point mutations in the acetohydroxyacid synthase gene. *BMC Biotechnology*, 17
5. Borg S, Brinch-Pedersen H, Tauris B, Madsen LH, Darbani B, Noeparvar S and Holm PB, 2012. Wheat ferritins: Improving the iron content of the wheat grain. *Journal of Cereal Science*, 56:204-213
6. Brand GD, Magalhães MTQ, Tinoco MLP, Aragão FJL, Nicoli J, Kelly SM, Cooper A and Bloch C, 2012. Probing Protein Sequences as Sources for Encrypted Antimicrobial Peptides. *PLoS ONE*, 7
7. Carvalho RF and Folta KM, 2017. Assessment of promoters and a selectable marker for development of strawberry intragenic vectors. *Plant Cell Tissue and Organ Culture*, 128:259-271
8. Cascone P, Radkova M, Arpaia S, Errico S, Lotz LAP, Magarelli RA, Djilianov D and Guerrieri E, 2018. Unintended effects of a Phytophthora-resistant cisgenic potato clone on the potato aphid Macrosiphum euphorbiae and its parasitoid Aphidius ervi. *Journal of Pest Science*, 91:565-574

9. Cavatorta J, Perez KW, Gray SM, Van Eck J, Yeam I and Jahn M, 2011. Engineering virus resistance using a modified potato gene. *Plant Biotechnology Journal*, 9:1014-1021
10. Chizzali C, Gusberti M, Schouten HJ, Gessler C and Broggin GAL, 2016. Cisgenic Rvi6 scab-resistant apple lines show no differences in Rvi6 transcription when compared with conventionally bred cultivars. *Planta*, 243:635-644
11. Corredoira E, San Jose MC, Vieitez AM, Allona I, Aragoncillo C and Ballester A, 2016. Agrobacterium-mediated transformation of European chestnut somatic embryos with a *Castanea sativa* (Mill.) endochitinase gene. *New Forests*, 47:669-684
12. Corredoira E, Valladares S, Allona I, Aragoncillo C, Vieitez AM and Ballester A, 2012. Genetic transformation of European chestnut somatic embryos with a native thaumatin-like protein (CsTL1) gene isolated from *Castanea sativa* seeds. *Tree Physiology*, 32:1389-1402
13. Cseh A, Soos V, Rakszegi M, Tuerkoesi E, Balazs E and Molnar-Lang M, 2013. Expression of HvCslF9 and HvCslF6 barley genes in the genetic background of wheat and their influence on the wheat beta-glucan content. *Annals of Applied Biology*, 163:142-150
14. Dalla Costa L, Bozzoli M, Pompili V, Piazza S, Broggin GAL, Patocchi A and Malnoy M, 2019. Development of a Taqman real-time PCR method to quantify nptII in apple lines obtained with 'established' or 'new breeding' techniques of genetic modification. *European Food Research and Technology*, 245:643-652
15. Dalla Costa L, Piazza S, Campa M, Flachowsky H, Hanke M-V and Malnoy M, 2016. Efficient heat-shock removal of the selectable marker gene in genetically modified grapevine. *Plant Cell Tissue and Organ Culture*, 124:471-481
16. Dermawan H, Karan R, Jung JH, Zhao Y, Parajuli S, Sanahuja G and Altpeter F, 2016. Development of an intragenic gene transfer and selection protocol for sugarcane resulting in resistance to acetolactate synthase-inhibiting herbicide. *Plant Cell Tissue and Organ Culture*, 126:459-468
17. Dhekney SA, Li ZT and Gray DJ, 2011. Grapevines engineered to express cisgenic *Vitis vinifera* thaumatin-like protein exhibit fungal disease resistance. *In Vitro Cellular & Developmental Biology-Plant*, 47:458-466
18. Duan H, Richael C and Rommens CM, 2012. Overexpression of the wild potato eIF4E-1 variant Eva1 elicits Potato virus Y resistance in plants silenced for native eIF4E-1. *Transgenic Research*, 21:929-938
19. Erpen L, Tavano ECR, Harakava R, Dutt M, Grosser JW, Piedade SMS, Mendes BMJ and Mourao Filho FAA, 2018. Isolation, characterization, and evaluation of three *Citrus sinensis*-derived constitutive gene promoters. *Plant Cell Reports*, 37:1113-1125
