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Marker-assisted selection: an approach for precision plant breeding in the twenty-first century

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1406	A marker-assisted backcross approach for developing submergence-tolerant rice cultivars. 2007 , 115, 767-76		324
1405	Integration of genomic tools to assist breeding in the japonica subspecies of rice. 2008 , 22, 159-168		18
1404	Introgression of Xa4, Xa7 and Xa21 for resistance to bacterial blight in thermosensitive genetic male sterile rice (<i>Oryza sativa</i> L.) for the development of two-line hybrids. 2008 , 164, 627-636		44
1403	Stressed genomics-bringing relief to rice fields. 2008 , 11, 201-8		40
1402	Molecular plant breeding as the foundation for 21st century crop improvement. 2008 , 147, 969-77		461
1401	Agricultural sustainability: concepts, principles and evidence. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 447-65	5.8	812
1400	Characterization of a resistance locus (Pfs-1) to the spinach downy mildew pathogen (<i>Peronospora farinosa</i> f. sp. <i>spinaciae</i>) and development of a molecular marker linked to Pfs-1. 2008 , 98, 894-900		21
1399	Introduction. Sustainable agriculture. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008 , 363, 445-446	5.8	15
1398	Rice molecular breeding laboratories in the genomics era: Current status and future considerations. 2008 , 2008, 524847		60
1397	. 2009 ,		4
1396	. 2009 , 31, 779-792		24
1395	Development of submergence-tolerant rice cultivars: the Sub1 locus and beyond. 2009 , 103, 151-60		336
1394	SNP identification in crop plants. 2009 , 12, 211-7		310
1393	Genetic resistance for the sustainable control of plant virus diseases: breeding, mechanisms and durability. 2009 , 125, 1-22		72
1392	Genetic improvement of C4 grasses as cellulosic biofuel feedstocks. 2009 , 45, 291-305		89
1391	Comparative analysis of marker-assisted and phenotypic selection for yield components in cucumber. 2009 , 119, 621-34		25

1390	Fine mapping, physical mapping and development of diagnostic markers for the Rrs2 scald resistance gene in barley. 2009 , 119, 1507-22	36
1389	Functional marker-assisted selection for bacterial leaf blight resistance genes in rice (<i>Oryza sativa</i> L.). 2009 , 129, 400	18
1388	Marker Assisted Breeding. 2009 , 451-469	10
1387	<i>Solanum lycopersicum</i> (Tomato). 2009 ,	1
1386	Molecular Improvement of Tropical Maize for Drought Stress Tolerance in Sub-Saharan Africa. 2009 , 28, 16-35	26
1385	GMO Detection. 2009 , 515-532	
1384	Novel Genomic Tools and Modern Genetic and Breeding Approaches for Crop Improvement. 2009 , 18, 127-138	56
1383	Genetic Approaches toward Improving Heat Tolerance in Plants. 221-260	
1382	From genetics to genomics in plants and animals. 2010 , 42, 177-194	1
1381	Application of molecular markers in predicting production quality of cultivated <i>Cistanche deserticola</i> . 2010 , 33, 334-9	5
1380	Quantitative disease resistance and quantitative resistance Loci in breeding. 2010 , 48, 247-68	226
1379	Marker-assisted selection of diploid and tetraploid potatoes carrying Rpi-phu1, a major gene for resistance to <i>Phytophthora infestans</i> . 2010 , 51, 133-40	21
1378	Combining DNA pooling with selective recombinant genotyping for increased efficiency in fine mapping. 2010 , 120, 775-83	
1377	Validation of QTLs for <i>Orobanche crenata</i> resistance in faba bean (<i>Vicia faba</i> L.) across environments and generations. 2010 , 120, 909-19	44
1376	Development and application of gene-based markers for the major rice QTL Phosphorus uptake 1. 2010 , 120, 1073-86	90
1375	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. 2010 , 121, 549-65	6
1374	Testing water-soluble carbohydrate QTL effects in perennial ryegrass (<i>Lolium perenne</i> L.) by marker selection. 2010 , 121, 1405-17	6
1373	Molecular marker survey and expression analyses of the rice submergence-tolerance gene SUB1A. 2010 , 121, 1441-53	73

1372	Traditional Breeding in Sugar Beet. 2010 , 12, 181-186	2
1371	Science and Society in Dialogue About Marker Assisted Selection. 2010 , 23, 317-329	2
1370	Rice genomics moves ahead. 2010 , 26, 257-273	5
1369	Three AFLP markers tightly linked to the genic male sterility ms 3 gene in chili pepper (<i>Capsicum annuum</i> L.) and conversion to a CAPS marker. 2010 , 173, 55-61	29
1368	Isolation of IGF2 and association of IGF2 polymorphism with growth trait in genetically improved farmed tilapias, <i>Oreochromis niloticus</i> L.. 2010 , 41, e743-e750	10
1367	Insertion site-based polymorphism markers open new perspectives for genome saturation and marker-assisted selection in wheat. 2010 , 8, 196-210	103
1366	Discovering plant metabolic biomarkers for phenotype prediction using an untargeted approach. 2010 , 8, 900-11	95
1365	Identification and application of a DNA-based marker that is diagnostic for the pepper (<i>Capsicum annuum</i>) bacterial spot resistance gene Bs3. 2010 , 129, 737-740	12
1364	Germplasm-regression-combined marker-trait association identification in plants. 2010 , 9, 573-580	12
1363	Molecular marker-assisted selection of the ae alleles in maize. 2010 , 9, 1074-84	2
1362	Understanding and using quantitative genetic variation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 73-85	5.8 195
1361	An improved method to quantify <i>Puccinia coronata</i> f. sp. <i>avenae</i> DNA in the host <i>Avena sativa</i> . 2010 , 32, 215-224	4
1360	Identification of grain variety and quality type. 2010 , 311-341	1
1359	Halophyte Improvement for a Salinized World. 2010 , 29, 329-359	119
1358	Development of genome-wide SNP assays for rice. 2010 , 60, 524-535	149
1357	Using genetic variability available in the breeder's pool to engineer fruit quality. 2010 , 1, 120-7	4
1356	Germplasm-regression-combined (GRC) marker-trait association identification in plant breeding: a challenge for plant biotechnological breeding under soil water deficit conditions. 2010 , 30, 192-9	8
1355	Marker-Assisted Selection as a Component of Conventional Plant Breeding. 2010 , 145-217	26

1354	Nitrogen Assimilation and its Relevance to Crop Improvement. 2010 , 1-40		16
1353	A single origin and moderate bottleneck during domestication of soybean (<i>Glycine max</i>): implications from microsatellites and nucleotide sequences. 2010 , 106, 505-14		100
1352	Genetic engineering for modern agriculture: challenges and perspectives. 2010 , 61, 443-62		702
1351	Strategic research, education and policy goals for seed science and crop improvement. 2010 , 179, 645-652		16
1350	QTL Analysis in Plant Breeding. 2010 , 3-21		4
1349	Genetic effects of major QTLs controlling low-temperature germinability in different genetic backgrounds in rice (<i>Oryza sativa</i> L.). 2010 , 53, 763-8		26
1348	Breeding technologies to increase crop production in a changing world. 2010 , 327, 818-22		1426
1347	Food security: contributions from science to a new and greener revolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010 , 365, 61-71	5.8	232
1346	Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. 2011 , 62, 439-52		216
1345	Metabolomics: creating new potentials for unraveling the mechanisms in response to salt and drought stress and for the biotechnological improvement of xero-halophytes. 2011 , 31, 153-69		50
1344	Tomato: Breeding for Improved Disease Resistance in Fresh Market and Home Garden Varieties. 2011 , 239-249		3
1343	Next generation DNA sequencing technology delivers valuable genetic markers for the genomic orphan legume species, <i>Bituminaria bituminosa</i> . 2011 , 12, 104		24
1342	Biofuels. 2011 ,		13
1341	A semi-automatic non-destructive method to quantify grapevine downy mildew sporulation. 2011 , 84, 265-71		31
1340	Assessment of genetic diversity among maize accessions using inter simple sequence repeats (ISSR) markers. 2011 , 10,		1
1339	Marker-Assisted Selection to Pyramid Nematode Resistance and the High Oleic Trait in Peanut. 2011 , 4, 110-117		125
1338	Use of molecular markers in reciprocal recurrent selection of maize increases heterosis effects. 2011 , 10, 2589-96		15
1337	Effectiveness of major resistance genes and identification of new sources for disease resistance in wheat. 2011 , 59, 241-248		2

1336	PLANT BREEDING IN BULBOUS ORNAMENTALS: ADDING WIT TO CHANCE. 2011 , 329-342	3
1335	Plant Breeding: A Success Story to be Continued Thanks to the Advances in Genomics. 2011 , 2, 51	28
1334	Locus-dependent selection in crop-wild hybrids of lettuce under field conditions and its implication for GM crop development. 2011 , 4, 648-59	20
1333	Green systems biology - From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. 2011 , 75, 284-305	148
1332	Classical Breeding in Diatoms: Scientific Background and Practical Perspectives. 2011 , 167-194	5
1331	Role of DREBs in regulation of abiotic stress responses in plants. 2011 , 62, 4731-48	573
1330	Rapid and high-precision marker assisted backcrossing to introgress the SUB1 QTL into BR11, the rainfed lowland rice mega variety of Bangladesh. 2011 , 178, 83-97	77
1329	Characterization of genes Rpp2, Rpp4, and Rpp5 for resistance to soybean rust. 2011 , 182, 53-64	41
1328	Quantitative trait loci mapping of Cercospora leaf spot resistance in mungbean, <i>Vigna radiata</i> (L.) Wilczek. 2011 , 28, 255-264	52
1327	Development, characterization, and cross-species/genera transferability of SSR markers for rubber tree (<i>Hevea brasiliensis</i>). 2011 , 30, 335-44	29
1326	SSR and EST-SSR-based genetic linkage map of cassava (<i>Manihot esculenta</i> Crantz). 2011 , 122, 1161-70	66
1325	Selection strategies for marker-assisted backcrossing with high-throughput marker systems. 2011 , 123, 251-60	41
1324	High-throughput SNP discovery and genotyping in durum wheat (<i>Triticum durum</i> Desf.). 2011 , 123, 555-69	104
1323	Comparative linkage mapping in the white button mushroom <i>Agaricus bisporus</i> provides foundation for breeding management. 2011 , 57, 39-50	20
1322	Crops that feed the world 4. Barley: a resilient crop? Strengths and weaknesses in the context of food security. 2011 , 3, 141-178	146
1321	Leaf dehydroascorbate reductase and catalase activity is associated with soil drought tolerance in bread wheat. 2011 , 33, 2169-2177	20
1320	Genome-wide patterns of genetic variation in sweet and grain sorghum (<i>Sorghum bicolor</i>). 2011 , 12, R114	194
1319	Gene expression biomarkers provide sensitive indicators of in planta nitrogen status in maize. 2011 , 157, 1841-52	70

1318	Breeding crop plants with deep roots: their role in sustainable carbon, nutrient and water sequestration. 2011 , 108, 407-18	233
1317	Association of an SNP in a novel DREB2-like gene SiDREB2 with stress tolerance in foxtail millet [<i>Setaria italica</i> (L.)]. 2011 , 62, 3387-401	111
1316	Developing rice with high yield under phosphorus deficiency: Pup1 sequence to application. 2011 , 156, 1202-16	124
1315	Tolerance of prolonged drought among a set of bread wheat chromosome substitution Lines. 2011 , 39, 343-351	5
1314	Marker-assisted breeding as next-generation strategy for genetic improvement of productivity and quality: can it be realized in cotton?. 2011 , 2011, 670104	9
1313	Molecular Breeding to Improve Salt Tolerance of Rice (<i>Oryza sativa</i> L.) in the Red River Delta of Vietnam. 2012 , 2012, 949038	59
1312	Inheritance and Genetic Mapping of Russian Wheat Aphid Resistance in Iranian Wheat Landrace Accession PI 626580. 2012 , 52, 676-682	32
1311	Genetic Linkage Map and Diversity Analysis of Tahitian Vanilla (<i>Vanilla bahitensis</i> , Orchidaceae). 2012 , 52, 795-806	8
1310	Exploitation of Elite Maize (<i>Zea mays</i> L.) Germplasm across Maturity Zones. 2012 , 52, 1534-1542	4
1309	Comparison of phenotypic versus marker-assisted background selection for the SUB1 QTL during backcrossing in rice. 2012 , 62, 216-22	15
1308	SNP markers and their impact on plant breeding. 2012 , 2012, 728398	236
1307	Assessing grain quality. 2012 , 149-187	1
1306	Fractionation, stability, and isolate-specificity of QTL for resistance to <i>Phytophthora infestans</i> in cultivated tomato (<i>Solanum lycopersicum</i>). 2012 , 2, 1145-59	24
1305	Development and Rapid Adoption of Submergence-Tolerant (Sub1) Rice Varieties. 2012 , 299-352	86
1304	Quantitative genetics in the genomics era. 2012 , 13, 196-206	36
1303	Application of genomic tools in plant breeding. 2012 , 13, 179-95	175
1302	Impact of Genomic Technologies on Chickpea Breeding Strategies. 2012 , 2, 199-221	96
1301	New aspects in quality related wheat research: II. New methodologies for better quality wheat. 2012 , 40, 307-333	19

1300	Genetic relationships and hybrid vigour in olive (<i>Olea europaea</i> L.) by microsatellites. 2012 , 131, 767-774	20
1299	Conducting molecular biomarker discovery studies in plants. 2012 , 918, 127-50	6
1298	Sequence-based marker development in wheat: advances and applications to breeding. 2012 , 30, 1071-88	98
1297	Rapid sex identification of papaya (<i>Carica papaya</i>) using multiplex loop-mediated isothermal amplification (mLAMP). 2012 , 236, 1239-46	17
1296	Analysis of RAPD and AFLP markers linked to resistance to <i>Fusarium oxysporum</i> f. sp. <i>lactucae</i> race 2 in lettuce (<i>Lactuca sativa</i> L.). 2012 , 187, 1-9	14
1295	Mapping QTLs with epistatic effects and QTL-by-environment interactions for seed coat cracking in soybeans. 2012 , 186, 933-942	20
1294	Development and characterization of genomic simple sequence repeat markers in eggplant and their application to the study of diversity and relationships in a collection of different cultivar types and origins. 2012 , 30, 647-660	44
1293	Determining resistance to <i>Pseudomonas syringae</i> in tomato, a comparison of different molecular markers. 2012 , 30, 967-974	2
1292	Evaluation of rice (<i>Oryza sativa</i> L.) near iso-genic lines with root QTLs for plant production and root traits in rainfed target populations of environment. 2012 , 137, 89-96	26
1291	Controlling rice bacterial blight in Africa: needs and prospects. 2012 , 159, 320-8	67
1290	Clarifying omics concepts, challenges, and opportunities for <i>Prunus</i> breeding in the postgenomic era. 2012 , 16, 268-83	27
1289	Genetic linkage maps of <i>Dendrobium moniliforme</i> and <i>D. officinale</i> based on EST-SSR, SRAP, ISSR and RAPD markers. 2012 , 137, 1-10	30
1288	Approaches to Increasing Salt Tolerance in Crop Plants. 2012 , 63-88	10
1287	A high-throughput apple SNP genotyping platform using the GoldenGate assay. 2012 , 494, 196-201	28
1286	Quantitative Trait Locus (QTL) meta-analysis and comparative genomics for candidate gene prediction in perennial ryegrass (<i>Lolium perenne</i> L.). 2012 , 13, 101	35
1285	An approach for jatropha improvement using pleiotropic QTLs regulating plant growth and seed yield. 2012 , 5, 42	30
1284	Re-orienting crop improvement for the changing climatic conditions of the 21st century. 2012 , 1, 7	62
1283	Increasing Food Production in Africa by Boosting the Productivity of Understudied Crops. 2012 , 2, 240-283	34

1282	Marker-assisted selection in plant breeding. 2012 , 163-184	25
1281	Marker Assisted Selection. 2012 , 424-435	2
1280	Integrating genomics and genetics to accelerate development of drought and salinity tolerant crops. 2012 , 271-286	1
1279	Biotechnologies for the management of genetic resources for food and agriculture. 2012 , 78, 1-167	24
1278	Sunflower: Improving Crop Productivity and Abiotic Stress Tolerance. 2012 , 1203-1249	9
1277	Whole genome sequencing and future breeding of rice. 2012 , 21, 10-14	1
1276	Kernel morphometric traits in hexaploid wheat (<i>Triticum aestivum</i> L.) are modulated by intricate QTL-QTL and genotype × environment interactions. 2012 , 56, 432-439	26
1275	Cloning and characterization of resistance gene candidate sequences and molecular marker development in gerbera (<i>Gerbera hybrida</i>). 2012 , 145, 68-75	9
1274	Genetic diversity and marker-assisted inbreeding in papaya. 2012 , 147, 20-28	6
1273	Marker-assisted selection in plant breeding for salinity tolerance. 2012 , 913, 305-33	14
1272	Molecular Marker Applications for Improving Sugar Content in Sugarcane. 2012 , 1-49	3
1271	Nutritionally Enhanced Staple Food Crops. 2012 , 169-291	35
1270	New Approaches to Cassava Breeding. 2012 , 427-504	29
1269	Improvement of Drought Resistance in Crops: From Conventional Breeding to Genomic Selection. 2012 , 225-259	6
1268	High-Throughput Phenotyping in Plants. 2012 ,	4
1267	Wheat: Mechanisms and Genetic Means for Improving Heat Tolerance. 2012 , 657-694	6
1266	Genetic linkage maps for Asian and American lotus constructed using novel SSR markers derived from the genome of sequenced cultivar. 2012 , 13, 653	28
1265	Impact of Molecular Technologies on Faba Bean (<i>Vicia faba</i> L.) Breeding Strategies. 2012 , 2, 132-166	43

1264	EST-SSR Marker Sets for Practical Authentication of All Nine Registered Ginseng Cultivars in Korea. 2012 , 36, 298-307	33
1263	Applied Genetics and Genomics in Alfalfa Breeding. 2012 , 2, 40-61	82
1262	Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress. 2012 ,	5
1261	Fostering molecular breeding in developing countries. 2012 , 29, 857-873	31
1260	Application of Molecular Marker-Assisted Selection (MAS) for Disease Resistance in a Practical Potato Breeding Programme. 2012 , 55, 1-13	56
1259	Molecular Markers and Their Application to Cassava Breeding: Past, Present and Future. 2012 , 5, 95-109	28
1258	RIKEN Cassava Initiative: Establishment of a Cassava Functional Genomics Platform. 2012 , 5, 110-116	9
1257	Characterization and genetic analysis of an EIN4-like sequence (CaETR-1) located in QTL(AR1) implicated in ascochyta blight resistance in chickpea. 2012 , 31, 1033-42	27
1256	Parent-offspring correlation estimate of heritability for late blight resistance conferred by an accession of the tomato wild species <i>Solanum pimpinellifolium</i> . 2012 , 131, 203-210	20
1255	Bulk segregant analysis: An effective approach for mapping consistent-effect drought grain yield QTLs in rice 2012 , 134, 185-192	42
1254	Agricultural biotechnology and smallholder farmers in developing countries. 2012 , 23, 278-85	29
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1251	Potential to improve oilseed rape and canola breeding in the genomics era. 2012 , 131, 351-360	50
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1247	Inheritance of resistance to powdery mildew in the watermelon and development of a molecular marker for selecting resistant plants. 2013 , 54, 134-140	11