20. Gao Y, e Bang TC and Schjoerring JK, 2019. Cisgenic overexpression of cytosolic glutamine synthetase improves nitrogen utilization efficiency in barley and prevents grain protein decline under elevated CO₂. *Plant Biotechnology Journal*, 17:1209-1221
21. Haesaert G, Vossen JH, Custers R, De Loose M, Haverkort A, Heremans B, Hutten R, Kessel G, Landschoot S, Van Droogenbroeck B, Visser RGF and Gheysen G, 2015. Transformation of the potato variety Desiree with single or multiple resistance genes increases resistance to late blight under field conditions. *Crop Protection*, 77:163-175
22. Han KM, Dharmawardhana P, Arias RS, Ma C, Busov V and Strauss SH, 2011. Gibberellin-associated cisgenes modify growth, stature and wood properties in *Populus*. *Plant Biotechnology Journal*, 9:162-178
23. Higuera-Sobrino JJ, Blanco-Portales R, Moyano E, Rodríguez-Franco A, Muñoz-Blanco J and Caballero JL, 2021. Silencing of strawberry pathogen defence related candidate genes by using specific strawberry fruit ripening-related promoters: An intragenic approach to improve fruit quality and resistance. *Acta Horticulturae*, 1309:83-91
24. Holme IB, Dionisio G, Brinch-Pedersen H, Wendt T, Madsen CK, Vincze E and Holm PB, 2012. Cisgenic barley with improved phytase activity. *Plant Biotechnology Journal*, 10:237-247
25. Holme IB, Madsen CK, Wendt T and Brinch-Pedersen H, 2020. Horizontal Stacking of PAPHy_a Cisgenes in Barley Is a Potent Strategy for Increasing Mature Grain Phytase Activity. *Frontiers in Plant Science*, 11
26. Hu L, Li H, Qin R, Xu R, Li J, Li L, Wei P and Yang J, 2016. Plant phosphomannose isomerase as a selectable marker for rice transformation. *Scientific Reports*, 6
27. Jaensch M, Paris R, Amoako-Andoh F, Keulemans W, Davey MW, Pagliarani G, Tartarini S and Patocchi A, 2014. A Phenotypic, Molecular and Biochemical Characterization of the First Cisgenic Scab-Resistant Apple Variety 'Gala'. *Plant Molecular Biology Reporter*, 32:679-690

28. Jo K, Kim C, Kim S, Kim T, Bergervoet M, Jongsma MA, Visser RGF, Jacobsen E and Vossen JH, 2014. Development of late blight resistant potatoes by cisgene stacking. *BMC Biotechnology*, 14:(29 May 2014)-(2029 May 2014)
29. Joshi SG, Schaart JG, Groenwold R, Jacobsen E, Schouten HJ and Krens FA, 2011. Functional analysis and expression profiling of HcrVf1 and HcrVf2 for development of scab resistant cisgenic and intragenic apples. *Plant Molecular Biology*, 75:579-591
30. Jung JH, Kannan B, Dermawan H, Moxley GW and Altpeter F, 2016. Precision breeding for RNAi suppression of a major 4-coumarate:coenzyme A ligase gene improves cell wall saccharification from field grown sugarcane. *Plant Molecular Biology*, 92:505-517
31. Kamrani M, Kohnehouz BB and Gholizadeh A, 2011. Cisgenic inhibition of the potato cold induced phosphorylase L gene expression and decrease in sugar contents. *African Journal of Biotechnology*, 10:10076-10082
32. Kandel R, Dutt M, Grosser JW, Gray DJ, Li ZT, Sittler V, Bergey DR and Dhekney SA, 2014. Evaluation of plant-based reporter systems for improvement of cold-hardy grape cultivars. 29th International Horticultural Congress on Horticulture - Sustaining Lives, Livelihoods and Landscapes (IHC) / 4th International Symposium on Tropical Wines / International Symposium on Grape and Wine Production in Diverse Regions, 1115:57-61