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1243	Genome-wide InDel marker system for application in rice breeding and mapping studies. 2013 , 192, 131-143	28
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1240	Functional molecular markers and high-resolution melting curve analysis of low phytic acid mutations for marker-assisted selection in rice. 2013 , 31, 517-528	26
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1237	Experimental assessment of the accuracy of genomic selection in sugarcane. 2013 , 126, 2575-86	71
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1235	What is the SMARTest way to breed plants and increase agrobiodiversity?. 2013 , 194, 53-66	21
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1233	Enabling Tools for Modern Breeding of Cowpea for Biotic Stress Resistance. 2013 , 183-199	6
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1231	Molecular markers: Implementation in crop plant breeding for identification, introgression and gene pyramiding. 2013 , 3, 464-473	12
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1229	Biotechnology of Neglected and Underutilized Crops. 2013 ,	12

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1226	Evaluation of genetic diversity in Korean soybean landraces by protein banding patterns using high-throughput screening. 2013 , 16, 189-195	2
1225	QTL analysis reveals the genetic architecture of domestication traits in Crisphead lettuce. 2013 , 60, 1487-1500	23
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1223	A microfluidic droplet platform for multiplexed single nucleotide polymorphism analysis of an array plant genomic DNA samples. 2013 ,	0
1222	Field-based experimental evolution of three cereal pathogens using a markereleasecapture strategy. 2013 , 62, 106-114	21
1221	Conversion of Microsatellite Markers to Single Nucleotide Polymorphism (SNP) Markers for Genetic Fingerprinting of <i>Theobroma cacao</i> L.. 2013 , 27, 215-241	6
1220	The reliability of leaf bioassays for predicting disease resistance on fruit: a case study on grapevine resistance to downy and powdery mildew. 2013 , 62, 533-544	27
1219	QTLs associated with root traits increase yield in upland rice when transferred through marker-assisted selection. 2013 , 126, 101-8	64
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1217	Bringing the voice of consumers into plant breeding with Bayesian modelling. 2013 , 189, 365-378	5
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1215	Molecular approaches unravel the mechanism of acid soil tolerance in plants. 2013 , 1, 91-104	85
1214	Mapping epistasis and environmentQTX interaction based on four -omics genotypes for the detected QTX loci controlling complex traits in tobacco. 2013 , 1, 151-159	6
1213	An efficient marker-assisted backcrossing strategy for enhancing barley (<i>Hordeum vulgare</i> L.) production under acidity and aluminium toxicity. 2013 , 31, 855-866	8
1212	A conceptual framework for restoration of threatened plants: the effective model of American chestnut (<i>Castanea dentata</i>) reintroduction. 2013 , 197, 378-393	130
1211	Choice of shrinkage parameter and prediction of genomic breeding values in elite maize breeding populations. 2013 , 132, 99-106	14

1210	Marker-assisted breeding of Pi-1 and Piz-5 genes imparting resistance to rice blast in PRR78, restorer line of Pusa RH-10 Basmati rice hybrid. 2013 , 132, 61-69	23
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1208	Improving Salt Tolerance in Rice: Looking Beyond the Conventional. 2013 , 219-260	17
1207	Marker-Assisted Breeding for Stress Resistance in Crop Plants. 2013 , 387-426	8
1206	Application of TILLING for Orphan Crop Improvement. 2013 , 83-113	18
1205	Validation of molecular markers for pathogen resistance in potato. 2013 , 132, 246-251	21
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1203	Bioinformatics Tools for Marker Discovery in Plant Breeding. 2013 , 53, 173-179	1
1202	Genetic diversity among and within Iranian and non-Iranian barely (<i>Hordeum vulgare</i> L.) genotypes using SSR and storage proteins markers. 2013 , 46, 7-17	11
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1200	Sequence-based SNP genotyping in durum wheat. 2013 , 11, 809-17	55
1199	Validation assay of p3_VvAGL11 marker in a wide range of genetic background for early selection of stenopermy in <i>Vitis vinifera</i> L. 2013 , 54, 1021-30	23
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1197	Non-DNA Biomarkers. 2013 , 11-37	1
1196	Validation of yield-enhancing quantitative trait loci from a low-yielding wild ancestor of rice. 2013 , 32, 101-120	27
1195	Disease Resistance. 2013 , 291-314	9
1194	Increasing the density of markers around a major QTL controlling resistance to angular leaf spot in common bean. 2013 , 126, 2451-65	26
1193	Polymorphism in the insulin-related peptide gene and its association with growth traits in the Pacific oyster <i>Crassostrea gigas</i> . 2013 , 46, 36-43	19

1192	Genomics Applications to Salinity Tolerance Breeding in Rice. 2013 , 31-46	3
1191	Foxtail millet: a model crop for genetic and genomic studies in bioenergy grasses. 2013 , 33, 328-43	157
1190	Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. 2013 , 189, 183-190	32
1189	Linkage relationships among multiple QTL for horticultural traits and late blight (<i>P. infestans</i>) resistance on chromosome 5 introgressed from wild tomato <i>Solanum habrochaites</i> . 2013 , 3, 2131-46	24
1188	Development and Phenotyping of Recombinant Inbred Line (RIL) Populations for Peanut (<i>Arachis hypogaea</i>). 2013 , 40, 89-94	24
1187	Increased genomic prediction accuracy in wheat breeding through spatial adjustment of field trial data. 2013 , 3, 2105-14	62
1186	Genetic diversity revealed by single nucleotide polymorphism markers in a worldwide germplasm collection of durum wheat. 2013 , 14, 7061-88	66
1185	Proteomics: a biotechnology tool for crop improvement. 2013 , 4, 35	66
1184	Association mapping and the genomic consequences of selection in sunflower. 2013 , 9, e1003378	80
1183	Applying Genomics Tools for Breeding Submergence Tolerance in Rice. 2013 , 9-30	35
1182	Improving the content and composition of dietary fibre in wheat. 2013 , 153-169	3
1181	Genome-wide SNP Database for Marker-assisted Background Selection in Tomato. 2013 , 45, 232-239	7
1180	The UDP-glucuronate decarboxylase gene family in <i>Populus</i> : structure, expression, and association genetics. 2013 , 8, e60880	21
1179	Development and Utilization of Plant Genetic Resources for Plant Breeding. 2013 , 864-867, 2537-2540	
1178	Converting restriction fragment length polymorphism to single-strand conformation polymorphism markers and its application in the fine mapping of a trichome gene in cotton. 2013 , 132, 337-343	9
1177	Genomic prediction of northern corn leaf blight resistance in maize with combined or separated training sets for heterotic groups. 2013 , 3, 197-203	83
1176	Organization of Genes Conferring Resistance to Anthracnose in Common Bean. 2013 , 151-181	32
1175	Do transgenesis and marker-assisted backcross breeding produce substantially equivalent plants? A comparative study of transgenic and backcross rice carrying bacterial blight resistant gene Xa21. 2013 , 14, 738	21

1174	Molecular Breeding for Phosphorus-efficient Rice. 2013 , 65-82	4
1173	Plant Marker-Assisted Breeding and Conventional Breeding: Challenges and Perspectives. 2013 , 01,	6
1172	Single Nucleotide Polymorphism Genotyping for Breeding and Genetics Applications in Chickpea and Pigeonpea using the BeadXpress Platform. 2013 , 6, plantgenome2013.05.0017	45
1171	Floral transcriptome sequencing for SSR marker development and linkage map construction in the tea plant (<i>Camellia sinensis</i>). 2013 , 8, e81611	58
1170	Molecular Markers and Marker-Assisted Breeding in Plants. 2013 ,	85
1169	Genomics approaches for crop improvement against abiotic stress. 2013 , 2013, 361921	50
1168	. 2013 ,	4
1167	Evidence for Outcrossing in the Perennial Forage Legume Tедера. 2014 , 54, 2406-2412	4
1166	New cultivation approaches of <i>Artemisia annua</i> L. for a sustainable production of the antimalarial drug artemisinin. 2014 , 8, 441-447	8
1165	Construction of a SSR-based genetic map and identification of QTLs for catechins content in tea plant (<i>Camellia sinensis</i>). 2014 , 9, e93131	54
1164	Identification and validation of a new male sex-specific ISSR marker in pointed gourd (<i>Trichosanthes dioica</i> Roxb.). 2014 , 2014, 216896	6
1163	Improvement of Oat as a Winter Forage Crop in the Southern United States. 2014 , 54, 1336-1346	5
1162	Plant breeding with marker-assisted selection in Brazil. 2014 , 14, 54-60	21
1161	THE RELATIONSHIP BETWEEN HETEROSIS AND GENETIC DISTANCES BASED ON SSR MARKERS IN <i>HELIANTHUS ANNUUS</i> . 2014 , 9, 270-276	8
1160	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. 2014 , 7, plantgenome2013.12.0042	66
1159	Candidate gene analysis for determinacy in pigeonpea (<i>Cajanus</i> spp.). 2014 , 127, 2663-78	43
1158	Natural Variation as a Tool to Investigate Nutrient Use Efficiency in Plants. 2014 , 29-50	4
1157	Introgression of the high grain protein gene <i>Gpc-B1</i> in an elite wheat variety of Indo-Gangetic Plains through marker assisted backcross breeding. 2014 , 1, 60-67	42

1156	Next-generation genebanking: plant genetic resources management and utilization in the sequencing era. 2014 , 12, 298-307	30
1155	Accelerating resistance breeding in wheat by integrating marker-assisted selection and doubled haploid technology. 2014 , 31, 35-43	16
1154	Development of Plant Genetic Diversity by Biotechnology and Genomics. 2014 , 522-524, 1047-1050	
1153	Moving toward a precise nutrition: preferential loading of seeds with essential nutrients over non-essential toxic elements. 2014 , 5, 51	28
1152	Crop immunity against viruses: outcomes and future challenges. 2014 , 5, 660	168
1151	Harvesting the promising fruits of genomics: applying genome sequencing technologies to crop breeding. 2014 , 12, e1001883	256
1150	Identification and confirmation of quantitative trait loci controlling resistance to mungbean yellow mosaic disease in mungbean [<i>Vigna radiata</i> (L.) Wilczek]. 2014 , 34, 1497-1506	22
1149	Challenges and prospects in genome-wide quantitative trait loci mapping of standing genetic variation in natural populations. 2014 , 1320, 35-57	37
1148	Breeding and Transgenic Approaches for Development of Abiotic Stress Tolerance in Rice. 2014 , 153-190	1
1147	Mapping genomic loci for cotton plant architecture, yield components, and fiber properties in an interspecific (<i>Gossypium hirsutum</i> L. × <i>G. barbadense</i> L.) RIL population. 2014 , 289, 1347-67	30
1146	Targeting environmental adaptation in the monocot model <i>Brachypodium distachyon</i> : a multi-faceted approach. 2014 , 15, 801	21
1145	Application of in silico bulked segregant analysis for rapid development of markers linked to Bean common mosaic virus resistance in common bean. 2014 , 15, 903	40
1144	An Application of Molecular Tools in Plant Genetic Diversity Conservation. 2014 , 955-959, 830-833	
1143	Breeding: Plants, Modern. 2014 , 187-200	2
1142	Early Selection of <i>Larix principis-rupprechtii</i> . 2014 , 1073-1076, 1095-1098	
1141	Beyond landraces: developing improved germplasm resources for underutilized species - a case for Bambara groundnut. 2014 , 30, 127-41	16
1140	Use of Major Quantitative Trait Loci to Improve Grain Yield of Rice. 2014 , 21, 65-82	27
1139	Cadmium minimization in rice. A review. 2014 , 34, 155-173	162

1138	Mapping of quantitative trait loci (QTLs) for oil yield using SSRs and gene-based markers in African oil palm (<i>Elaeis guineensis</i> Jacq.). 2014 , 10, 1-14	42
1137	Development of novel EST-derived resistance gene markers in hop (<i>Humulus lupulus</i> L.). 2014 , 33, 61-74	5
1136	Tagging quantitative trait loci for heading date and plant height in important breeding parents of rice (<i>Oryza sativa</i>). 2014 , 197, 191-200	12
1135	Genetic and physical mapping of the QTLAR3 controlling blight resistance in chickpea (<i>Cicer arietinum</i> L.). 2014 , 198, 69-78	16
1134	Heritability and identification of QTLs and underlying candidate genes associated with the architecture of the grapevine cluster (<i>Vitis vinifera</i> L.). 2014 , 127, 1143-62	34
1133	Achieving sustainable plant disease management through evolutionary principles. 2014 , 19, 570-5	73
1132	Marker-assisted pyramiding of eight QTLs/genes for seven different traits in common wheat (<i>Triticum aestivum</i> L.). 2014 , 34, 167-175	50
1131	From genomics to functional markers in the era of next-generation sequencing. 2014 , 36, 417-26	29
1130	Quantitative Trait Loci for Resistance to <i>Stenocarpella maydis</i> and <i>Fusarium graminearum</i> Cob Rots in Tropical Maize. 2014 , 28, 214-228	5
1129	Combating Mineral Malnutrition through Iron and Zinc Biofortification of Cereals. 2014 , 13, 329-346	86
1128	Comparison of three QTL detection models on biochemical, sensory, and yield characters in <i>Coffea canephora</i> . 2014 , 10, 1541-1553	9
1127	Quantitative trait loci for quality and agronomic traits in two advanced backcross populations in oat (<i>Avena sativa</i> L.). 2014 , 133, 588-601	8
1126	Nutrient Use Efficiency in Plants. 2014 ,	14
1125	Improving breeding efficiency in potato using molecular and quantitative genetics. 2014 , 127, 2279-92	46
1124	Population structure and association mapping of flower-related traits in lotus (<i>Nelumbo Adans.</i>) accessions. 2014 , 175, 214-222	5
1123	Development of SCAR marker associated with downy mildew disease resistance in pearl millet (<i>Pennisetum glaucum</i> L.). 2014 , 41, 7815-24	25
1122	Genomic selection: genome-wide prediction in plant improvement. 2014 , 19, 592-601	366
1121	The American cranberry: first insights into the whole genome of a species adapted to bog habitat. 2014 , 14, 165	61

1120	Detection of partial resistance quantitative trait loci against <i>Didymella pinodes</i> in <i>Medicago truncatula</i> . 2014 , 33, 589-599	7
1119	Transferring a major QTL for oil content using marker-assisted backcrossing into an elite hybrid to increase the oil content in maize. 2014 , 34, 739-748	17
1118	Stacking of five favorable alleles for amylase content, fragrance and disease resistance into elite lines in rice (<i>Oryza sativa</i>) by using four HRM-based markers and a linked gel-based marker. 2014 , 34, 805-815	8
1117	Development of STS markers for <i>Verticillium</i> wilt resistance in cotton based on RGA-FLP analysis. 2014 , 34, 917-926	
1116	Fine genetic mapping of a locus controlling short internode length in melon (<i>Cucumis melo</i> L.). 2014 , 34, 949-961	20
1115	Genome-wide single nucleotide polymorphisms and insertion-deletions of <i>Oryza sativa</i> L. subsp. japonica cultivars grown near the northern limit of rice cultivation. 2014 , 34, 1007-1021	8
1114	Identification of large-effect QTL for kernel row number has potential for maize yield improvement. 2014 , 34, 1087-1096	9
1113	Marker-assisted selection and evaluation of high oil in vivo haploid inducers in maize. 2014 , 34, 1147-1158	26
1112	Genetic architecture of rind penetrometer resistance in two maize recombinant inbred line populations. 2014 , 14, 152	23
1111	QTL architecture of reproductive fitness characters in <i>Brassica rapa</i> . 2014 , 14, 66	17
1110	Linking ecophysiological modelling with quantitative genetics to support marker-assisted crop design for improved yields of rice (<i>Oryza sativa</i>) under drought stress. 2014 , 114, 499-511	32
1109	Microalgae and Biotechnology. 2014 , 57-115	
1108	Allelic variation within the S-adenosyl-L-homocysteine hydrolase gene family is associated with wood properties in Chinese white poplar (<i>Populus tomentosa</i>). 2014 , 15 Suppl 1, S4	7
1107	Genetic basis of maize kernel starch content revealed by high-density single nucleotide polymorphism markers in a recombinant inbred line population. 2015 , 15, 288	20
1106	Extreme-phenotype genome-wide association study (XP-GWAS): a method for identifying trait-associated variants by sequencing pools of individuals selected from a diversity panel. 2015 , 84, 587-96	57
1105	Genomic basis of the differences between cider and dessert apple varieties. 2015 , 8, 650-61	26
1104	Gene pyramiding and omics approaches for stress tolerance in leguminous plants. 2015 , 265-283	
1103	Biotechnological applications to improve salinity stress in wheat. 2015 , 1-27	

1102	Plant Mutation Breeding: Current Progress and Future Assessment. 2015 , 23-88	8
1101	Combining Ability for Phytophthora infestans Quantitative Resistance from Wild Tomato. 2015 , 55, 240-254	5
1100	Plant Mutation Breeding: Current Progress and Future Assessment. 2015 , 23-88	4
1099	Application of whole genome re-sequencing data in the development of diagnostic DNA markers tightly linked to a disease-resistance locus for marker-assisted selection in lupin (<i>Lupinus angustifolius</i>). 2015 , 16, 660	28
1098	The severity of wheat diseases increases when plants and pathogens are acclimatized to elevated carbon dioxide. 2015 , 21, 2661-2669	65
1097	High-Density Single Nucleotide Polymorphism Linkage Maps of Lowland Switchgrass using Genotyping-by-Sequencing. 2015 , 8, eplantgenome2014.10.0065	6
1096	Genetic characterization of angular leaf spot resistance in selected common bean landraces from Tanzania. 2015 , 14, 2943-2948	1
1095	Marker Assisted Selection: Biotechnology Tool for Rice Molecular Breeding. 2015 , 03,	7
1094	CR Dhan 407, a high-yielding rice cultivar released for the rainfed shallow lowland ecosystem of eastern India. 2015 , 15, 120-124	
1093	Molecular-assisted selection for resistance to cassava mosaic disease in <i>Manihot esculenta</i> Crantz. 2015 , 72, 520-527	7
1092	Genetic Diversity Studies on Selected Rice (<i>Oryza Sativa</i> L.) Genotypes Based on Amylose Content and Gelatinization Temperature. 2015 , 04,	1
1091	Assessing the Barley Genome Zipper and Genomic Resources for Breeding Purposes. 2015 , 8, eplantgenome2015.06.004	
1090	Genetic variation of selected quality protein maize inbred lines. 2015 , 10, 4087-4093	0
1089	Genetic Map Construction and Quantitative Trait Locus (QTL) Detection of Six Economic Traits Using an F2 Population of the Hybrid from <i>Saccharina longissima</i> and <i>Saccharina japonica</i> . 2015 , 10, e0128588	7
1088	Large-Scale SNP Discovery and Genotyping for Constructing a High-Density Genetic Map of Tea Plant Using Specific-Locus Amplified Fragment Sequencing (SLAF-seq). 2015 , 10, e0128798	54
1087	Epi-fingerprinting and epi-interventions for improved crop production and food quality. 2015 , 6, 397	26
1086	Identification of novel drought-tolerant-associated SNPs in common bean (<i>Phaseolus vulgaris</i>). 2015 , 6, 546	27
1085	Molecular Breeding Strategy and Challenges Towards Improvement of Blast Disease Resistance in Rice Crop. 2015 , 6, 886	85

1084	Validation of molecular markers associated with boron tolerance, powdery mildew resistance and salinity tolerance in field peas. 2015 , 6, 917	20
1083	Introgression of Blast Resistance Genes (Putative Pi-b and Pi-kh) into Elite Rice Cultivar MR219 through Marker-Assisted Selection. 2015 , 6, 1002	23
1082	Biotechnology: Can It Really Solve the Problems of Food Production?. 2015 , 89-95	
1081	Segregation analysis of microsatellite (SSR) markers in sugarcane polyploids. 2015 , 14, 18384-95	7
1080	Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. 2015 , 2015, 431487	268
1079	Genetic variation of 12 rice cultivars grown in Brunei Darussalam and assessment of their tolerance to saline environment. 2015 , 14, 1029-1038	2
1078	Identification of QTL for ear row number and two-ranked versus many-ranked ear in maize across four environments. 2015 , 206, 33-47	14
1077	Marker-assisted backcrossing: a useful method for rice improvement. 2015 , 29, 237-254	104
1076	Prospects of breeding high-quality rice using post-genomic tools. 2015 , 128, 1449-66	41
1075	Efficient data reduction for large-scale genetic mapping. 2015 ,	1
1074	First insights into the genotype-phenotype map of phenotypic stability in rye. 2015 , 66, 3275-84	16
1073	Decision support for cost-efficient and logistically feasible marker-assisted seedling selection in fruit breeding. 2015 , 35, 1	20
1072	A novel genetic map of pomegranate based on transcript markers enriched with QTLs for fruit quality traits. 2015 , 11, 1	23
1071	A new window of opportunity to reject process-based biotechnology regulation. 2015 , 6, 233-42	22
1070	Molecular Marker-Assisted Breeding: A Plant Breeder's Review. 2015 , 431-472	21
1069	Conventional Plant Breeding Principles and Techniques. 2015 , 115-158	21
1068	Potentials of Proteomics in Crop Breeding. 2015 , 513-537	3
1067	Marker-assisted breeding for TaALMT1, a major gene conferring aluminium tolerance to wheat. 2015 , 59, 83-91	19

1066	Molecular mapping of a stripe rust resistance gene in Chinese wheat cultivar Mianmai 41. 2015 , 14, 295-304	4
1065	Current applications, challenges, and perspectives of marker-assisted seedling selection in Rosaceae tree fruit breeding. 2015 , 11, 1	58
1064	Next-generation transcriptome sequencing, SNP discovery and validation in four market classes of peanut, <i>Arachis hypogaea</i> L. 2015 , 290, 1169-80	34
1063	Identification of SNPs linked to eight apple disease resistance loci. 2015 , 35, 1	23
1062	Planning for food security in a changing climate. 2015 , 66, 3435-50	42
1061	Marker-assisted introgression improves <i>Striga</i> resistance in an Eritrean Farmer-Preferred Sorghum Variety. 2015 , 173, 22-29	23
1060	Application of Marker Assisted Selection for Potato Virus Y Resistance in the University of Wisconsin Potato Breeding Program. 2015 , 92, 444-450	27
1059	Applied oilseed rape marker technology and genomics. 2015 , 253-295	7
1058	qEL7.2 is a pleiotropic QTL for kernel number per row, ear length and ear weight in maize (<i>Zea mays</i> L.). 2015 , 203, 429-436	11
1057	Quantitative Trait Loci from Two Genotypes of Oat (<i>Avena sativa</i>) Conditioning Resistance to <i>Puccinia coronata</i> . 2015 , 105, 239-45	16
1056	Evaluation of marker-assisted selection for the stripe rust resistance gene , introgressed from wild emmer wheat. 2015 , 35, 1	57
1055	Multiple QTLs Linked to Agro-Morphological and Physiological Traits Related to Drought Tolerance in Potato. 2015 , 33, 1286-1298	23
1054	Single-nucleotide polymorphism identification and genotyping in. 2015 , 35, 35	23
1053	Sequence-related amplified polymorphism primer screening on Chinese fir (<i>Cunninghamia lanceolata</i> (Lamb.) Hook). 2015 , 26, 101-106	5
1052	Carotenoid identification and molecular analysis of carotenoid isomerase-encoding BrCRTISO, the candidate gene for inner leaf orange coloration in Chinese cabbage. 2015 , 35, 1	8
1051	Marker-assisted breeding for transgressive seed protein content in soybean [<i>Glycine max</i> (L.) Merr]. 2015 , 128, 1061-72	21
1050	Sequence-characterized amplified polymorphism markers for selecting rind stripe pattern in watermelon (<i>Citrullus lanatus</i> L.). 2015 , 56, 341-349	16
1049	Validation of QTL for resistance to <i>Aphanomyces euteiches</i> in different pea genetic backgrounds using near-isogenic lines. 2015 , 128, 2273-88	36

1048	A SCAR marker for identifying susceptibility to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> in banana. 2015 , 191, 108-112	9
1047	Genomic selection and association mapping in rice (<i>Oryza sativa</i>): effect of trait genetic architecture, training population composition, marker number and statistical model on accuracy of rice genomic selection in elite, tropical rice breeding lines. 2015 , 11, e1004982	277
1046	Identification of Rubisco <i>rbcL</i> and <i>rbcS</i> in <i>Camellia oleifera</i> and their potential as molecular markers for selection of high tea oil cultivars. 2015 , 6, 189	16
1045	Marker-assisted introgression of bacterial blight and blast resistance into DRR17B, an elite, fine-grain type maintainer line of rice. 2015 , 35, 1	34
1044	Haploids: Constraints and opportunities in plant breeding. 2015 , 33, 812-29	141
1043	Genetic Markers, Trait Mapping and Marker-Assisted Selection in Plant Breeding. 2015 , 65-88	4
1042	Creating new interspecific hybrid and polyploid crops. 2015 , 33, 436-41	41
1041	Introduction to Marker-Assisted Crop Improvement. 2015 , 3-16	3
1040	Marker-Assisted Selection. 2015 , 259-293	0
1039	Genome-wide association mapping for yield and other agronomic traits in an elite breeding population of tropical rice (<i>Oryza sativa</i>). 2015 , 10, e0119873	105
1038	Mapping quantitative trait loci in selected breeding populations: A segregation distortion approach. 2015 , 115, 538-46	22
1037	Marker-Assisted Plant Breeding: Principles and Practices. 2015 ,	74
1036	Enhanced resistance in wheat against stem rust achieved by marker assisted backcrossing involving three independent <i>Sr</i> genes. 2015 , 2, 25-33	17
1035	Infection processes of xylem-colonizing pathogenic bacteria: possible explanations for the scarcity of qualitative disease resistance genes against them in crops. 2015 , 128, 1219-29	28
1034	Genomic variation across landscapes: insights and applications. 2015 , 207, 953-67	96
1033	Embracing new-generation 'omics' tools to improve drought tolerance in cereal and food-legume crops. 2015 , 59, 413-428	37
1032	Sequencing consolidates molecular markers with plant breeding practice. 2015 , 128, 779-95	65
1031	Introgression of multiple disease resistance into a maintainer of Basmati rice CMS line by marker assisted backcross breeding. 2015 , 203, 97-107	13

1030	Genetic diversity and assessment of markers linked to resistance and pungency genes in Capsicum germplasm. 2015 , 204, 103-119	20
1029	Gene-based molecular marker system for multiple disease resistances in tomato against Tomato yellow leaf curl virus, late blight, and verticillium wilt. 2015 , 205, 599-613	9
1028	Development and GBS-genotyping of introgression lines (ILs) using two wild species of rice, and in a common recurrent parent, 'cv. Curinga. 2015 , 35, 81	57
1027	Construction of a genetic linkage map and mapping of drought tolerance trait in Indian beverage tea. 2015 , 35, 1	15
1026	Assessing microsatellite linkage disequilibrium in wild, cultivated, and mapping populations of Theobroma cacao L. and its impact on association mapping. 2015 , 11, 1	11
1025	Review of Potato Molecular Markers to Enhance Trait Selection. 2015 , 92, 455-472	47
1024	Getting the 'MOST' out of crop improvement. 2015 , 20, 372-9	10
1023	Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. 2015 , 16, 248	17
1022	Loci and candidate gene identification for resistance to Sclerotinia sclerotiorum in soybean (Glycine max L. Merr.) via association and linkage maps. 2015 , 82, 245-55	86
1021	Salinity: Physiological Impacts on Legume Nitrogen Fixation. 2015 , 35-65	4
1020	The impact of SNP fingerprinting and parentage analysis on the effectiveness of variety recommendations in cacao. 2015 , 11, 1	28
1019	Multiple QTL for horticultural traits and quantitative resistance to Phytophthora infestans linked on Solanum habrochaites chromosome 11. 2014 , 5, 219-33	18
1018	Development of DArT-based PCR markers for selecting drought-tolerant spring barley. 2015 , 56, 299-309	14
1017	Development of genome-wide insertion/deletion markers in rice based on graphic pipeline platform. 2015 , 57, 980-91	16
1016	Development of a large set of SNP markers for assessing phylogenetic relationships between the olive cultivars composing the Israeli olive germplasm collection. 2015 , 35, 1	34
1015	Marker-Assisted Breeding. 2015 , 95-144	2
1014	Achieving crop stress tolerance and improvement--an overview of genomic techniques. 2015 , 177, 1395-408	5
1013	Dynamic Quantitative Trait Locus Analysis of Plant Phenomic Data. 2015 , 20, 822-833	44

1012	Population Improvement. 2015 , 61-77	1
1011	Cytosolic glutamine synthetase is important for photosynthetic efficiency and water use efficiency in potato as revealed by high-throughput sequencing QTL analysis. 2015 , 128, 2143-53	13
1010	Single nucleotide polymorphism markers linked to QTL for wheat yield traits. 2015 , 206, 89-101	20
1009	Multi-trait multi-environment quantitative trait loci mapping for a sugarcane commercial cross provides insights on the inheritance of important traits. 2015 , 35, 175	16
1008	Chickpea. 2015 , 85-109	6
1007	Marker-assisted backcross breeding for development of pepper varieties (<i>Capsicum annuum</i>) containing capsinoids. 2015 , 35, 1	22
1006	RNA-Seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. 2015 , 13, 613-24	151
1005	Advances in Host Plant and Rhizobium Genomics to Enhance Symbiotic Nitrogen Fixation in Grain Legumes. 2015 , 1-116	55
1004	Genomic resources in fruit plants: an assessment of current status. 2015 , 35, 438-47	13
1003	Advances to improve the eating and cooking qualities of rice by marker-assisted breeding. 2016 , 36, 87-98	23
1002	Targeted Discovery of Single-Nucleotide Polymorphisms in an Unmarked Wheat Chromosomal Region Containing the Hessian Fly Resistance Gene H33. 2016 , 56, 1106-1114	6
1001	Food Production and Ecosystem Protection. 2016 ,	0
1000	Molecular Approaches to Genetically Improve the Accumulation of Health-Promoting Secondary Metabolites in Staple Crops-A Case Study: The Lipoxygenase-B1 Genes and Regulation of the Carotenoid Content in Pasta Products. 2016 , 17,	12
999	Emerging Genetic Technologies for Improving the Security of Food Crops. 2016 , 23-41	1
998	Genomic Prediction of Manganese Efficiency in Winter Barley. 2016 , 9, plantgenome2015.09.0085	6
997	Heterotic Patterns of IITA and CIMMYT Early-Maturing Yellow Maize Inbreds under Contrasting Environments. 2016 , 108, 1321-1336	22
996	Marker Development for Rice Blast Resistance Gene Pi66(t) and Application in the USDA Rice Mini-Core Collection. 2016 , 56, 1001-1008	4
995	Exploration and Utilization of Drought-Tolerant Barley Germplasm. 2016 , 115-152	1

994	Exploration and Utilization of Waterlogging-Tolerant Barley Germplasm. 2016 , 153-179	0
993	Sorghum [<i>Sorghum bicolor</i> (L.) Moench] Genotypes with Contrasting Polyphenol Compositions Differentially Modulate Inflammatory Cytokines in Mouse Macrophages. 2016 , 2016, 1-10	8
992	Antioxidant activity, S-alk(en)yl-l-cysteine sulfoxide and polyphenol content in onion (<i>Allium cepa</i> L.) cultivars are associated with their genetic background. 2016 , 34, 127-132	2
991	Application of Genomic, Transcriptomic, and Metabolomic Technologies in <i>Arachis</i> Species. 2016 , 209-240	2
990	Successful Technologies and Approaches Used to Develop and Manage Resistance against Crop Diseases and Pests. 2016 , 43-66	11
989	Genomic Selection in the of Next Generation Sequencing for Complex Traits in Plant Breeding. 2016 , 7, 221	137
988	Novel QTL for Stripe Rust Resistance on Chromosomes 4A and 6B in Soft White Winter Wheat Cultivars. 2016 , 6, 4	14
987	Development of a RAD-Seq Based DNA Polymorphism Identification Software, AgroMarker Finder, and Its Application in Rice Marker-Assisted Breeding. 2016 , 11, e0147187	5
986	Improvement of Rice Biomass Yield through QTL-Based Selection. 2016 , 11, e0151830	17
985	CandiSSR: An Efficient Pipeline used for Identifying Candidate Polymorphic SSRs Based on Multiple Assembled Sequences. 2015 , 6, 1171	29
984	Development and Identification of SSR Markers Associated with Starch Properties and β -Carotene Content in the Storage Root of Sweet Potato (<i>Ipomoea batatas</i> L.). 2016 , 7, 223	16
983	Public Availability of a Genotyped Segregating Population May Foster Marker Assisted Breeding (MAB) and Quantitative Trait Loci (QTL) Discovery: An Example Using Strawberry. 2016 , 7, 619	10
982	Into the Wild: <i>Oryza</i> Species as Sources for Enhanced Nutrient Accumulation and Metal Tolerance in Rice. 2016 , 7, 974	12
981	Exploring New Alleles Involved in Tomato Fruit Quality in an Introgression Line Library of <i>Solanum pimpinellifolium</i> . 2016 , 7, 1172	26
980	QTLomics in Soybean: A Way Forward for Translational Genomics and Breeding. 2016 , 7, 1852	17
979	Association analysis for oxalate concentration in spinach. 2016 , 212, 17-28	23
978	A next-generation marker genotyping platform (AmpSeq) in heterozygous crops: a case study for marker-assisted selection in grapevine. 2016 , 3, 16002	57
977	Modeling of genetic gain for single traits from marker-assisted seedling selection in clonally propagated crops. 2016 , 3, 16015	5

976	Potato breeding now and into the genomics era. 2016 , 1-10	1
975	Open access resources for genome-wide association mapping in rice. 2016 , 7, 10532	229
974	Development of salt tolerant IR64 near isogenic lines through marker-assisted breeding. 2016 , 19, 373-381	12
973	Sustainable Agriculture and Plant Breeding. 2016 , 3-34	2
972	Molecular Breeding to Improve Plant Resistance to Abiotic Stresses. 2016 , 283-326	7
971	Single Nucleotide Polymorphism (SNP) Marker for Abiotic Stress Tolerance in Crop Plants. 2016 , 327-343	3
970	Association Mapping in Turkish Olive Cultivars Revealed Significant Markers Related to Some Important Agronomic Traits. 2016 , 54, 506-533	21
969	Implications of genomic selection for obtaining F2:3 families of tomato. 2016 , 207, 7-13	2
968	Construction of a genetic linkage map and QTL analysis in bambara groundnut. 2016 , 59, 459-72	23
967	Genetic diversity and population structure of Bambara groundnut (<i>Vigna subterranea</i> (L.) Verdc.): synopsis of the past two decades of analysis and implications for crop improvement programmes. 2016 , 63, 925-943	21
966	Production and Breeding of Chilli Peppers (<i>Capsicum</i> spp.). 2016 ,	5
965	Molecular Markers in <i>Capsicum</i> spp. Breeding. 2016 , 81-95	1
964	Development of SNP-based assays for disease resistance and fruit quality traits in apple (<i>Malus domestica</i> Borkh.) and validation in breeding pilot studies. 2016 , 12, 1	24
963	Recurrent parent genome recovery in different populations with the introgression of Sub1 gene from a cross between MR219 and Swarna-Sub1. 2016 , 207, 605-618	9
962	Identification of the target region including the Foc0 1 /foc0 1 gene and development of near isogenic lines for resistance to Fusarium Wilt race 0 in chickpea. 2016 , 210, 119-133	10
961	Characterization of genome-wide simple sequence repeats and application in interspecific genetic map integration in kiwifruit. 2016 , 12, 1	4
960	Effect of Lr34/Yr18 on agronomic and quality traits in a spring wheat mapping population and implications for breeding. 2016 , 36, 1	16
959	Association mapping of caffeine content with TCS1 in tea plant and its related species. 2016 , 105, 251-259	14

958	Construction of a genetic linkage map and analysis of quantitative trait loci associated with the agronomically important traits of <i>Pleurotus eryngii</i> . 2016 , 92, 50-64	16
957	The Onion Genomic Resource: A genomics and bioinformatics driven resource for onion breeding. 2016 , 8, 9-15	6
956	When more is better: how data sharing would accelerate genomic selection of crop plants. 2016 , 212, 814-826	51
955	Advances in breeding and biotechnology of legume crops. 2016 , 127, 561-584	27
954	Sorghum. 2016 , 163-203	7
953	QTL and candidate genes associated with common bacterial blight resistance in the common bean cultivar Longyundou 5 from China. 2016 , 4, 344-352	11
952	Isolated Microspore Culture and Its Applications in Plant Breeding and Genetics. 2016 , 487-507	15
951	Using genomic information to improve soybean adaptability to climate change. 2017 , 68, 1823-1834	15
950	Identification and mapping of resistance to stem rust in the European winter wheat cultivars Spark and Rialto. 2016 , 36, 1	2
949	Methods of high-throughput plant phenotyping for large-scale breeding and genetic experiments. 2016 , 52, 688-701	23
948	Association of single nucleotide polymorphisms with form traits in three New Zealand populations of radiata pine in the presence of genotype by environment interactions. 2016 , 12, 1	13
947	Cold tolerance during juvenile development in sorghum: a comparative analysis by genomewide association and linkage mapping. 2016 , 135, 598-606	18
946	Genetic Linkage Map of Cassava (<i>Manihot esculenta</i> Crantz) Based on Rubber Tree and Cassava Simple Sequence Repeat Markers. 2016 , 30, 552-561	
945	Ex Ante Welfare Analysis of Technological Change: The Case of Nitrogen Efficient Maize for African Soils. 2016 , 64, 147-168	5
944	The future of food. 2016 , 41, 192-196	
943	Molecular Markers and Crop Improvement. 2016 , 381-410	2
942	QTL mapping of grain appearance quality traits and grain weight using a recombinant inbred population in rice (<i>Oryza sativa</i> L.). 2016 , 15, 1693-1702	5
941	Evaluation of the Ph-3 gene-specific marker developed for marker-assisted selection of late blight-resistant tomato. 2016 , 135, 636-642	3

940	Development and Validation of High-Resolution Melting Markers Derived from Ry STS Markers for High-Throughput Marker-Assisted Selection of Potato Carrying Ry. 2016 , 106, 1366-1375	11
939	Building strong relationships between conservation genetics and primary industry leads to mutually beneficial genomic advances. 2016 , 25, 5267-5281	12
938	Mapping of male sterility gene ms10 in chilli pepper (<i>Capsicum annuum</i> L.). 2016 , 135, 531-535	10
937	Genetic diversity and association analysis of leafminer (<i>Liriomyza langei</i>) resistance in spinach (<i>Spinacia oleracea</i>). 2016 , 59, 581-8	11
936	A high-density genetic map and growth related QTL mapping in bighead carp (<i>Hypophthalmichthys nobilis</i>). 2016 , 6, 28679	58
935	Smart Engineering of Genetic Resources for Enhanced Salinity Tolerance in Crop Plants. 2016 , 35, 146-189	130
934	Biomass traits and candidate genes for bioenergy revealed through association genetics in coppiced European Populus nigra (L.). 2016 , 9, 195	24
933	Application of subtracted gDNA microarray-assisted Bulk Segregant Analysis for rapid discovery of molecular markers associated with day-neutrality in strawberry (<i>Fragaria x ananassa</i>). 2016 , 6, 32551	3
932	Identification of QTL for maize grain yield and kernel-related traits. 2016 , 95, 239-47	15
931	Genome-wide association mapping of glyphosate-resistance in <i>Gossypium hirsutum</i> races. 2016 , 209, 209-221	7
930	SSR-based genetic mapping and QTL analysis for timing of spring bud flush, young shoot color, and mature leaf size in tea plant (<i>Camellia sinensis</i>). 2016 , 12, 1	33
929	Rapid identification of rice blast resistance gene by specific length amplified fragment sequencing. 2016 , 30, 462-468	5
928	Potential for oilseed rape resistance in pollen beetle control. 2016 , 10, 463-475	13
927	Association mapping of leaf traits in spinach (<i>Spinacia oleracea</i> L.). 2016 , 135, 399-404	17
926	The first genetic linkage map of <i>Primulina eburnea</i> (Gesneriaceae) based on EST-derived SNP markers. 2016 , 95, 377-82	2
925	Biotechnology Towards Energy Crops. 2016 , 58, 149-58	7
924	Genetic diversity and association analysis of two duplicated ODC genes polymorphisms with weight gain in <i>Cyprinus carpio</i> L.. 2016 , 459, 14-18	
923	Towards development of new ornamental plants: status and progress in wide hybridization. 2016 , 244, 1-17	34