33. Kessel GJT, Mullins E, Evenhuis A, Stellingwerf J, Cortes VO, Phelan S, van den Bosch T, Forch MG, Goedhart P, van der Voet H and Lotz LAP, 2018. Development and validation of IPM strategies for the cultivation of cisgenically modified late blight resistant potato. *European Journal of Agronomy*, 96:146-155
34. Konagaya K-i, Tsuda M, Okuzaki A, Ando S and Tabei Y, 2013. Application of the acetolactate synthase gene as a cisgenic selectable marker for *Agrobacterium*-mediated transformation in Chinese cabbage (*Brassica rapa ssp pekinensis*). *Plant Biotechnology*, 30:125-U125
35. Kost TD, Gessler C, Jaensch M, Flachowsky H, Patocchi A and Broggini GAL, 2015. Development of the First Cisgenic Apple with Increased Resistance to Fire Blight. *PLoS ONE*, 10
36. Kost TD, Jansch M, Gessler C, Flachowsky H, Patocchi A and Broggini GAL, 2017. Generation of a cisgenic apple line of cultivar 'Gala' with increased fire blight resistance. *Acta Horticulturae*, 1172:79-84
37. Krause SMB, Naether A, Ortiz Cortes V, Mullins E, Kessel GJT, Lotz LAP and Tebbe CC, 2020. No Tangible Effects of Field-Grown Cisgenic Potatoes on Soil Microbial Communities. *Frontiers in Bioengineering and Biotechnology*, 8
38. Krens FA, Schaart JG, van der Burgh AM, Tnennenbroek-Capel IEM, Groenwold R, Kodde LP, Broggini GAL, Gessler C and Schouten HJ, 2015. Cisgenic apple trees; development, characterization, and performance. *Frontiers in Plant Science*, 6
39. Kumari M, Devanna BN, Singh PK, Rajashekara H, Sharma V and Sharma TR, 2017. Stacking of blast resistance orthologue genes in susceptible indica rice line improves resistance against *Magnaporthe oryzae*. *3 Biotech*, 8
40. Lazebnik J, Dicke M, ter Braak CJF and van Loon JJA, 2017. Biodiversity analyses for risk assessment of genetically modified potato. *Agriculture Ecosystems & Environment*, 249:196-205
41. Li ZT, Kim K-H, Jasinski JR, Creech MR and Gray DJ, 2012. Large-scale characterization of promoters from grapevine (*Vitis spp.*) using quantitative anthocyanin and GUS assay systems. *Plant Science*, 196:132-142
42. Lu H, Viswanath V, Ma C, Etherington E, Dharmawardhana P, Shevchenko O, Strauss SH, Pearce DW, Rood SB and Busov V, 2015. Recombinant DNA modification of gibberellin metabolism alters growth rate and biomass allocation in *Populus*. *Tree Genetics & Genomes*, 11
43. Lutken H, Laura M, Borghi C, Orgaard M, Allavena A and Rasmussen SK, 2011. Expression of KxhKN4 and KxhKN5 genes in *Kalanchoe* << *blossfeldiana* 'Molly' results in novel compact plant phenotypes: towards a cisgenesis alternative to growth retardants. *Plant Cell Reports*, 30:2267-2279
44. Maltseva E, Iskakova G, Ismagul A, Chirkin A, Naizabayeva D, Ismagulova G, Malakhova N, Aitkhozhina N, Eliby S and Skiba Y, 2021. A cisgenic approach in the transformation of bread wheat cv. saratovskaya 29 with class I chitinase gene. *Open Biotechnology Journal*, 15:29-35
45. Martinez-Alarcon D, Mora-Aviles A, Espinoza-Nunez A, Serrano Jamaica LM, Cruz-Hernandez A, Rodriguez-Torres A, Castro-Guillen JL, Blanco-Labra A and Garcia-Gasca T, 2019. Rhizosecretion of a cisgenic lectin by genetic manipulation of Tepary bean plants (*Phaseolus acutifolius*). *Journal of Biotechnology*, 306

46. Merritt BA, Zhang X, Triplett EW, Mou Z and Orbovic V, 2021. Selection of transgenic citrus plants based on glyphosate tolerance conferred by a citrus 5-enolpyruvylshikimate-3-phosphate synthase variant. *Plant Cell Reports*,
47. Miroshnichenko I, Timerbaev V, Okuneva A, Klementyeva A, Sidorova T, Pushin A and Dolgov S, 2020. Enhancement of resistance to PVY in intragenic marker-free potato plants by RNAi-mediated silencing of eIF4E translation initiation factors. *Plant Cell Tissue and Organ Culture*, 140:691-705