922	Genetic mapping and inheritance of Russian wheat aphid resistance gene in accession IG 100695. 2016 , 135, 21-25	7
921	High-density genetic map of <i>Miscanthus sinensis</i> reveals inheritance of zebra stripe. 2016 , 8, 616-630	16
920	Genetic dissection of fruiting body-related traits using quantitative trait loci mapping in <i>Lentinula edodes</i> . 2016 , 100, 5437-52	11
919	Manufacturing a natural advantage: capturing place-based technology rents in the genetically modified corn seed industry. 2016 , 2, 41-52	4
918	Introgression and Exploitation of Biotic Stress Tolerance from Related Wild Species in Wheat Cultivars. 2016 , 269-324	4
917	Single nucleotide polymorphism tightly linked to a major QTL on chromosome 7A for both kernel length and kernel weight in wheat. 2016 , 36, 1	29
916	Verification of marker-trait associations in biparental winter barley (<i>Hordeum vulgare</i> L.) DH populations. 2016 , 36, 1	6
915	Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. 2016 , 116, 395-408	173
914	A DNA test for routine prediction in breeding of sweet cherry fruit color, Pav-Rf-SSR. 2016 , 36, 1	14
913	Association analysis of cowpea bacterial blight resistance in USDA cowpea germplasm. 2016 , 208, 143-155	30
912	Discovery of QTL for stay-green and heat-stress in barley (<i>Hordeum vulgare</i>) grown under simulated abiotic stress conditions. 2016 , 207, 305-317	32
911	Identification of potato cyst nematode resistant genotypes using molecular markers. 2016 , 198, 21-26	5
910	Why India Needs Biotechnology to Ensure Food and Nutrition Security?. 2016 , 313-324	
909	Improving salt tolerance of lowland rice cultivar 'Rassi' through marker-aided backcross breeding in West Africa. 2016 , 242, 288-299	43
908	Maize hybrids derived from GM positive and negative segregant inbreds are compositionally equivalent: any observed differences are associated with conventional backcrossing practices. 2016 , 25, 83-96	5
907	Advances in <i>Dendrobium</i> molecular research: Applications in genetic variation, identification and breeding. 2016 , 95, 196-216	38
906	Development of molecular markers linked to disease resistance genes in common bean based on whole genome sequence. 2016 , 242, 351-357	67
905	Enhancing spot blotch resistance in wheat by marker-aided backcross breeding. 2016 , 207, 119-133	10

904	Transgenic trait deployment using designed nucleases. 2016 , 14, 503-9	24
903	Fine mapping for double podding gene in chickpea. 2016 , 129, 77-86	15
902	Can functional hologenomics aid tackling current challenges in plant breeding?. 2016 , 15, 288-97	34
901	From QTL to variety-harnessing the benefits of QTLs for drought, flood and salt tolerance in mega rice varieties of India through a multi-institutional network. 2016 , 242, 278-287	126
900	Haplotypic Diversity and Virulence of <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> Population Infecting the First Superfine Aromatic Basmati Hybrid. 2017 , 87, 1005-1014	1
899	Benefits of the development and dissemination of climate-smart rice: ex ante impact assessment of drought-tolerant rice in South Asia. 2017 , 22, 879-901	24
898	Wheat defense response to <i>Fusarium</i> head blight and possibilities of its improvement. 2017 , 98, 9-17	3
897	The importance of yellow horn (<i>Xanthoceras sorbifolia</i>) for restoration of arid habitats and production of bioactive seed oils. 2017 , 99, 504-512	17
896	Identification of the QTL underlying the vitamin E content of soybean seeds. 2017 , 136, 147-154	5
895	Role of Biotechnology in Rice Production. 2017 , 487-547	5
894	Cadmium in rice: Transport mechanisms, influencing factors, and minimizing measures. 2017 , 224, 622-630	205
893	Genome-wide SNP identification, linkage map construction and QTL mapping for seed mineral concentrations and contents in pea (<i>Pisum sativum</i> L.). 2017 , 17, 43	44
892	Mapping QTLs for 100-seed weight in an interspecific soybean cross of Williams 82 (<i>Glycine max</i>) and PI 366121 (<i>Glycine soja</i>). 2017 , 68, 148	11
891	High-Throughput Phenotyping and QTL Mapping Reveals the Genetic Architecture of Maize Plant Growth. 2017 , 173, 1554-1564	133
890	A DNA test for routine prediction in breeding of peach blush, Ppe-RF-SSR. 2017 , 37, 1	11
889	Speed breeding for multiple disease resistance in barley. 2017 , 213, 1	59
888	Beyond the dichotomy of instrumentality and non-instrumentality of knowledge production: The case of generation challenge programme. 2017 , 44, 583-597	4
887	Molecular stacking of wide compatibility gene, S5 n and elongated uppermost internode (eui) gene into IR 58025B, an elite maintainer line of rice. 2017 , 26, 425-435	3

886	Verification and fine mapping of qGW1.05, a major QTL for grain weight in maize (<i>Zea mays</i> L.). 2017 , 292, 871-881	12
885	RAPD assisted selection of black gram (<i>Vigna mungo</i> L. Hepper) towards the development of multiple disease resistant germplasm. 2017 , 7, 1	66
884	Introgression of Pi2 and Pi5 Genes for Blast (<i>Magnaporthe oryzae</i>) Resistance in Rice and Field Evaluation of Introgression Lines for Resistance and Yield Traits. 2017 , 165, 397-405	2
883	Towards new sources of resistance to the currant-lettuce aphid (). 2017 , 37, 4	10
882	Genetic diversity of tropical maize inbred lines combining resistance to <i>Striga hermonthica</i> with drought tolerance using SNP markers. 2017 , 136, 338-343	20
881	Identification and validation of root length QTLs for water stress resistance in hexaploid wheat (<i>Triticum aestivum</i> L.). 2017 , 213, 1	21
880	Development of a high-resolution melting approach for reliable and cost-effective genotyping of PPVres locus in apricot (<i>P. armeniaca</i>). 2017 , 37, 1	6
879	A genome-wide association study of 23 agronomic traits in Chinese wheat landraces. 2017 , 91, 861-873	64
878	Marker assisted selection (MAS) towards generating stress tolerant crop plants. 2017 , 11, 205-218	8
877	High-resolution mapping reveals linkage between genes in common bean cultivar Ouro Negro conferring resistance to the rust, anthracnose, and angular leaf spot diseases. 2017 , 130, 1705-1722	14
876	Genome-wide SNP discovery and QTL mapping for fruit quality traits in inbred backcross lines (IBLs) of <i>solanum pimpinellifolium</i> using genotyping by sequencing. 2017 , 18, 1	249
875	Validation of Fusarium Head Blight Resistance QTL in US Winter Wheat. 2017 , 57, 1-12	177
874	Marker-Assisted Selection and Genomic Selection. 2017 , 275-291	1
873	Genome-wide study of an elite rice pedigree reveals a complex history of genetic architecture for breeding improvement. 2017 , 7, 45685	10
872	DNA-informed breeding of rosaceous crops: promises, progress and prospects. 2017 , 4, 17006	44
871	Biometric and biotechnology strategies in <i>Jatropha</i> genetic breeding for biodiesel production. 2017 , 76, 894-904	27
870	Molecular Markers and Marker-Assisted Selection in Crop Plants. 2017 , 295-328	4
869	Breeding for Disease Resistance. 2017 , 69-76	10

868	Marker-Assisted Selection. 2017 , 183-197	5
867	Construction of a High-Density American Cranberry (Ait.) Composite Map Using Genotyping-by-Sequencing for Multi-pedigree Linkage Mapping. 2017 , 7, 1177-1189	18
866	Modelling the effect of gene deployment strategies on durability of plant resistance under selection. 2017 , 97, 10-17	13
865	Canalization of Tomato Fruit Metabolism. 2017 , 29, 2753-2765	34
864	Cisgenesis and Intragenesis as New Strategies for Crop Improvement. 2017 , 191-216	2
863	Morphological variation and marker-fruit trait associations in a collection of grape (<i>Vitis vinifera</i> L.). 2017 , 225, 771-782	12
862	Arbuscular Mycorrhizal Technology Based on Ecosystem Services Rendered by Native Flora for Improving Phosphorus Nutrition of Upland Rice: Status and Prospect. 2017 , 87-105	1
861	Increased genomic prediction accuracy in wheat breeding using a large Australian panel. 2017 , 130, 2543-2555	25
860	The Tartary Buckwheat Genome Provides Insights into Rutin Biosynthesis and Abiotic Stress Tolerance. 2017 , 10, 1224-1237	134
859	Exploring new alleles for frost tolerance in winter rye. 2017 , 130, 2151-2164	16
858	Association mapping revealed SNP markers for adaptation to low phosphorus conditions and rock phosphate response in USDA cowpea (<i>Vigna unguiculata</i> (L.) Walp.) germplasm. 2017 , 213, 1	6
857	New insight into the mechanism of heterofertilization during maize haploid induction. 2017 , 213, 1	5
856	Strategies for Enhancing Phytonutrient Content in Plant-Based Foods. 2017 , 203-232	2
855	Molecular Analysis of Date Palm Genetic Diversity Using Random Amplified Polymorphic DNA (RAPD) and Inter-Simple Sequence Repeats (ISSRs). 2017 , 1638, 143-152	4
854	Towards CRISPR/Cas crops - bringing together genomics and genome editing. 2017 , 216, 682-698	165
853	Inheritance and a major quantitative trait locus of seed starch content in mungbean (<i>Vigna radiata</i> (L.) Wilczek). 2017 , 213, 1	3
852	Rapid location of <i>Glomerella</i> leaf spot resistance gene locus in apple by whole genome re-sequencing. 2017 , 37, 1	7
851	Oxidative discolouration in whole-head and cut lettuce: biochemical and environmental influences on a complex phenotype and potential breeding strategies to improve shelf-life. 2017 , 213, 180	14

850	Genetic Aspects and Strategies for Obtaining Hybrids. 2017 , 35-87	4
849	Novel technologies in doubled haploid line development. 2017 , 15, 1361-1370	63
848	Identification of transposable element markers associated with yield and quality traits from an association panel of independent mutants in peanut (<i>Arachis hypogaea</i> L.). 2017 , 213, 1	7
847	Assessment of SNP and InDel Variations Among Rice Lines of Tulaipanji x Ranjit. 2017 , 24, 336-348	4
846	Current Status of Conventional and Molecular Interventions for Blast Resistance in Rice. 2017 , 24, 299-321	38
845	Quantitative trait loci analysis for net ginning energy requirements in upland cotton (<i>Gossypium hirsutum</i> L.). 2017 , 213, 1	1
844	Molecular progress in sugar beet breeding for resistance to biotic stresses in sub-arid conditions-current status and perspectives. 2017 , 20, 99-105	7
843	Analysis of a major rice blast resistance gene in the rice restorer line Hanghui 1179. 2017 , 213, 1	3
842	Genotyping-by-sequencing approaches to characterize crop genomes: choosing the right tool for the right application. 2017 , 15, 149-161	159
841	Plant Biotechnology and Agriculture. 2017 , 415-452	2
840	Marker-assisted introgression of broad-spectrum blast resistance genes into the cultivated MR219 rice variety. 2017 , 97, 2810-2818	13
839	Identification of loci controlling forage yield and nutritive value in diploid alfalfa using GBS-GWAS. 2017 , 130, 261-268	40
838	Breeding approaches and genomics technologies to increase crop yield under low-temperature stress. 2017 , 36, 1-35	75
837	Identification and Mapping of Adult Plant Resistance Loci to Leaf Rust and Stripe Rust in Common Wheat Cultivar Kundan. 2017 , 101, 456-463	24
836	Genomics-assisted breeding [A revolutionary strategy for crop improvement. 2017 , 16, 2674-2685	33
835	MSDB: A Comprehensive Database of Simple Sequence Repeats. 2017 , 9, 1797-1802	14
834	. 2017 ,	4
833	Development of Species-Specific Microsatellite Markers for Broomcorn Millet (<i>Panicum miliaceum</i> L.) via High-Throughput Sequencing. 2017 , 05,	1

832	Wheat resistance to Fusarium head blight and possibilities of its improvement using molecular marker-assisted selection. 2017 , 53, 47-54	5
831	Calcium Biofortification: Three Pronged Molecular Approaches for Dissecting Complex Trait of Calcium Nutrition in Finger Millet () for Devising Strategies of Enrichment of Food Crops. 2016 , 7, 2028	51
830	Genome Analysis Identified Novel Candidate Genes for Ascochyta Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. 2017 , 8, 359	29
829	Elite Haplotypes of a Protein Kinase Gene Associated with Important Agronomic Traits in Common Wheat. 2017 , 8, 368	22
828	Insight into MAS: A Molecular Tool for Development of Stress Resistant and Quality of Rice through Gene Stacking. 2017 , 8, 985	65
827	Genome-Wide Association Study Reveals Natural Variations Contributing to Drought Resistance in Crops. 2017 , 8, 1110	30
826	Searching for an Accurate Marker-Based Prediction of an Individual Quantitative Trait in Molecular Plant Breeding. 2017 , 8, 1182	17
825	Identification of Major Quantitative Trait Loci for Seed Oil Content in Soybeans by Combining Linkage and Genome-Wide Association Mapping. 2017 , 8, 1222	48
824	Quantitative Resistance to Plant Pathogens in Pyramiding Strategies for Durable Crop Protection. 2017 , 8, 1838	93
823	Marker-Assisted Selection in Disease Resistance Breeding. 2017 , 187-213	4
822	Identification of Grain Variety and Quality Type. 2017 , 453-492	0
821	Rosaceae Fruit Development, Ripening and Post-harvest: An Epigenetic Perspective. 2017 , 8, 1247	41
820	Fusarium 'Wilt' Affecting 'Chickpea' Crop. 2017 , 7, 23	36
819	Potential Uses of Wild Germplasms of Grain Legumes for Crop Improvement. 2017 , 18,	40
818	Trade, Diplomacy, and Warfare: The Quest for Elite Rhizobia Inoculant Strains. 2017 , 8, 2207	47
817	A Multidisciplinary Phenotyping and Genotyping Analysis of a Mapping Population Enables Quality to Be Combined with Yield in Rice. 2017 , 4, 32	7
816	Breeding DifferentlyThe Digital Revolution: High-Throughput Phenotyping and Genotyping. 2017 , 60, 337-352	9
815	Assessment of genetic diversity and yield performance in Jordanian barley (<i>Hordeum vulgare</i> L.) landraces grown under Rainfed conditions. 2017 , 17, 191	20

814	Reproducible genomic DNA preparation from diverse crop species for molecular genetic applications. 2017 , 13, 106	10
813	Application of sequence specific amplified polymorphism (SSAP) and simple sequence repeat (SSR) markers for variability and molecular assisted selection (MAS) studies of the Mexican guava. 2017 , 12, 2372-2387	3
812	Modified Method of High Quality Genomic DNA Extraction from Mungbean [Vigna radiata(L.) Wilczek] Suitable for PCR Based Amplification. 2017 , 10, 1-7	4
811	Introgressed Genomic Regions in a Set of Near-Isogenic Lines of Common Bean Revealed by Genotyping-by-Sequencing. 2017 , 10, plantgenome2016.08.0081	8
810	Wheat in Kenya: Past and Twenty-First Century Breeding. 2017 ,	2
809	Genetic diversity and association mapping of mineral element concentrations in spinach leaves. 2017 , 18, 941	20
808	Genetic diversity and population structure analysis of spinach by single-nucleotide polymorphisms identified through genotyping-by-sequencing. 2017 , 12, e0188745	23
807	Genetic Mapping Populations for Conducting High-Resolution Trait Mapping in Plants. 2018 , 164, 109-138	38
806	Transcriptomic signature of drought response in pearl millet (Pennisetum glaucum (L.) and development of web-genomic resources. 2018 , 8, 3382	31
805	Identification of quantitative trait loci for leaf-related traits in an IBM Syn10 DH maize population across three environments. 2018 , 137, 127-138	11
804	Population genomics of sorghum (Sorghum bicolor) across diverse agroclimatic zones of Niger. 2018 , 61, 223-232	13
803	Current status and future possibilities of molecular genetics techniques in Brassica napus. 2018 , 40, 479-492	6
802	Efficient genome-wide genotyping strategies and data integration in crop plants. 2018 , 131, 499-511	38
801	Plant genetic resources for food and agriculture: opportunities and challenges emerging from the science and information technology revolution. 2018 , 217, 1407-1419	59
800	Induced mutation analysis with biochemical and molecular characterization of high yielding lentil mutant lines. 2018 , 109, 167-179	18
799	funRiceGenes dataset for comprehensive understanding and application of rice functional genes. 2018 , 7, 1-9	55
798	The validation of two major QTLs related to the timing of spring bud flush in Camellia sinensis. 2018 , 214, 1	4
797	From Pinot to Xinomavro in the world's future wine-growing regions. 2018 , 8, 29-37	57

796	Molecular Markers and Their Role in Producing Salt-Tolerant Crop Plants. 2018 , 381-399	0
795	Identification of SSR and retrotransposon-based molecular markers linked to morphological characters in oily sunflower (<i>Helianthus annuus</i>) L.) under natural and water-limited states. 2018 , 97, 189-203	3
794	Marker-assisted introgression of three dominant blast resistance genes into an aromatic rice cultivar Mushk Budji. 2018 , 8, 4091	19
793	Seeds of accumulation: Molecular breeding and the seed corn industry in Hawaii 2018 , 18, 370-384	5
792	Synthetic genetic circuits in crop plants. 2018 , 49, 16-22	32
791	Effectiveness of predictive markers for marker assisted selection of pro-vitamin A carotenoids in medium-late maturing maize (<i>Zea mays</i> L.) inbred lines. 2018 , 79, 27-34	19
790	Association analysis of salt tolerance in cowpea (<i>Vigna unguiculata</i> (L.) Walp) at germination and seedling stages. 2018 , 131, 79-91	24
789	Understanding and engineering plant form. 2018 , 79, 68-77	7
788	Development of CACTA transposon derived SCAR markers and their use in population structure analysis in <i>Zea mays</i> . 2018 , 146, 1-12	8
787	Unlocking the diversity of genebanks: whole-genome marker analysis of Swiss bread wheat and spelt. 2018 , 131, 407-416	20
786	A Review of Genetic Advances Related to Sex Control and Manipulation in Tilapia. 2018 , 49, 277-291	21
785	Rust resistance in faba bean (<i>Vicia faba</i> L.): status and strategies for improvement. 2018 , 47, 71-81	9
784	Marker assisted backcrossing for introgression of Fusarium wilt resistance gene into melon. 2018 , 214, 1	2
783	Trends in plant research using molecular markers. 2018 , 247, 543-557	63
782	Adaptation and mitigation of climate change in vegetable cultivation: a review. 2018 , 9, 17-36	8
781	Molecular breeding technologies and strategies for rust resistance in wheat (<i>Triticum aestivum</i>) for sustained food security. 2018 , 67, 771-791	23
780	Bruchid pest management in pulses: past practices, present status and use of modern breeding tools for development of resistant varieties. 2018 , 172, 4-19	22
779	Strategies for Enhanced Crop Resistance to Insect Pests. 2018 , 69, 637-660	82

778	Breeding of the new Saccharina variety Banhai with high-yield. 2018 , 485, 59-65	4
777	DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. 2018 , 32, 261-285	272
776	Securing Diversity for Food Security: The Case of Conservation and Use of Rice Genetic Resources. 2018 ,	
775	Advances in DNA Markers and Breeding for Warm- and Cool-Season Turfgrasses. 2018 , 119-165	3
774	Marker-assisted pyramiding of Xa21 and Xa7 genes conferring resistance to bacterial leaf blight in indica cultivar Bacthomb7. 2018 , 17, 1389-1396	1
773	Iron Biofortification of Rice: Progress and Prospects. 2018 ,	10
772	Alternative markers linked to the Phg-2 angular leaf spot resistance locus in common bean using the Phaseolus genes marker database. 2018 , 17, 818-828	11
771	Breeding Low-Cadmium Wheat: Progress and Perspectives. 2018 , 8, 249	17
770	Molecular Breeding for Plant Factory: Strategies and Technology. 2018 , 301-323	1
769	QTL-seq and marker development for resistance to Fusarium oxysporum f. sp. niveum race 1 in cultivated watermelon. 2018 , 38, 1	13
768	Association mapping of quantitative resistance to charcoal root rot in mulberry germplasm. 2018 , 13, e0200099	8
767	Molecular marker assisted selection for increasing inbreeding in S1 populations of cassava. 2018 , 90, 3853-3869	2
766	Genome-wide association study of kernel moisture content at harvest stage in maize. 2018 , 68, 622-628	12
765	Generation and Evaluation of Modified Popcorn Suggests a Route to Quality Protein Popcorn. 2018 , 9, 1803	14
764	Multivariate GBLUP Improves Accuracy of Genomic Selection for Yield and Fruit Weight in Biparental Populations of Ait. 2018 , 9, 1310	25
763	Genomic Prediction in a Multiploid Crop: Genotype by Environment Interaction and Allele Dosage Effects on Predictive Ability in Banana. 2018 , 11, 170090	33
762	Broad resistance of RD6 introgression lines with xa5 gene from IR62266 rice variety to bacterial leaf blight disease for rice production in Northeastern Thailand. 2018 , 52, 241-245	4
761	Three new approaches to genomic selection. 2018 , 137, 673-681	5

760	Molecular breeding for resistance to black rot [<i>Xanthomonas campestris</i> pv. <i>campestris</i> (Pammel) Dowson] in Brassicas: recent advances. 2018 , 214, 1	20
759	Selection criteria for SNP loci to maximize robustness of high-resolution melting analysis for plant breeding. 2018 , 68, 488-498	8
758	Importance of Mineral Nutrition for Mitigating Aluminum Toxicity in Plants on Acidic Soils: Current Status and Opportunities. 2018 , 19,	73
757	Breeding for Anthracnose Disease Resistance in Chili: Progress and Prospects. 2018 , 19,	20
756	Unraveling the Roles of Regulatory Genes during Domestication of Cultivated : Evidence and Insights from Comparative and Evolutionary Genomics. 2018 , 9,	8
755	Identification, analysis and development of salt responsive candidate gene based SSR markers in wheat. 2018 , 18, 249	19
754	Plant Genetics and Molecular Biology. 2018 ,	4
753	Genome-Wide Association Mapping in a Rice MAGIC Plus Population Detects QTLs and Genes Useful for Biofortification. 2018 , 9, 1347	53
752	Simple Sequence Repeat (SSR) Genetic Linkage Map of D Genome Diploid Cotton Derived from an Interspecific Cross between <i>Gossypium davidsonii</i> and <i>Gossypium klotzschianum</i> . 2018 , 19,	21
751	Crop Productivity in Changing Climate. 2018 , 213-241	3
750	Association mapping in rice: basic concepts and perspectives for molecular breeding. 2018 , 21, 159-176	16
749	An Update on Genetic Modification of Chickpea for Increased Yield and Stress Tolerance. 2018 , 60, 651-663	15
748	Molecular and genetic characterization of the Ry locus on chromosome XI from Andigena potatoes conferring extreme resistance to potato virus Y. 2018 , 131, 1925-1938	19
747	Molecular validation of Rpp5 gene linked to soybean rust resistance in Indian genotypes. 2018 , 71, 275-278	1
746	Variance, Inter-Trait Correlation, Heritability, and Marker-Trait Association of Rubber Yield-Related Characteristics in <i>Taraxacum kok-saghyz</i> . 2018 , 36, 576-587	5
745	Marker-assisted backcross breeding for improvement of drought tolerance in bread wheat (<i>Triticum aestivum</i> L. em Thell). 2018 , 137, 514-526	23
744	Genomic prediction of crown rust resistance in <i>Lolium perenne</i> . 2018 , 19, 35	17
743	Recombinant Promoter (MUASCsV8CP) Driven Totiviral Killer Protein 4 (KP4) Imparts Resistance Against Fungal Pathogens in Transgenic Tobacco. 2018 , 9, 278	13

742	Breeding of Coconut (<i>Cocos Nucifera</i> L.): The Tree of Life. 2018 , 673-725	4
741	QTL Mapping of Fiber Quality and Yield-Related Traits in an Intra-Specific Upland Cotton Using Genotype by Sequencing (GBS). 2018 , 19,	35
740	Maize Combined Insect Resistance Genomic Regions and Their Co-localization With Cell Wall Constituents Revealed by Tissue-Specific QTL Meta-Analyses. 2018 , 9, 895	14
739	Triticale Improvement for Forage and Cover Crop Uses in the Southern Great Plains of the United States. 2018 , 9, 1130	25
738	Identification and expression of genes in response to cassava bacterial blight infection. 2018 , 59, 391-403	3
737	Virulence adaptation in a rice leafhopper: Exposure to ineffective genes compromises pyramided resistance. 2018 , 113, 40-47	4
736	Genetic Engineering of Horticultural Crops. 2018 , 23-46	9
735	Identification of Phenotypic Variation and Genetic Diversity in Rice (<i>Oryza sativa</i> L.) Mutants. 2018 , 8, 30	15
734	Sensing Technologies for Precision Phenotyping in Vegetable Crops: Current Status and Future Challenges. 2018 , 8, 57	47
733	Genome-Wide Linkage Mapping of Quantitative Trait Loci for Late-Season Physiological and Agronomic Traits in Spring Wheat under Irrigated Conditions. 2018 , 8, 60	8
732	Identifying molecular markers suitable for Frl selection in tomato breeding. 2018 , 131, 2099-2105	11
731	Genetic Dissection and Simultaneous Improvement of Drought and Low Nitrogen Tolerances by Designed QTL Pyramiding in Rice. 2018 , 9, 306	29
730	Advanced Innovative Tools in Lemon (<i>Citrus limon</i> L.) Breeding. 2018 , 437-463	2
729	Genome-wide characterization of simple sequence repeats in <i>Pyrus bretschneideri</i> and their application in an analysis of genetic diversity in pear. 2018 , 19, 473	14
728	IR64: a high-quality and high-yielding mega variety. 2018 , 11, 18	82
727	The Spring of Systems Biology-Driven Breeding. 2018 , 23, 706-720	27
726	Carbohydrate reserves and seed development: an overview. 2018 , 31, 263-290	25
725	Development and validation of diagnostic markers for Fhb1 region, a major QTL for Fusarium head blight resistance in wheat. 2018 , 131, 2371-2380	40

724	Mapping of Quantitative Trait Loci for Resistance to Fall Armyworm and Southwestern Corn Borer Leaf-Feeding Damage in Maize. 2018 , 58, 529-539	12
723	Marker-Assisted Breeding for Disease Resistance in Crop Plants. 2018 , 41-57	3
722	Nitrogen Assimilation and its Relevance to Crop Improvement. 2018 , 1-40	10
721	Combined bulked segregant sequencing and traditional linkage analysis for identification of candidate gene for purple leaf sheath in maize. 2018 , 13, e0190670	4
720	History of Plant Biotechnology Development. 2018 , 3-37	
719	Fruit Ripening and QTL for Fruit Quality in the Octoploid Strawberry. 2018 , 95-113	2
718	Genetic dissection of the relationships between grain yield components by genome-wide association mapping in a collection of tetraploid wheats. 2018 , 13, e0190162	33
717	Harnessing Genetic Resources in Field Crops for Developing Resilience to Climate Change. 2018 , 597-621	3
716	Quantitative and comparative analysis of whole-plant performance for functional physiological traits phenotyping: New tools to support pre-breeding and plant stress physiology studies. 2019 , 282, 49-59	27
715	Review: High-throughput phenotyping to enhance the use of crop genetic resources. 2019 , 282, 40-48	54
714	Gene Pyramiding and Multiple Character Breeding. 2019 , 83-124	15
713	Genetic Mapping of Prince Rupprecht's Larch (Mayr) by Specific-Locus Amplified Fragment Sequencing. 2019 , 10,	2
712	Drought Stress in Chickpea: Physiological, Breeding, and Omics Perspectives. 2019 , 189-227	1
711	Methodology: -: a single seed-based sampling strategy for marker-assisted selection in rice. 2019 , 15, 78	11
710	VigSatDB: genome-wide microsatellite DNA marker database of three species of Vigna for germplasm characterization and improvement. 2019 , 2019,	5
709	Identification of TaPPH-7A haplotypes and development of a molecular marker associated with important agronomic traits in common wheat. 2019 , 19, 296	13
708	PASTIC: An online toolkit to estimate plant abiotic stress indices. 2019 , 7, e11278	19
707	Review: Improving global food security through accelerated plant breeding. 2019 , 287, 110207	60

706	Dynamic Physiological Phenotyping of Drought-Stressed Pepper Plants Treated With "Productivity-Enhancing" and "Survivability-Enhancing" Biostimulants. 2019 , 10, 905	16
705	Development and application of high-resolution melting DNA markers for the polygenic control of tuber skin colour in autotetraploid potato. 2019 , 39, 1	
704	Genome Studies by Means of DNA Markers of the Blackcurrant. 2019 , 55, 1061-1071	2
703	Genome-wide mining, characterization, and development of microsatellite markers in Tartary buckwheat (<i>Fagopyrum tataricum</i> Garetn.). 2019 , 215, 1	4
702	Genomic Selection Considerations for Successful Implementation in Wheat Breeding Programs. 2019 , 9, 479	20
701	. 2019 ,	3
700	Discovery of Functional SNPs via Genome-Wide Exploration of Malaysian Pigmented Rice Varieties. 2019 , 2019, 4168045	2
699	The complex evolutionary history of apricots: Species divergence, gene flow and multiple domestication events. 2019 , 28, 5299-5314	16
698	The Fondazione Edmund Mach grapevine breeding program for downy and powdery mildew resistances: toward a green viticulture. 2019 , 109-114	4
697	Genomic Selection for Antioxidant Production in a Panel of and Lines. 2019 , 10,	8
696	Marker-Assisted Selection (MAS): A Fast-Track Tool in Tomato Breeding. 2019 ,	3
695	GLADS: A gel-less approach for detection of STMS markers in wheat and rice. 2019 , 14, e0224572	
694	Marker-assisted Selection for Abiotic Stress Tolerance in Crop Plants. 2019 , 335-368	2
693	Screening for <i>Sclerotinia sclerotiorum</i> resistance using detached leaf assays and simple sequence repeat markers in soybean cultivars. 2019 , 125, 104909	1
692	Evaluation of SSR and SNP markers in <i>Rubus glaucus</i> Benth progenitors selection. 2019 , 41,	1
691	Evaluation of Various <i>Rosa Damascena</i> Mill. Genotypes Grown under Rainfed Semi-arid Condition. 2019 , 50, 2534-2543	2
690	Evaluation of Genomic Prediction for Pasm Resistance in Flax. 2019 , 20,	21
689	De Novo Sequencing and Hybrid Assembly of the Biofuel Crop <i>L.</i> : Identification of Quantitative Trait Loci for Geminivirus Resistance. 2019 , 10,	15

688	High-Throughput Field-Phenotyping Tools for Plant Breeding and Precision Agriculture. 2019 , 9, 258	73
687	Salt Tolerance Improvement in Rice through Efficient SNP Marker-Assisted Selection Coupled with Speed-Breeding. 2019 , 20,	38
686	Conclusions and Future Directions. 2019 , 213-220	
685	Dispersal and local persistence shape the genetic structure of a widespread Neotropical plant species with a patchy distribution. 2019 , 124, 499-512	6
684	Genome-wide association mapping of root system architecture traits in common wheat (<i>Triticum aestivum</i> L.). 2019 , 215, 1	12
683	Expression profiles of 12 drought responsive genes in two European (deciduous) oak species during a two-year drought experiment with consecutive drought periods. 2019 , 19, 100193	1
682	Development and Validation of a Gene-Targeted dCAPS Marker for Marker-Assisted Selection of Low-Alkaloid Content in Seeds of Narrow-Leafed Lupin (L.). 2019 , 10,	11
681	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (<i>Glycine max</i> L.). 2019 , 123, 579-592	23
680	Common Bean Genetics, Breeding, and Genomics for Adaptation to Changing to New Agri-environmental Conditions. 2019 , 1-106	2
679	Is Chickpea a Potential Substitute for Soybean? Phenolic Bioactives and Potential Health Benefits. 2019 , 20,	37
678	Molecular Mapping and Synteny. 2019 , 33-40	
677	Genomic Designing for Climate-Smart Pea. 2019 , 265-358	2
676	The Omics Approach for Crop Improvement Against Drought Stress. 2019 , 183-204	3
675	QTLian breeding for climate resilience in cereals: progress and prospects. 2019 , 19, 685-701	16
674	Carrot Genetics, Omics and Breeding Toolboxes. 2019 , 225-245	3
673	Allele specific DNA marker for fusarium resistance gene in. 2019 , 69, 308-315	3
672	Effect of drought stress on the genetic architecture of photosynthate allocation and remobilization in pods of common bean (<i>Phaseolus vulgaris</i> L.), a key species for food security. 2019 , 19, 171	24
671	Recent Trends in Research on the Genetic Diversity of Plants: Implications for Conservation. 2019 , 11, 62	20

670	Marker-assisted transfer of gene to develop soft grain wheat cultivars. 2019 , 9, 183	6
669	Development and Validation of Markers for the Fertility Restorer Gene in Sunflower. 2019 , 20,	6
668	Quantitative Trait Loci for Freezing Tolerance in a Lowland x Upland Switchgrass Population. 2019 , 10, 372	12
667	Evaluation of RR-BLUP Genomic Selection Models that Incorporate Peak Genome-Wide Association Study Signals in Maize and Sorghum. 2019 , 12, 180052	43
666	Plant breeding at the speed of light: the power of CRISPR/Cas to generate directed genetic diversity at multiple sites. 2019 , 19, 176	82
665	Comparative transcriptomics-based selection of suitable reference genes for normalization of RT-qPCR experiments in drought-stressed leaves of three European Quercus species. 2019 , 15, 1	10
664	Genomic Strategies for Improving Abiotic Stress Tolerance in Crop Plants. 2019 , 205-230	1
663	Modern biotechnology and sustainable intensification: chances and limitations. 2019 , 159-179	
662	Marker-assisted breeding for Downy mildew, Powdery mildew and Phylloxera resistance at FEM. 2019 , 13, 01002	1
661	Application of Molecular Markers in Genetic Improvement of Jatropha. 2019 , 131-143	1
660	Plant Breeding. 2019 , 29-68	1
659	Mapping QTL Associated with Stripe Rust, Leaf Rust, and Leaf Spotting in a Canadian Spring Wheat Population. 2019 , 59, 650-658	9
658	Identification of optimal prediction models using multi-omic data for selecting hybrid rice. 2019 , 123, 395-406	16
657	Selection of Bread Wheat for Low Grain Cadmium Concentration at the Seedling Stage Using Hydroponics versus Molecular Markers. 2019 , 59, 945-956	4
656	Identification of genomic SSRs in cluster bean (<i>Cyamopsis tetragonoloba</i>) and demonstration of their utility in genetic diversity analysis. 2019 , 133, 221-231	13
655	Marker-assisted selection and gene pyramiding for resistance to bacterial leaf blight disease of rice (<i>Oryza sativa</i> L.). 2019 , 33, 440-455	30
654	Identification of drought responsive proteins and related proteomic QTLs in barley. 2019 , 70, 2823-2837	13
653	Development of an SNP-based high-density linkage map and QTL analysis for bruchid (<i>Callosobruchus maculatus</i> F.) resistance in black gram (<i>Vigna mungo</i> (L.) Hepper). 2019 , 9, 3930	11

652	Elymus nutans genes for seed shattering and candidate gene-derived EST-SSR markers for germplasm evaluation. 2019 , 19, 102	7
651	Genomic Prediction using Existing Historical Data Contributing to Selection in Biparental Populations: A Study of Kernel Oil in Maize. 2019 , 12, 180025	10
650	Genetic mapping of QTL for agronomic traits and grain mineral elements in rice. 2019 , 7, 560-572	35
649	Genetic diversity and population structure of early-maturing tropical maize inbred lines using SNP markers. 2019 , 14, e0214810	21
648	Development of marama bean, an orphan legume, as a crop. 2019 , 8, e00164	5
647	Low-cost assembly of a cacao crop genome is able to resolve complex heterozygous bubbles. 2019 , 6, 44	3
646	Genomic Resources and Marker-Assisted Selection in Jatropha curcas. 2019 , 145-160	1
645	Origin and evolution of the octoploid strawberry genome. 2019 , 51, 541-547	242
644	ADAM-Plant: A Software for Stochastic Simulations of Plant Breeding From Molecular to Phenotypic Level and From Simple Selection to Complex Speed Breeding Programs. 2018 , 9, 1926	13
643	Genome-wide association mapping of grain yield in a diverse collection of spring wheat (Triticum aestivum L.) evaluated in southern Australia. 2019 , 14, e0211730	33
642	Marker-Assisted Breeding for Enrichment of Provitamin A in Maize. 2019 , 139-157	8
641	Gene-Based Approaches to Durable Disease Resistance in Triticeae Cereals. 2019 , 165-182	1
640	Genetic mapping of a major gene for leaf rust resistance in soft red winter wheat cultivar AGS 2000. 2019 , 39, 1	8
639	A DNA test for routinely predicting mildew resistance in descendants of crabapple [White Angel]. 2019 , 39, 1	2
638	Capsicum Breeding: History and Development. 2019 , 25-55	3
637	Exploring sources of resistance to brown rot in an interspecific almond [peach population. 2019 , 99, 4105-4113	8
636	Development of multiple SNP marker panels affordable to breeders through genotyping by target sequencing (GBTS) in maize. 2019 , 39, 1	36
635	Marker-Assisted Breeding for Improving the Cooking and Eating Quality of Rice. 2019 , 23-39	2