48. Mishra S, Alavilli H, Lee B-h, Panda SK and Sahoo L, 2015. Cloning and characterization of a novel vacuolar Na⁺/H⁺ antiporter gene (VuNHX1) from drought hardy legume, cowpea for salt tolerance. *Plant Cell Tissue and Organ Culture*, 120:19-33
49. Mlalazi B, Welsch R, Namanya P, Khanna H, Geijskes RJ, Harrison MD, Harding R, Dale JL and Bateson M, 2012. Isolation and functional characterisation of banana phytoene synthase genes as potential cisgenes. *Planta*, 236:1585-1598
50. Muratova OA, Beketova MP, Kuznetsova MA, Rogozina EV and Khavkin EE, 2020. South American species *Solanum alandiae* Card. and *S. Okadae* Hawkes et Hjerting as potential sources of genes for potato late blight resistance. *Proceedings on Applied Botany, Genetics and Breeding*, 181:73-83
51. Nietsch J, Bruegmann T, Becker D and Fladung M, 2017. Old methods rediscovered: application and improvement of two direct transformation methods to hybrid poplar (*Populus tremula* x *P-alba*). *Plant Cell Tissue and Organ Culture*, 130:183-196
52. Ortega JL, Rajapakse W, Bagga S, Apodaca K, Lucero Y and Sengupta-Gopalan C, 2018. An intragenic approach to confer glyphosate resistance in chile (*Capsicum annuum*) by introducing an in vitro mutagenized chile EPSPS gene encoding for a glyphosate resistant EPSPS protein. *PLoS ONE*, 13
53. Ortiz V, Phelan S and Mullins E, 2016. A temporal assessment of nematode community structure and diversity in the rhizosphere of cisgenic *Phytophthora infestans*-resistant potatoes. *BMC Ecology*, 16:(1 December 2016)-(2011 December 2016)
54. Paez-Valencia J, Sanchez-Lares J, Marsh E, Dorneles LT, Santos MP, Sanchez D, Winter A, Murphy S, Cox J, Trzaska M, Metler J, Kozic A, Facanha AR, Schachtman D, Sanchez CA and Gaxiola RA, 2013. Enhanced Proton Translocating Pyrophosphatase Activity Improves Nitrogen Use Efficiency in Romaine Lettuce. *Plant Physiology*, 161:1557-1569
55. Paul S, Ali N, Gayen D, Datta SK and Datta K, 2012. Molecular breeding of Osfer 2 gene to increase iron nutrition in rice grain. *GM crops & food*, 3:310-316
56. Radkova M, Lyubenova A, Slavov S, Batchvarova R, Kalushkov P and Djilianov D, 2017. FEEDING COLORADO POTATO BEETLE ON LATE BLIGHT RESISTANT CISGENIC POTATO LINES HAS NO EFFECT ON THE INSECT AS A NON TARGET ORGANISM. *Comptes Rendus De L Academie Bulgare Des Sciences*, 70:895-902
57. Raj RS, Singh C, Modi A and Subhash N, 2015. Genetic transformation of lowland rice variety GR11 for drought tolerance and its ratification for upland paddy cultivation. *Indian Journal of Genetics and Plant Breeding*, 75:30-40
58. Righetti L, Djennane S, Berthelot P, Cournol R, Wilmot N, Loridon K, Vergne E and Chevreau E, 2014. Elimination of the nptII marker gene in transgenic apple and pear with a chemically inducible R/Rs recombinase. *Plant Cell Tissue and Organ Culture*, 117:335-348
59. Rojas M, Tiessen A, Ascencio F, Angulo C and Gomez-Anduro G, 2015. Two Promoters of Beta-Glucosidase Paralogs (ZmBGlu2 and ZmBGlu5) Highly Active in Tropical Young Maize Hybrid Seedlings. *Plant Molecular Biology Reporter*, 33:1666-1674
60. Sabbadini S, Capriotti L, Limeria C, Navacchi O, Tempesta G and Mezzetti B, 2018. A plant regeneration platform to apply new breeding techniques for improving disease resistance in grapevine rootstocks and cultivars. *41st World Congress of Vine and Wine*, 12