634	Leaf-associated microbiomes of grafted tomato plants. 2019 , 9, 1787	28
633	Genotypic characterization of an F1 Japanese plum progeny through genotyping by sequencing (GBS) and preliminary quantitative trait locus (QTL) analysis for important agronomic traits. 2019 , 49-58	1
632	Recombination fraction and genetic linkage among key disease resistance genes (// "P.ult") in common bean. 2019 , 18,	
631	Genome-Wide Association Study of a Worldwide Collection of Wheat Genotypes Reveals Novel Quantitative Trait Loci for Leaf Rust Resistance. 2019 , 12, 1-14	11
630	Dissection of Phenotypic and Genetic Variation of Drought-Related Traits in Diverse Chinese Wheat Landraces. 2019 , 12, 1-14	20
629	Genome-wide association study of drought tolerance and biomass allocation in wheat. 2019 , 14, e0225383	24
628	Association Mapping Considering Allele Dosage: An Example of Forage Traits in an Interspecific Segmental Allotetraploid Urochloa spp. Panel. 2019 , 59, 2062-2076	1
627	Back to the future: revisiting MAS as a tool for modern plant breeding. 2019 , 132, 647-667	66
626	Production of wheat-doubled haploids resistant to eyespot supported by marker-assisted selection. 2019 , 37, 11-17	3
625	Zinc biofortification of maize (<i>Zea mays</i> L.): Status and challenges. 2019 , 138, 1-28	32
624	Recent understanding of starch biosynthesis in cassava for quality improvement: A review. 2019 , 83, 167-180	25
623	Enhanced resistance to sclerotinia stem rot in transgenic soybean that overexpresses a wheat oxalate oxidase. 2019 , 28, 103-114	12
622	Criteria for evaluating molecular markers: Comprehensive quality metrics to improve marker-assisted selection. 2019 , 14, e0210529	37
621	Introgression of Two Drought QTLs into FUNAABOR-2 Early Generation Backcross Progenies Under Drought Stress at Reproductive Stage. 2019 , 26, 32-41	8
620	TaARF4 genes are linked to root growth and plant height in wheat. 2019 , 124, 903-915	18
619	Association genetics of carbon isotope discrimination and leaf morphology in a breeding population of <i>Juglans regia</i> L.. 2019 , 15, 1	14
618	Salinity stress response and 'omics' approaches for improving salinity stress tolerance in major grain legumes. 2019 , 38, 255-277	39
617	Genetic Dissection of Grain Nutritional Traits and Leaf Blight Resistance in Rice. 2019 , 10,	10

616	Multiplex restriction amplicon sequencing: a novel next-generation sequencing-based marker platform for high-throughput genotyping. 2020 , 18, 254-265	5
615	Hybrid breeding of rice via genomic selection. 2020 , 18, 57-67	49
614	Molecular identification and chromosomal localization of new powdery mildew resistance gene Pm11 in oat. 2020 , 133, 179-185	4
613	MSDB: a comprehensive, annotated database of microsatellites. 2020 , 48, D155-D159	6
612	Advances in Omics Approaches to tackle drought stress in grain legumes. 2020 , 139, 1-27	17
611	Identification of single nucleotide polymorphism markers for population genetic studies in <i>Zizania palustris</i> L.. 2020 , 12, 451-455	2
610	Development and utilization of an InDel marker linked to the fertility restorer genes of CMS-D8 and CMS-D2 in cotton. 2020 , 47, 1275-1282	2
609	Development of a core SNP panel for cacao (<i>C. L.</i>) identity analysis. 2020 , 63, 103-114	4
608	Applications and Trends of Machine Learning in Genomics and Phenomics for Next-Generation Breeding. 2019 , 9,	25
607	Legume genomics and transcriptomics: From classic breeding to modern technologies. 2020 , 27, 543-555	20
606	Molecular mapping of major QTL conferring resistance to orange wheat blossom midge (<i>Sitodiplosis mosellana</i>) in Chinese wheat varieties with selective populations. 2020 , 133, 491-502	4
605	The Effects of Domestication on Secondary Metabolite Composition in Legumes. 2020 , 11, 581357	11
604	SNP-based QTL mapping for panicle traits in the japonica super rice cultivar Liaoxing 1. 2020 , 8, 769-780	2
603	Marker-assisted selection for fast-track breeding of high oleic lines in safflower (<i>Carthamus tinctorius</i> L.). 2020 , 158, 112983	5
602	Characterization of Radiation-Induced DNA Polymorphisms in the M1 Population of the Japonica Rice Variety Gaogengnuo by Whole-Genome Resequencing. 2020 , 56, 693-705	2
601	Phenotyping and QTL mapping for cold tolerance at the germination and seedling stages in Argentine temperate rice. 2020 , 216, 1	1
600	Data synthesis for crop variety evaluation. A review. 2020 , 40, 25	3
599	Elusive Diagnostic Markers for Russian Wheat Aphid Resistance in Bread Wheat: Deliberating and Reviewing the Status Quo. 2020 , 21,	2

598	Exploration of genetic structure and association mapping for fibre quality traits in global flax (<i>Linum usitatissimum</i> L.) collections utilizing SSRs markers. 2020 , 24, 100256	0
597	Transgenic Crops for Biofortification. 2020 , 4,	16
596	Harnessing High-throughput Phenotyping and Genotyping for Enhanced Drought Tolerance in Crop Plants. 2020 , 324, 248-260	11
595	Intricate genetic variation networks control the adventitious root growth angle in apple. 2020 , 21, 852	0
594	Marker assisted improvement of low soil phosphorus tolerance in the bacterial blight resistant, fine-grain type rice variety, Improved Samba Mahsuri. 2020 , 10, 21143	5
593	A Weak Allele of FASCIATED EAR 2 (FEA2) Increases Maize Kernel Row Number (KRN) and Yield in Elite Maize Hybrids. 2020 , 10, 1774	5
592	Application of Genomic Big Data in Plant Breeding:Past, Present, and Future. 2020 , 9,	6
591	Development of EST-SSR Markers Linked to Flowering Candidate Genes in L. Based on RNA Sequencing. 2020 , 9,	2
590	De novo transcriptome assembly and mining of EST-SSR markers in <i>Gloriosa superba</i> . 2020 , 99, 1	
589	Gene Pyramiding for Sustainable Crop Improvement against Biotic and Abiotic Stresses. 2020 , 10, 1255	20
588	Advancements in molecular marker technologies and their applications in diversity studies. 2020 , 45, 1	6
587	Accelerating Tomato Breeding by Exploiting Genomic Selection Approaches. 2020 , 9,	13
586	Faba Bean Gall (<i>Olpidium viciae</i> K.) as a Priority Biosecurity Threat for Producing Faba Bean in Ethiopia: Current Status and Future Perspectives. 2020 , 2020, 1-12	1
585	Marker-assisted pyramiding of potato late blight resistance genes <i>Rpi-rzc1</i> and <i>Rpi-phu1</i> on di- and tetraploid levels. 2020 , 40, 1	12
584	Application of Pedimap: a pedigree visualization tool to facilitate the decisioning of rice breeding in Sri Lanka. 2020 , 10, 14255	1
583	Marker aided introgression of allele improving lysine and tryptophan in maize (L.). 2020 , 26, 1925-1930	3
582	Fine mapping of <i>qKRN8</i> , a QTL for maize kernel row number, and prediction of the candidate gene. 2020 , 133, 3139-3150	1
581	Genetic basis of ion exclusion in salinity stressed wheat: implications in improving crop yield. 2020 , 92, 479-496	14

580	Genetic mapping of Fusarium wilt resistance in a wild banana <i>Musa acuminata</i> ssp. <i>malaccensis</i> accession. 2020 , 133, 3409-3418	10
579	Assessment of the Potential for Genomic Selection To Improve Husk Traits in Maize. 2020 , 10, 3741-3749	6
578	Epistasis and Quantitative Resistance to <i>Pyricularia oryzae</i> Revealed by GWAS in Advanced Rice Breeding Populations. 2020 , 10, 622	0
577	Recovery of Recurrent Parent Genome in a Marker-Assisted Backcrossing Against Rice Blast and Blight Infections Using Functional Markers and SSRs. 2020 , 9,	7
576	RAD-seq-Based High-Density Linkage Map Construction and QTL Mapping of Biomass-Related Traits in Sorghum using the Japanese Landrace Takakibi NOG. 2020 , 61, 1262-1272	10
575	LEPStr: A database for <i>Mycobacterium leprae</i> short tandem repeats. 2020 , 19, 100322	
574	Principles and approaches of association mapping in plant breeding. 2020 , 13, 212-224	16
573	Identification, deployment, and transferability of quantitative trait loci from genome-wide association studies in plants. 2020 , 24, 100145	7
572	Mapping QTLs underpin nutrition components in aromatic rice germplasm. 2020 , 15, e0234395	5
571	A novel intragenic marker targeting the ectodomain of bacterial blight-resistance gene <i>Xa21</i> for marker-assisted selection in rice. 2020 , 34, 824-841	0
570	Genetic dissection of husk number and length across multiple environments and fine-mapping of a major-effect QTL for husk number in maize (<i>Zea mays</i> L.). 2020 , 8, 1071-1080	3
569	Mapping quantitative trait loci for resistance to watermelon bud necrosis orthotospovirus in watermelon [<i>Citrullus lanatus</i> (Thunb.) Matsum & Nakai]. 2020 , 216, 1	0
568	Combining High Oleic Acid Trait and Resistance to Late Leaf Spot and Rust Diseases in Groundnut (L.). 2020 , 11, 514	8
567	Innovative breeding technologies in lettuce for improved post-harvest quality. 2020 , 168, 111266	9
566	Development of SNP markers for marker-assisted breeding in Chinese cabbage using Fluidigm genotyping assays. 2020 , 61, 327-338	2
565	Abiotic and biotic stress interactions in plants: A cross-tolerance perspective. 2020 , 267-302	7
564	Marker-assisted selection for grain number and yield-related traits of rice (L.). 2020 , 26, 885-898	8
563	TeaMiD: a comprehensive database of simple sequence repeat markers of tea. 2020 , 2020,	12

562	Assessing Salinity Tolerance in Rice Mutants by Phenotypic Evaluation Alongside Simple Sequence Repeat Analysis. 2020 , 10, 191	1
561	Systems biology of crop improvement: Drought tolerance as a model to integrate molecular biology, physiology, and breeding. 2020 , 209-231	2
560	Advancements in plant disease control strategies. 2020 , 141-157	2
559	CitGVD: a comprehensive database of citrus genomic variations. 2020 , 7, 12	12
558	Evaluation of Cross-Species Transferability of SSR Markers in. 2020 , 9,	4
557	Characteristics of Microsatellites Mined from Transcriptome Data and the Development of Novel Markers in. 2020 , 11,	3
556	Submergence Tolerance in Rice: Review of Mechanism, Breeding and, Future Prospects. 2020 , 12, 1632	18
555	High-density NGS-based map construction and genetic dissection of fruit shape and rind netting in <i>Cucumis melo</i> . 2020 , 133, 1927-1945	10
554	High-density genetic linkage map based on arbitrary and microsatellite markers using inter-specific recombinant inbred lines in eggplant (<i>Solanum melongena</i> L.). 2020 , 29, 427-438	2
553	Lack of effective resistance to the virulent race of <i>Colletotrichum lentis</i> in <i>Lens culinaris</i> Medikus subsp. <i>culinaris</i> . 2020 , 18, 81-87	6
552	Genetic Analysis of Agronomic Traits and Grain Iron and Zinc Concentrations in a Doubled Haploid Population of Rice (<i>Oryza sativa</i> L.). 2020 , 10, 2283	28
551	Inheritance and mapping of drought tolerance in soybean at seedling stage using bulked segregant analysis. 2020 , 18, 63-70	5
550	Diallelic SNP marker development and genetic linkage map construction in octoploid strawberry (<i>Fragaria × ananassa</i>) through next-generation resequencing and high-resolution melting analysis. 2020 , 61, 371-383	6
549	Mechanisms of powdery mildew resistance of wheat: a review of molecular breeding. 2020 , 69, 601-617	16
548	Diversity analysis of selected rice landraces from West Bengal and their linked molecular markers for salinity tolerance. 2020 , 26, 669-682	3
547	Characterization of haplotypes and single nucleotide polymorphisms associated with Gn1a for high grain number formation in rice plant. 2020 , 112, 2647-2657	7
546	Molecular bases for drought tolerance in common vetch: designing new molecular breeding tools. 2020 , 20, 71	11
545	Overexpression of the chitinase gene CmCH1 from <i>Coniothyrium minitans</i> renders enhanced resistance to <i>Sclerotinia sclerotiorum</i> in soybean. 2020 , 29, 187-198	8

544	Photosynthetic Metabolism under Stressful Growth Conditions as a Bases for Crop Breeding and Yield Improvement. 2020 , 9,	47
543	Development and characterization of an EMS-mutagenized wheat population and identification of salt-tolerant wheat lines. 2020 , 20, 18	14
542	The Lupin Genome. 2020 ,	2
541	Quantitative trait loci analysis of seed oil content and composition of wild and cultivated soybean. 2020 , 20, 51	17
540	Breeder friendly phenotyping. 2020 , 295, 110396	62
539	High-Density Genetic Linkage Mapping of Based on Genotyping-by-Sequencing SNPs and Segregating Contig Tag Haplotypes. 2020 , 11, 448	6
538	Efficient genomic selection using ensemble learning and ensemble feature reduction. 2020 , 23, 311-323	3
537	A systematic analysis of apple root resistance traits to infection and the underpinned molecular regulations of defense activation. 2020 , 7, 62	10
536	Construction of a single nucleotide polymorphism marker based QTL map and validation of resistance loci to bacterial wilt caused by <i>Ralstonia solanacearum</i> species complex in tomato. 2020 , 216, 1	7
535	Multigene CRISPR/Cas9 genome editing of hybrid proline rich proteins (HyPRPs) for sustainable multi-stress tolerance in crops: the review of a promising approach. 2020 , 26, 857-869	7
534	GWAS and co-expression network combination uncovers multigenes with close linkage effects on the oleic acid content accumulation in <i>Brassica napus</i> . 2020 , 21, 320	6
533	Molecular marker assisted gene stacking for disease resistance and quality genes in the dwarf mutant of an elite common wheat cultivar Xiaoyan22. 2020 , 21, 45	9
532	Exploring the genetic base of the soybean germplasm from Africa, America and Asia as well as mining of beneficial allele for flowering and seed weight. 2020 , 10, 195	1
531	The Rubber Tree Genome. 2020 ,	2
530	Long-term trends and genetic architecture of seed characteristics, grain yield and correlated agronomic traits in triticale (<i>Triticosecale</i> Wittmack). 2020 , 139, 717-729	8
529	Genome-Wide Association Study Reveals Novel Candidate Genes Associated with Productivity and Disease Resistance to spp. in Cacao (<i>C. L.</i>). 2020 , 10, 1713-1725	5
528	Morphological, genetic and essential oil variation of Greek sage (<i>Salvia fruticosa</i> Mill.) populations from Greece. 2020 , 150, 112346	6
527	Introgression of a drought insensitive grain yield QTL for improvement of four Indian bread wheat cultivars using marker assisted breeding without background selection. 2021 , 30, 172-183	13

526	Identification of loci for pre-harvest sprouting resistance in the highly dormant spring wheat RL4137. 2021 , 134, 113-124	3
525	Development of Heat Tolerant Two-Line Hybrid Rice Restorer Line Carrying Dominant Locus of OsHTAS. 2021 , 28, 99-108	1
524	Identification of QTL and candidate genes involved in early seedling growth in rice via high-density genetic mapping and RNA-seq. 2021 , 9, 360-371	1
523	Generation of new hybrids by crossbreeding between bottom-fermenting yeast strains. 2021 , 131, 61-67	2
522	Genomic prediction of agronomic traits in wheat using different models and cross-validation designs. 2021 , 134, 381-398	8
521	Application of genomics and transcriptomics to accelerate development of clubroot resistant canola. 2021 , 43, 189-208	5
520	Shallot (<i>Allium cepa</i> L. Aggregatum Group) Breeding. 2021 , 99-154	0
519	Bibliography. 2021 , 595-614	
518	Development of abiotic stress tolerant mustard genotype through induced mutagenesis. 2021 , 213-233	1
517	Utilizing Host-Plant Resistance to Circumvent Blast Disease in Rice. 2021 , 15-26	
516	Genomic Designing for Biotic Stress Resistance in Sorghum. 2021 , 213-255	1
515	Methods for Chromosome Doubling. 2021 , 2287, 127-148	0
514	A short review: Comparisons of high-throughput phenotyping methods for detecting drought tolerance. 2021 , 78,	5
513	Advancement in Molecular and Fast Breeding Programs for Climate-Resilient Agriculture Practices. 2021 , 73-98	
512	Advances in Genomic Designing for Abiotic Stress Tolerance in Sorghum. 2021 , 193-221	
511	Genomic Designing for Biotic Stress Resistant Rice. 2021 , 1-58	
510	Growing Rice with Less Water: Improving Productivity by Decreasing Water Demand. 2021 , 147-170	2
509	Genetics and Breeding of Apple Scions. 2021 , 73-103	2

508	Detection of quantitative trait loci regulating seed yield potential in two interspecific <i>S. bicolor</i> × <i>S. halepense</i> subpopulations. 2021 , 217, 1	1
507	Molecular Markers for Plant Variety Identification and Protection. 2021 , 84-102	
506	Potential of genomics for the improvement of underutilized legumes in sub-Saharan Africa. 2021 , 3, e69	3
505	Variability among <i>Festuca arundinacea</i> cultivars for tolerance to and recovery from waterlogging, salinity and their combination. 2021 , 72, 75	1
504	Genetic Variation and Unintended Risk in the Context of Old and New Breeding Techniques. 2021 , 40, 68-108	5
503	CRISPR/Cas system: A powerful approach for enhanced resistance against rice blast. 2021 , 649-658	
502	How the pan-genome is changing crop genomics and improvement. 2021 , 22, 3	43
501	Construction of a DArT-seq marker-based genetic linkage map and identification of QTLs for yield in tea (<i>Camellia sinensis</i> (L.) O. Kuntze). 2021 , 17, 1	1
500	Technological Innovations for Improving Cassava Production in Sub-Saharan Africa. 2020 , 11, 623736	11
499	The Wild Genetic Resources of Tomato: A Reservoir of Useful Genes for the Future. 2021 , 35-49	
498	Chromosome genomics uncovers plant genome organization and function. 2021 , 46, 107659	8
497	Application of CRISPR/Cas system for genome editing in cotton. 2021 , 277-301	1
496	Comparison of multiplex PCR kits for SCoT and SRAP genotyping in plants. 2021 , 19, 29-34	
495	Assessment of genetic diversity and agronomic traits of durum wheat germplasm under drought environment of the northern Great Plains. 2021 , 61, 1194-1206	3
494	Use of Contemporary Groups in the Construction of Multi-Environment Trial Datasets for Selection in Plant Breeding Programs. 2020 , 11, 623586	5
493	Breeding for Disease Resistance in Brassica Vegetables Using DNA Marker Selection.	1
492	Identification of Promising RILs for High Grain Zinc Through Genotype × Environment Analysis and Stable Grain Zinc QTL Using SSRs and SNPs in Rice (L.). 2021 , 12, 587482	5
491	Conversion and Validation of Uniplex SNP Markers for Selection of Resistance to Cassava Mosaic Disease in Cassava Breeding Programs. 2021 , 11, 420	4

490	Genomics Armed With Diversity Leads the Way in Improvement in a Changing Global Environment. 2021 , 12, 600789	8
489	Novel and Transgressive Salinity Tolerance in Recombinant Inbred Lines of Rice Created by Physiological Coupling-Uncoupling and Network Rewiring Effects. 2021 , 12, 615277	5
488	Genetic mapping of the dominant gene controlling weeping habit in Japanese chestnut (<i>Castanea crenata</i> Sieb. et Zucc.). 2021 , 17, 1	0
487	Genetic variation in carbon isotope discrimination-based water use efficiency of teak (<i>Tectona grandis</i> L. f.) and its association with growth and wood quality traits. 2021 , 35, 799-807	0
486	Association Mapping of Thousand Grain Weight using SSR and SNP Markers in Rice (<i>Oryza sativa</i> L.) Across Six Environments. 2021 , 14, 143-155	2
485	Ṫekiyėde Yayġ̇ Olarak̇̇ Eteleṅ̇ Oṅ̇ Bė̇Sȯ̇ṅ̇ İ̇̇diniṅ̇ Leek yellow stripe virus (LYSV)̇̇ė̇ Kaṙ̇ Reaksiyonlaṙ̇71-79	1
484	Regional association analysis coupled with transcriptome analyses reveal candidate genes affecting seed oil accumulation in <i>Brassica napus</i> . 2021 , 134, 1545-1555	1
483	Sorghum breeding in the genomic era: opportunities and challenges. 2021 , 134, 1899-1924	12
482	QTL Analysis of Adult Plant Resistance to Stripe Rust in a Winter Wheat Recombinant Inbred Population. 2021 , 10,	1
481	Dynamic changes in the genetic parameters of growth traits with age and their associations with heterosis in hybrid <i>Liriodendron</i> . 2021 , 17, 1	0
480	Development and validation of genome-wide InDel markers with high levels of polymorphism in bitter melon (<i>Momordica charantia</i>). 2021 , 22, 190	1
479	Understanding the metabolome and metagenome as extended phenotypes: The next frontier in macroalgae domestication and improvement. 2021 , 52, 1009-1030	1
478	Common Vetch, Valuable Germplasm for Resilient Agriculture: Genetic Characterization and Spanish Core Collection Development. 2021 , 12, 617873	5
477	High-throughput NGS-based genotyping and phenotyping: Role in genomics-assisted breeding for soybean improvement. 2021 , 3, e81	1
476	Introgression of dual abiotic stress tolerance QTLs (QTL and gene) into Rice (<i>L.</i>) variety Aiswarya through marker assisted backcross breeding. 2021 , 27, 497-514	6
475	Genomics assisted breeding: The need and current perspective for rice improvement in India. 2021 , 58, 61-68	2
474	Rice Adaptation to Climate Change: Opportunities and Priorities in Molecular Breeding. 2021 , 1-25	1
473	Developing Climate-Resilient, Direct-Seeded, Adapted Multiple-Stress-Tolerant Rice Applying Genomics-Assisted Breeding. 2021 , 12, 637488	3

472	Rice Breeding in Vietnam: Retrospects, Challenges and Prospects. 2021 , 11, 397	1
471	Variation in southern chinch bug (<i>Blissus insularis</i>) survival and damage on St. Augustinegrass germplasm.	
470	Attaining the promise of plant gene editing at scale. 2021 , 118,	20
469	Revisions to USDA biotechnology regulations: The SECURE rule. 2021 , 118,	6
468	Recent Advances of Genetic Resources, Genes and Genetic Approaches for Flooding Tolerance in Rice. 2021 , 22, 41-58	1
467	Meta-analysis of QTLome for grain zinc and iron contents in wheat (<i>Triticum aestivum</i> L.). 2021 , 217, 1	6
466	Integrated genomic selection for rapid improvement of crops. 2021 , 113, 1070-1086	7
465	Molecular and phenotypic evaluation for heading date and panicle length on F2 selected aromatic rice progenies derived from gene pyramiding effort. 2021 , 759, 012070	
464	Association Mapping for Improving Fiber Quality in Upland Cottons.	
463	Smart Breeding for Climate Resilient Agriculture.	1
462	Late blight in tomato: insights into the pathogenesis of the aggressive pathogen <i>Phytophthora infestans</i> and future research priorities. 2021 , 253, 119	7
461	Introgression of Maize Lethal Necrosis Resistance Quantitative Trait Loci Into Susceptible Maize Populations and Validation of the Resistance Under Field Conditions in Naivasha, Kenya. 2021 , 12, 649308	3
460	Synthetic Promoters from Strawberry Vein Banding Virus (SVBV) and Dahlia Mosaic Virus (DaMV). 2021 , 63, 792-806	0
459	Biotechnological approaches in management of oomycetes diseases. 2021 , 11, 274	0
458	Adaptive Evolution and Addressing the Relevance for Genetic Improvement of Sago Palm Commodity.	
457	Breeding Approaches for Biotic Stress Resistance in Vegetables.	1
456	Population structure and association mapping for hundred seed weight in mungbean minicore.	
455	The Development of the Genic SSR Markers for Analysis of Genetic Diversity in Gooseberry Cultivars. 2021 , 11, 1050	0

454	Insights into Marker Assisted Selection and Its Applications in Plant Breeding.	1
453	Goat : Indel Mutation Detection, Association Analysis With Litter Size and Alternative Splicing Variant Expression. 2021 , 12, 648256	1
452	Marker-assisted breeding of onion (<i>A. cepa</i> L.) maintainer line resistant to Downy mildew. 2021 , 34-39	
451	Soil pathogen, <i>Fusarium oxysporum</i> induced wilt disease in chickpea: a review on its dynamicity and possible control strategies. 2021 , 87, 260-274	1
450	Genome-Wide Association Study and Genomic Prediction for Soybean Cyst Nematode Resistance in USDA Common Bean () Core Collection. 2021 , 12, 624156	5
449	Identification and Fine-Mapping of a Novel QTL qMrdd2 Conferring Resistance to Maize Rough Dwarf Disease. 2021 ,	1
448	Harnessing translational research in wheat for climate resilience. 2021 , 72, 5134-5157	5
447	Development, characterization, functional annotation and validation of genomic and genic-SSR markers using de novo next generation sequencing in Cav. 2021 , 11, 310	1
446	Genome wide association study of agronomic and seed traits in a world collection of proso millet (<i>Panicum miliaceum</i> L.). 2021 , 21, 330	6
445	Detection of 15-bp Deletion Mutation within Gene and Its Effects on Growth Traits in Goats. 2021 , 11,	2
444	Mapping and Validation of a Stable Quantitative Trait Locus Conferring Maize Resistance to Gibberella Ear Rot. 2021 , 105, 1984-1991	0
443	Genetic diversity and population structure analysis of bambara groundnut (<i>Vigna subterrenea</i> L) landraces using DArT SNP markers. 2021 , 16, e0253600	1
442	Gene regulation at transcriptional and post-transcriptional levels to combat salt stress in plants. 2021 , 173, 1556-1572	4
441	Phytoexclusion of heavy metals using low heavy metal accumulating cultivars: A green technology. 2021 , 413, 125427	14
440	Genomics and Marker-Assisted Improvement of Vegetable Crops. 2021 , 40, 303-365	6
439	Abiotic Stress Responses in Plants: Current Knowledge and Future Prospects.	2
438	New approaches in the discovery and introgression of disease resistance genes from wild tomato. 2021 , 23-34	0
437	Recent molecular and breeding strategies in lettuce (<i>Lactuca</i> spp.). 2021 , 68, 3055	5

436	Using chlorate as an analogue to nitrate to identify candidate genes for nitrogen use efficiency in barley. 2021 , 41, 1	1
435	Analysis of genetic diversity in a collection of <i>Plantago</i> species: application of ISSR markers. 1	0
434	Advances in Developing Multigene Abiotic and Biotic Stress-Tolerant Rice Varieties.	
433	Mapping of Two New Rust Resistance Genes Uvf-2 and Uvf-3 in Faba Bean. 2021 , 11, 1370	8
432	Genetic Dissection of Seedling Root System Architectural Traits in a Diverse Panel of Hexaploid Wheat through Multi-Locus Genome-Wide Association Mapping for Improving Drought Tolerance. 2021 , 22,	4
431	Structural and Functional Genomics of the Resistance of Cacao to. 2021 , 10,	1
430	QTL mapping for Fusarium wilt resistance based on the whole-genome resequencing and their association with functional genes in <i>Raphanus sativus</i> . 2021 , 134, 3925-3940	1
429	High-Frequency Homologous Recombination Occurred Preferentially in. 2021 , 12, 703077	
428	Genome-wide development of lncRNA-derived-SSR markers for Dongxiang wild rice (<i>Oryza rufipogon</i> Griff.).	0
427	Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean.	
426	Advances in omics technology for improving crop yield and stress resilience. 2021 , 140, 719	4
425	Oat crown rust disease severity estimated at many time points using multispectral aerial photos. 2021 ,	1
424	Development of high-resolution multiple-SNP arrays for genetic analyses and molecular breeding through genotyping by target sequencing and liquid chip. 2021 , 2, 100230	4
423	Deciphering variation of 239 elite japonica rice genomes for whole genome sequences-enabled breeding. 2021 , 113, 3083-3091	1
422	Characterisation of a 4A QTL for Metribuzin Resistance in Wheat by Developing Near-Isogenic Lines. 2021 , 10,	
421	Enhancing genetic gains through marker-assisted recurrent selection: from phenotyping to genotyping. 1	3
420	New approaches to improve crop tolerance to biotic and abiotic stresses. 2021 ,	0
419	Insertion/deletion variants within the gene identified in reported genome-wide selective sweep analysis reveal a correlation with goat litter size. 2021 , 22, 757-766	3

418	Evolution of Fusarium Head Blight Management in Wheat: Scientific Perspectives on Biological Control Agents and Crop Genotypes Protocooperation. 2021 , 11, 8960	3
417	Integrating omics approaches to discover and prioritize candidate genes involved in oil biosynthesis in soybean. 2022 , 808, 145976	0
416	Exploration of genetic, morphological and essential oil variation reveals tools for the authentication and breeding of <i>Salvia pomifera</i> subsp. <i>calycina</i> (Sm.) Hayek. 2021 , 191, 112900	0
415	Contribution of Crop Biofortification in Mitigating Vitamin Deficiency Globally. 2021 , 112-130	1
414	Natural Insecticidal Proteins and Their Potential in Future IPM. 2021 , 265-303	
413	Genomics Assisted Breeding for Sustainable Agriculture: Meeting the Challenge of Global Food Security. 2021 , 23-51	
412	Doubled Haploids in Rice Improvement: Approaches, Applications, and Future Prospects. 2021 , 425-447	1
411	Zinc-Biofortified Rice: A Sustainable Food-Based Product for Fighting Zinc Malnutrition. 2021 , 449-470	1
410	Development and characterization of GR2E Golden rice introgression lines. 2021 , 11, 2496	7
409	Biotechnology and Genomics: Exploiting the Potential of CWR. 212-223	2
408	A Short History and Perspectives on Plant Genetic Transformation. 2020 , 2124, 39-68	8
407	Practical Workflow from High-Throughput Genotyping to Genomic Estimated Breeding Values (GEBVs). 2021 , 2264, 119-135	2
406	Red Clover. 2010 , 439-455	30
405	Encyclopedia of Sustainability Science and Technology. 2012 , 2527-2540	4
404	Legumes in Omic Era: Retrospects and Prospects. 2014 , 1-14	3
403	Common Bean Genomics and Its Applications in Breeding Programs. 2014 , 185-206	3
402	SSR genotyping. 2015 , 1245, 77-89	38
401	Genomic Approaches to Biotic Stresses. 2020 , 133-167	3

400	Genomic Applications and Resources to Dissect Flowering Time Control in Narrow-Leafed Lupin. 2020 , 109-137	1
399	Cacao (<i>Theobroma cacao</i> L.) Breeding. 2019 , 409-487	5
398	Safflower (<i>Carthamus tinctorius</i> L.) Breeding. 2019 , 537-575	3
397	Genomic Selection in Cereal Crops: Methods and Applications. 2020 , 51-88	3
396	Data-Driven Decisions for Accelerated Plant Breeding. 2020 , 89-119	4
395	The Reyan 7-33-97 Rubber Tree Genome: Insight into Its Structure, Composition and Application. 2020 , 13-40	2
394	Marker-Assisted Selection in Pea Breeding. 2020 , 137-154	2
393	Genetic-Based Biofortification of Staple Food Crops to Meet Zinc and Iron Deficiency-Related Challenges. 2020 , 173-223	5
392	History of Plant Biotechnology Development. 2018 , 1-35	2
391	A Mathematical Programming Approach to Marker-Assisted Gene Pyramiding. 2011 , 26-38	4
390	Impact Molecular Marker and Genomics-Led Technologies on Brassica Breeding. 2015 , 145-154	1
389	Cowpea. 2014 , 95-114	4
388	Application of Molecular Markers for Breeding Disease Resistant Varieties in Crop Plants. 2010 , 185-205	6
387	Marker-Assisted Breeding in Higher Plants. 2011 , 39-76	6
386	Marker-Aided Breeding Revolutionizes Twenty-First Century Crop Improvement. 2012 , 435-452	3
385	Biotechnology for Cotton Improvement. 2020 , 509-525	3
384	Genetic patterns recognition in crop species using self-organizing map: the example of the highly heterozygous autotetraploid potato (<i>Solanum tuberosum</i> L.). 2020 , 67, 947-966	1
383	Evolution in crop improvement approaches and future prospects of molecular markers to CRISPR/Cas9 system. 2020 , 753, 144795	6

382	Non-coding RNAs as emerging targets for crop improvement. 2020 , 297, 110521	9
381	Effect of marker segregation distortion on high density linkage map construction and QTL mapping in Soybean (<i>Glycine max</i> L.).	0
380	Existence of vigorous lineages of crop-wild hybrids in Lettuce under field conditions. 2009 , 8, 203-17	16
379	Influence of environmental factors and production practices on the growth and productivity of pawpaw (<i>Carica papaya</i> L.) in south western Nigeria [A review. 2016 , 71, 341-361	6
378	Transgressive segregation for salt tolerance in rice due to physiological coupling and uncoupling and genetic network rewiring.	2
377	A High-Throughput Physiological Functional Phenotyping System for Time- and Cost-Effective Screening of Potential Biostimulants.	2
376	Bael (<i>Aegle marmelos</i> L. Corrã), a Medicinal Tree with Immense Economic Potentials. 2020 , 2020, 1-13	6
375	Development of Whole-Genome Agarose-Resolvable LInDel Markers in Rice. 2020 , 13, 1	18
374	Omics: Modern Tools for Precise Understanding of Drought Adaptation in Plants. 2017 , 263-294	3
373	Omics Approaches in Tropical Fruit Crops. 2013 , 285-324	1
372	Maize (<i>Zea mays</i> L.) Genome Diversity as Revealed by RNA-Sequencing. 2014 , 329-356	1
371	Biotechnology of Trees:Chestnut. 2014 ,	3
370	Genomics assisted ancestry deconvolution in grape. 2013 , 8, e80791	25
369	Genetic rearrangements of six wheat-agropyron <i>crisatum</i> 6P addition lines revealed by molecular markers. 2014 , 9, e91066	43
368	Association mapping for epistasis and environmental interaction of yield traits in 323 cotton cultivars under 9 different environments. 2014 , 9, e95882	30
367	Molecular mapping and validation of a major QTL conferring resistance to a defoliating isolate of verticillium wilt in cotton (<i>Gossypium hirsutum</i> L.). 2014 , 9, e96226	21
366	Large-scale SNP discovery through RNA sequencing and SNP genotyping by targeted enrichment sequencing in cassava (<i>Manihot esculenta</i> Crantz). 2014 , 9, e116028	38
365	Ultrahigh-density linkage map for cultivated cucumber (<i>Cucumis sativus</i> L.) using a single-nucleotide polymorphism genotyping array. 2015 , 10, e0124101	20

364	Inclusive Composite Interval Mapping of QTL by Environment Interactions in Biparental Populations. 2015 , 10, e0132414	44
363	Major Quantitative Trait Loci and Putative Candidate Genes for Powdery Mildew Resistance and Fruit-Related Traits Revealed by an Intraspecific Genetic Map for Watermelon (<i>Citrullus lanatus</i> var. <i>lanatus</i>). 2015 , 10, e0145665	25
362	Genome-Assisted Prediction of Quantitative Traits Using the R Package sommer. 2016 , 11, e0156744	241
361	Leveraging genomic prediction to scan germplasm collection for crop improvement. 2017 , 12, e0179191	21
360	Pea Marker Database (PMD) - A new online database combining known pea (<i>Pisum sativum</i> L.) gene-based markers. 2017 , 12, e0186713	17
359	Genome wide identification of QTL associated with yield and yield components in two popular wheat cultivars TAM 111 and TAM 112. 2020 , 15, e0237293	6
358	Genotipado por secuenciación de variedades tradicionales de <i>Theobroma cacao</i> (Malvaceae) del Estado de Tabasco, México. 2019 , 97, 381	2
357	Modified Method of High Quality Genomic DNA Extraction from Mungbean [<i>Vigna radiata</i> (L.) Wilczek] Suitable for PCR Based Amplification. 2017 , 10, 1-7	1
356	Development of New Drought Tolerant Breeding Lines for Vietnam Using Marker-Assisted Backcrossing. 59, 1-13	5
355	Phenotypic Performance of Rice (<i>Oryza sativa</i> L.) Populations Induced by the MNU Mutant on the Adaptive Characteristics. 5, 13-24	3
354	Main and Epistatic Quantitative Trait Loci Associated with Seed Size in Watermelon. 2012 , 137, 452-457	18
353	Cisgenics - a sustainable approach for crop improvement. 2013 , 14, 468-76	43
352	Application of DNA Molecular Markers in Plant Breeding (Review article). 2019 , 6, 1-30	4
351	Registration of a Rice Gene-Mapping Population Consisting of 'Qingfeng' into 'Jemont' Backcross Introgression Lines. 2012 , 6, 128-135	14
350	Precision Genome Engineering for the Breeding of Tomatoes: Recent Progress and Future Perspectives. 2020 , 2, 612137	5
349	A High-Density Genetic Linkage Map of SLAFs and QTL Analysis of Grain Size and Weight in Barley (<i>L.</i>). 2020 , 11, 620922	3
348	MOLECULAR MARKER ANALYSIS OF SPIKE FERTILITY INDEX AND RELATED TRAITS IN A BREAD WHEAT RECOMBINANT INBRED LINE POPULATION. 2019 , 30, 7-20	0
347	Molecular Identification of Phytophthora Resistance Gene in Soybean Cultivar Yudou 25. 2009 , 35, 1844-1850	29

346	Impact of Marker Assisted Breeding for Bacterial Blight Resistance in Rice: A Review. 2020 , 19, 151-165	1
345	Application of Marker Assisted Backcrossing to Introgress the Submergence Tolerance QTL &i>SUB&i>1 into the Vietnam Elite Rice Variety-AS996. 2012 , 03, 528-536	21
344	Association Analysis and Identification of SNP Markers for Stemphylium Leaf Spot (&i>Stemphylium botryosum&i> f. sp. &i>spinacia&i>) Resistance in Spinach (&i>Spinacia oleracea&i>). 2016 , 07, 1600-1611	11
343	Performance of interspecific grapevine varieties in north-east Italy. 2013 , 04, 91-101	5
342	A Review on Hereditary Qualities Assorted Variety of American Cotton. 2018 , 09, 587-608	1
341	Multiplex Simple Sequence Repeat (SSR) Markers Discriminating <i>Pleurotus eryngii</i> Cultivar. 2014 , 42, 159-164	4
340	Development of an SNP set for marker-assisted breeding based on the genotyping-by-sequencing of elite inbred lines in watermelon. 2018 , 45, 242-249	2
339	Evaluation of Germplasm and Development of SSR Markers for Marker-assisted Backcross in Tomato. 2012 , 30, 557-567	3
338	Recent Advances in Rice Varietal Development for Durable Resistance to Biotic and Abiotic Stresses through Marker-Assisted Gene Pyramiding. 2021 , 13, 10806	2
337	Genetic Architecture of Multiphasic Growth Covariation as Revealed by a Nonlinear Mixed Mapping Framework. 2021 , 12, 711219	0
336	QTL Validation and Development of SNP-Based High Throughput Molecular Markers Targeting a Genomic Region Conferring Narrow Root Cone Angle in Aerobic Rice Production Systems. 2021 , 10,	1
335	LegumeSSRdb: A Comprehensive Microsatellite Marker Database of Legumes for Germplasm Characterization and Crop Improvement. 2021 , 22,	0
334	Transcription Factor TaWRKY51 Is a Positive Regulator in Root Architecture and Grain Yield Contributing Traits. 2021 , 12, 734614	1
333	Marker-assisted backcross breeding for enhancing Mungbean Yellow Mosaic Virus (MYMV) disease resistance in blackgram [<i>Vigna mungo</i> (L.) Hepper] cv MDU 1. 2021 , 116, 101732	
332	Metabolomics for Crop Breeding: General Considerations. 2021 , 12,	1
331	Genome-Wide Linkage Mapping for Preharvest Sprouting Resistance in Wheat Using 15K Single-Nucleotide Polymorphism Arrays. 2021 , 12, 749206	0
330	Cash Crops: An Introduction. 2022 , 1-19	1
329	Development of a Panel of Genotyping-in-Thousands by Sequencing in. 2021 , 12, 769473	0

- 328 Registration of the Coda/Brundage wheat recombinant inbred line mapping population.
- 327 Meta-QTLs, ortho-MQTLs and candidate genes for nitrogen use efficiency and root system architecture in bread wheat (L.). **2021**, 27, 2245-2267 9
- 326 Breeding for Sustainability. **2011**, 41-64
- 325 Sustainable Food Production. **2013**, 501-513
- 324 Sustainable Food Production. **2013**, 1201-1228 1
- 323 Genomics-Based Breeding Technology. **2013**, 329-348 1
- 322 Advances in Greengram and Blackgram Genomics. **2014**, 155-184 2
- 321 Practical Omics Approaches for Drought Tolerance in Rice. **2013**, 47-72
- 320 Monitoring Three Resistance Genes in Iranian Sunflower Inbred Lines. **2015**, 13, 45-50 1
- 319 Genetic Mapping and Detection of Quantitative Trait Loci. **2016**, 65-74
- 318 Toward the Rapid Domestication of Perennial Grains: Developing Genetic and Genomic Resources for Intermediate Wheatgrass. **2016**, 227-241
- 317 Stress in Plants and Crops Induced by Parasitic Weeds. **2016**, 765-776
- 316 Biotic Stress Management in Rice Through RNA Interference. **2016**, 363-394
- 315 Construction of a high-density American cranberry (*Vaccinium macrocarpon* Ait.) composite map using genotyping-by-sequencing for multi-pedigree linkage mapping.
- 314 Strategies for Breeding Cereal Crops to Attain Sustainability with Major Emphasis on Rice. **2017**, 443-459
- 313 Genomic and Proteomic Tools for Understanding Mysterious Protein Dioscorin from Dioscorea Tuber. **2017**, 97-114
- 312 Genetic analysis and development of submergence tolerance rice (*Oryza sativa* L.) lines through MAS. **2018**, 11, 2
- 311 Criteria for evaluating molecular markers: Comprehensive quality metrics to improve marker-assisted selection.