61. Schaart JG, Tinnenbroek-Capel IEM and Krens FA, 2011. Isolation and characterization of strong gene regulatory sequences from apple, *Malus x domestica*. *Tree Genetics & Genomes*, 7:135-142
62. Schlathölter I, Broggin GAL, Meissle M, Romeis J, Studer B and Patocchi A, 2021. Multi-level assessment of field-grown cisgenic apple trees. *Acta Horticulturae*, 1307:239-246
63. Scholey D, Burton E, Morgan N, Sanni C, Madsen CK, Dionisio G and Brinch-Pedersen H, 2017. P and Ca digestibility is increased in broiler diets supplemented with the high-phytase HIGHPHY wheat. *Animal*, 11:1457-1463

64. Stover E, Avila Y, Li ZT and Gray D, 2013. Transgenic expression in citrus of Vitis MybA1 from a bidirectional promoter resulted in variable anthocyanin expression and was not suitable as a screenable marker without antibiotic selection. *Proceedings of the Florida State Horticultural Society*, 126:84-88
65. Timerbaev VR, Mitiouchkina TY and Dolgov SV, 2019. Production of marker-free cisgenic apple plants using inducible site-specific recombinase and a bifunctional selectable gene. *Acta Horticulturae*, 1261:149-156
66. Vanblaere T, Flachowsky H, Gessler C and Broggin GAL, 2014. Molecular characterization of cisgenic lines of apple 'Gala' carrying the Rvi6 scab resistance gene. *Plant Biotechnology Journal*, 12:2-9
67. Vanblaere T, Szankowski I, Schaart J, Schouten H, Flachowsky H, Broggin GAL and Gessler C, 2011. The development of a cisgenic apple plant. *Journal of Biotechnology*, 154:304-311
68. Verzaux E, van Arkel G, Vleeshouwers VGAA, van der Vossen EAG, Niks RE, Jacobsen E, Vossen J and Visser RGF, 2012. High-Resolution Mapping of Two Broad-Spectrum Late Blight Resistance Genes from Two Wild Species of the Solanum circaeifolium Group. *Potato Research*, 55:109-123
69. Vossen JH, van Arkel G, Bergervoet M, Jo K-R, Jacobsen E and Visser RGF, 2016. The Solanum demissum R8 late blight resistance gene is an Sw-5 homologue that has been deployed worldwide in late blight resistant varieties. *Theoretical and Applied Genetics*, 129:1785-1796
70. Wuerdig J, Flachowsky H and Hanke M-V, 2013. Studies on heat shock induction and transgene expression in order to optimize the Flp/FRT recombinase system in apple (*Malus x domestica* Borkh.). *Plant Cell Tissue and Organ Culture*, 115:457-467
71. Wuerdig J, Flachowsky H, Sass A, Peil A and Hanke M-V, 2015. Improving resistance of different apple cultivars using the Rvi6 scab resistance gene in a cisgenic approach based on the Flp/FRT recombinase system. *Molecular Breeding*, 35
72. Yao JL, Karunaretnam S, Tomes S and Gleave AP, 2011. Developing Apple Intragenic Transformation Systems. *2nd Genetically Modified Organisms in Horticulture Symposium*, 974:109-115
73. Ying X, Redfern B, Gmitter FG and Jr D, 2020. Heterologous Expression of the Constitutive Disease Resistance 2 and 8 Genes from Poncirus trifoliata Restored the Hypersensitive Response and Resistance of Arabidopsis cdr1 Mutant to Bacterial Pathogen Pseudomonas syringae. *Plants-Basel*, 9

A.3. List of selected patents

Title	ID application
Construct and vector for intragenic plant transformation	WO2017185136A1
	AU2018253628A1
	SG11201809406PA
	AU2018253628B2
Method for modifying tuber shape in potato	WO2020008078A1
	NL2021271B1
Plant transformation using DNA minicircles	AU2010211450A1
Potato class T DNA elements and cisgenesis system and its application	CN104911180B
Recombinant DNA construct, expression cassette and usage	BR102019022248A2
Use of R-genes as a selection marker in plant transformation and use of cisgenes in plant transformation	US2010146662A1