310	Optimizing Trait Predictability in Hybrid Rice Using Superior Prediction Models and Selective Omic Datasets.	
309	Scientific and Technological Interventions for Attaining Precision in Plant Genetics and Breeding. 2017 , 1, 5-21	1
308	Functional Quantitative Trait Loci (QTL) analysis for adaptive traits in a three-generation Scots pine pedigree.	0
307	Do below-ground genotypes influence above-ground microbiomes of grafted tomato plants?.	
306	Using stepwise regression to identify ISSR molecular markers associated with agronomic traits in ispaghula (<i>Plantago ovata</i> Forssk.) ecotypes. 2018 , 5, 128-136	0
305	Molecular Breeding. 2019 , 509-539	
304	Gene Modification of Medicinal Plant Germplasm Resources. 2019 , 145-190	
303	Mung Bean (<i>Vigna radiata</i> (L.) R. Wilczek) Breeding. 2019 , 371-407	0
302	Genetic Diversity and Conservation of <i>Pterocarpus santalinus</i> L.f. Through Molecular Approaches. 2019 , 173-187	1
301	THE IMPACT OF MOLECULAR GENETICS IN PLANT BREEDING: REALITIES AND PERSPECTIVES. 2019 , 30, 11-15	
300	Recurrent parent genome (RPG) recovery analysis in a marker-assisted backcross breeding based on the genotyping-by-sequencing in tomato (<i>Solanum lycopersicum</i> L.). 2019 , 46, 165-171	
299	Genetic Variation Analysis of Chinese Jujube Cultivars Using ISSR Molecular Markers. 2019 , 7, 200-207	
298	Genome wide association study reveals novel candidate genes associated with productivity and disease resistance to <i>Moniliophthora</i> spp. in cacao (<i>Theobroma cacao</i> L.).	
297	Validation of Bread Wheat KASP Markers in Durum Wheat Lines in Kazakhstan. 2019 , 73, 462-465	
296	Molecular marker assisted gene stacking for disease resistance and quality genes in the dwarf mutant of an elite common wheat cultivar Xiaoyan22.	
295	Genetic Engineering of Rice for Resistance to Insect Pests. 2020 , 129-148	3
294	Advances in Big Data Analytics and Applications in Seed Technology. 2020 , 419-438	
293	Biotechnological Approaches to Develop Rice Tolerance to Low and High Temperature Stress. 2020 , 549-578	

- 292 Effect of Population Size on Genome-Wide Association Study of Agronomic Traits in Soybean. **2020**, 74, 244-251
- 291 Tag-SNP selection and online database construction for haplotype-based marker development in tomato. **2020**, 47, 218-226 2
- 290 The introgression of resistance to *Tuta absoluta* in tomato based on glandular trichomes. 1 0
- 289 Biotechnology: An Intervention for Genetic Resistance Against Seed-Borne Phytopathogens. **2020**, 683-716
- 288 Improvement of Rice Quality via Biofortification of Micronutrients. **2020**, 715-748
- 287 Specific-Locus Amplified Fragment Sequencing (SLAF-Seq) as High-Throughput SNP Genotyping Methods. **2021**, 2264, 75-87 1
- 286 Method for Improving Marker Selection Efficiency through a Graphical Representation of Molecular Markers. **2020**, 52, 374-381
- 285 Resistance Breeding and Exploitation of Wild Relatives for New Resistance Sources. **2021**, 211-247 1
- 284 Accelerated Improvement of Cole Vegetable Crops. **2020**, 101-135 1
- 283 Translational Genomics and Breeding in Soybean. **2020**, 343-367
- 282 Use of Biotechnology for Crop Improvement in Sri Lanka: Current Status and Future Prospects. **2020**, 89-106 1
- 281 Efficient Breeding of Pulse Crops. **2020**, 1-30 1
- 280 Improving Cotton Crop Tolerance to Drought Stress Through Molecular Approaches. **2020**, 17-37
- 279 Accelerated Breeding of Plants: Methods and Applications. **2020**, 1-29
- 278 Increasing Rice Grain Yield Under Biotic Stresses: Mutagenesis, Transgenics and Genomics Approaches. **2020**, 149-178 2
- 277 Advances of Next-Generation Sequencing (NGS) Technologies to Enhance the Biofortifications in Crops. **2020**, 427-450 1
- 276 GWAS and co-expression network combination uncovers multigenes with close linkage effects on oleic acid content accumulation in *Brassica napus*.
- 275 GWAS and co-expression network combination uncovers multigenes with close linkage effects on oleic acid content accumulation in *Brassica napus*.

274 QTL mapping of seed protein and oil traits in two recombinant inbred line soybean populations. 1-16

273 Oakleaf Hydrangea (*Hydrangeaquercifolia* Bartr.). **2022**, 1-33

272 Analysis of genetic diversity and association of seed and mucilage yields with inter simple sequence repeats (ISSR) polymorphism in a collection of Plantago species.

271 Identification of ISSR and RAPD Molecular Markers Associated with Agronomic Traits in Lemon Balm (*Melissa Officinalis*). **2018**, 10, 64-72

0

270 Genetic divergence in pumpkin genotypes using ISSR markers. **2020**, 29-34

1

269 Breeding Strategies of Garden Pea (*Pisum sativum* L.). **2021**, 331-377

1

268 High-oleic oils: Future developments and technologies. **2022**, 143-188

267 Introduction to Marker-Assisted Selection in Wheat Breeding. **2022**, 77-117

1

266 Promising versions of a commercial pearl millet hybrid for terminal drought tolerance identified through MAS. **2021**, 100, 1

2

265 Disease resistance of improved MR220 lines against *Pyricularia oryzae* Cavara and their preliminary agronomic performance.

264 Soybean Yield Formation Physiology - A Foundation for Precision Breeding Based Improvement. **2021**, 12, 719706

7

263 The barley immune receptor *Mla* recognizes multiple pathogens and contributes to host range dynamics. **2021**, 12, 6915

2

262 A super PPR cluster for restoring fertility revealed by genetic mapping, homocap-seq and de novo assembly in cotton. **2021**, 1

0

261 A multiplex PCR marker distinguishes between a series of four *LanFTc1* alleles regulating flowering time in narrow-leafed lupin (*Lupinus angustifolius*). **2021**, 140, 1090-1101

260 Wheat Breeding, Fertilizers, and Pesticides: Do They Contribute to the Increasing Immunogenic Properties of Modern Wheat?. **2021**, 3, 247-264

1

259 A compressed variance component mixed model framework for detecting small and linked QTL-by-environment interactions.. **2022**,

0

258 Advances of Biotechnology in Quinoa Production: A Global Perspective. **2021**, 79-111

0

257 Asparagus (*Asparagus officinalis* L.) Breeding. **2021**, 425-469

0

256 of Host Resistance to Hemibiotrophs and. **2021**, 233-348

255 Meta-QTLs, ortho-meta-QTLs and candidate genes for grain yield and associated traits in wheat (*Triticum aestivum* L.).. **2022**, 1 4

254 Management of stored grain pest with special reference to , a major pest of cowpea: A review.. **2022**, 8, e08703 4

253 Feasibility of Genomic Prediction for Brown Rot (*Monilinia* spp.) Resistance in Peach. **2022**, 2, 1-12 0

252 Genomics-Assisted Breeding for Resistance to Leaf Spots and Rust Diseases in Peanut. **2022**, 239-278 1

251 Development and Genetic Characterization of Peanut Advanced Backcross Lines That Incorporate Root-Knot Nematode Resistance From .. **2021**, 12, 785358 0

250 Agronomical and breeding approaches to improve the nutritional status of forage crops for better livestock productivity. 2

249 Pear genetics: Recent advances, new prospects, and a roadmap for the future.. **2022**, 9, 1

248 Improvement of *Cercospora* leaf spot and powdery mildew resistance of mungbean variety KING through marker-assisted selection. 1-12 1

247 Response to selection to different breeding methods for soybean flood tolerance. 0

246 A Single Nucleotide Deletion in the Third Exon of FT-D1 Increases the Spikelet Number and Delays Heading Date in Wheat (*Triticum aestivum* L.).. **2022**, 1

245 Validation of SNP markers for marker-assisted selection of genotypes with increased carotenoid and dry matter contents in cassava. 1

244 Automating microsatellite screening and primer design from multi-individual libraries using Micro-Primers.. **2022**, 12, 295 0

243 Strategies, Opportunities, and Challenges in Crop Genetic Diversity Conservation: A Plant Breeder's Perspective. **2022**, 151-169

242 Genome-wide development of lncRNA-derived-SSR markers for Dongxiang wild rice (*Oryza rufipogon* Griff.). 1-4 0

241 The genome sequence of Ciherang, an Indonesian rice mega variety, revealed the footprints of modern rice breeding. **2022**,

240 Expressed sequence tag simple sequence repeats (EST-SSRs) mining and marker development from *Leucaena leucocephala* root transcriptome. **2022**, 959, 012022

239 Ecophysiological Crop Modelling Combined with Genetic Analysis Is a Powerful Tool for Ideotype Design. **2022**, 12, 215 1

238	Identification of true male parents in F1 populations of cacao using SSR markers. 2022 , 974, 012051	
237	Development and validation of a novel core set of KASP markers for the traits improving grain yield and adaptability of rice under direct seeded cultivation conditions.. 2022 , 110269	0
236	Marker-Assisted Pyramiding of Genes for Multilocular Ovaries, Self-Compatibility, and Clubroot Resistance in Chinese Cabbage (<i>Brassica rapa</i> L. ssp. <i>pekinensis</i>). 2022 , 8, 139	0
235	Salinity Stress in Wheat: Effects, Mechanisms and Management Strategies. 2022 , 91, 667-694	11
234	Identification of SSR and retrotransposon-based molecular markers linked to morphological characters in oily sunflower (<i>Helianthus annuus</i> L.) under natural and water-limited states. 2018 , 97, 189-203	
233	Molecular Linkage Mapping: Map Construction and Mapping of Genes/QTLs. 2022 , 121-144	
232	Common Bean Genetics, Breeding, and Genomics for Adaptation to Biotic Stress Conditions. 2022 , 1-116	
231	Identification of the Powdery Mildew Resistance in Chinese Wheat Cultivar Heng 4568 and its Evaluation in Marker-Assisted Selection.. 2022 , 13, 819844	0
230	Combination of Marker-Assisted Backcross Selection of Yr59 and Phenotypic Selection to Improve Stripe Rust Resistance and Agronomic Performance in Four Elite Wheat Cultivars. 2022 , 12, 497	2
229	Exploring the correlation between salt tolerance and yield: research advances and perspectives for salt-tolerant forage sorghum selection and genetic improvement.. 2022 , 255, 71	1
228	High-Density Genetic Variation Map Reveals Key Candidate Loci and Genes Associated With Important Agronomic Traits in Peanut.. 2022 , 13, 845602	1
227	Marker assisted introgression of semi-dwarfing (<i>sd1</i>) gene in Katarni rice (<i>Oryza sativa</i> L.) landrace. 2022 , 1-9	
226	Impacts, Tolerance, Adaptation, and Mitigation of Heat Stress on Wheat under Changing Climates.. 2022 , 23,	7
225	Genetic diversity and population structure of an African yam bean (<i>Sphenostylis stenocarpa</i>) collection from IITA GenBank.. 2022 , 12, 4437	
224	Genomic prediction of morphometric and colorimetric traits in Solanaceous fruits.	0
223	Genetic diversity and population structure analysis reveals the unique genetic composition of South African selected macadamia accessions. 2022 , 18, 1	0
222	A new strategy for using historical imbalanced yield data to conduct genome-wide association studies and develop genomic prediction models for wheat breeding. 2022 , 42, 1	
221	Advances from Conventional to Modern Plant Breeding Methodologies. 2022 , 10, 1-14	2

220	Can Epigenetics Guide the Production of Better Adapted Cultivars?. 2022 , 12, 838	1
219	Breaking Yield Ceiling in Wheat: Progress and Future Prospects.	1
218	Pyramiding of genes for grain protein content, grain quality, and rust resistance in eleven Indian bread wheat cultivars: a multi-institutional effort. 2022 , 42, 1	2
217	Recent Advances and Applicability of GBS, GWAS, and GS in Soybean. 2022 , 218-249	
216	Screening of different wheat genotypes against leaf rust and role of environmental factors affecting disease development. 2022 , 34, 101991	0
215	Meta-QTL Analysis in Rice and Cross-Genome Talk of the Genomic Regions Controlling Nitrogen Use Efficiency in Cereal Crops Revealing Phylogenetic Relationship.. 2021 , 12, 807210	3
214	Exploring the legacy of Central European historical winter wheat landraces.. 2021 , 11, 23915	2
213	Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (spp.).. 2021 , 12, 779386	2
212	A cross-scale approach to unravel the molecular basis of plant phenology in temperate and tropical climates. 2021 ,	0
211	Advances in Multi-Omics Approaches for Molecular Breeding of Black Rot Resistance in L.. 2021 , 12, 742553	0
210	GBS and a newly developed mRNA-GBS approach to link population genetic and transcriptome analyses reveal pattern differences between sites and treatments in red clover (<i>Trifolium pratense</i> L.).	
209	Genomic dissection reveals QTLs for grain biomass and correlated traits under drought stress in Ethiopian durum wheat (<i>Triticum turgidum</i> ssp . durum).	0
208	Climate-Smart Maize Breeding: The Potential of Arbuscular Mycorrhizal Symbiosis in Improving Yield, Biotic and Abiotic Stress Resistance, and Carbon and Nitrogen Sink Efficiency.	
207	Novel Plant Breeding Techniques Shake Hands with Cereals to Increase Production.. 2022 , 11,	1
206	Image_1.TIF. 2018 ,	
205	Image_2.TIF. 2018 ,	
204	Image_3.TIF. 2018 ,	
203	Image_4.TIF. 2018 ,	

202 Table_1.docx. **2018,**

201 Table_2.docx. **2018,**

200 Data_Sheet_1.DOCX. **2018,**

199 Image_1.TIFF. **2018,**

198 Table_1.XLSX. **2018,**

197 Table_2.XLSX. **2018,**

196 Table_1.DOCX. **2018,**

195 Data_Sheet_1.pdf. **2018,**

194 Presentation_1.pptx. **2019,**

193 Table_1.docx. **2019,**

192 Table_10.xlsx. **2019,**

191 Table_11.xlsx. **2019,**

190 Table_2.xlsx. **2019,**

189 Table_3.xlsx. **2019,**

188 Table_4.xlsx. **2019,**

187 Table_5.xlsx. **2019,**

186 Table_6.xlsx. **2019,**

185 Table_7.xlsx. **2019,**

184 Table_8.xlsx. 2019,

183 Table_9.xlsx. 2019,

182 Table_1.xlsx. 2018,

181 Table_2.docx. 2018,

180 Table_3.docx. 2018,

179 Table_4.docx. 2018,

178 Table_5.docx. 2018,

177 Image_1.TIF. 2018,

176 Image_10.TIF. 2018,

175 Image_11.TIF. 2018,

174 Image_12.TIF. 2018,

173 Image_13.TIF. 2018,

172 Image_14.TIF. 2018,

171 Image_2.TIF. 2018,

170 Image_3.TIF. 2018,

169 Image_4.TIF. 2018,

168 Image_5.TIF. 2018,

167 Image_6.TIF. 2018,

166 Image_7.TIF. 2018,

165 Image_8.TIF. 2018,

164 Image_9.TIF. 2018,

163 Table_1.csv. 2018,

162 Table_2.XLSX. 2018,

161 Table_3.XLSX. 2018,

160 Table_4.XLSX. 2018,

159 Table_5.XLSX. 2018,

158 Table_1.DOCX. 2020,

157 Presentation_1.ZIP. 2018,

156 Image_1.TIFF. 2019,

155 Table_1.XLSX. 2019,

154 Table_2.XLSX. 2019,

153 Table_3.XLSX. 2019,

152 Image_1.TIFF. 2020,

151 Table_1.XLSX. 2020,

150 Table_2.XLSX. 2020,

149 Table_3.XLSX. 2020,

- 148 A High-Density Genetic Map and QTL Fine Mapping for Growth- and Sex-Related Traits in Red Swamp Crayfish (*Procambarus clarkii*). **2022**, 13, 852280 0
- 147 Integrated Management Practices for Incremental Wheat Productivity. **2022**, 367-392 1
- 146 Advances in agricultural bioinformatics: an outlook of multi-omics approaches. **2022**, 3-21 0
- 145 Promises and benefits of omics approaches to data-driven science industries. **2022**, 23-36 0
- 144 Perspectives on the Marker-Assisted Breeding of the Cd-PSCs. **2022**, 197-211 0
- 143 Bioinformatics intervention in identification and development of molecular markers: an overview. **2022**, 537-559 0
- 142 Wheat Breeding. **2022**, 39-111 0
- 141 Powdery Mildew of Wheat: Research Progress, Opportunities, and Challenges. **2022**, 133-178 0
- 140 Evaluation of Population Structure and Estimation of Genetic Parameters in Breeding Lines and Landraces Populations of Durum Wheat Using ISSR Markers. **2022**, 8, 23-32 0
- 139 Current Strategies and Future of Mutation Breeding in Soybean Improvement. **2022**, 1-11 1
- 138 A Comparative Study of Flavonoids and Carotenoids Revealed Metabolite Responses for Various Flower Colorations Between L. and L.. **2022**, 13, 828042 1
- 137 Faster marker-assisted selection of pollination-constant non-astringent persimmon offspring by crude-sample PCR. **2022**, 43-50 0
- 136 The Development of Two High-Yield and High-Quality Functional Rice Cultivars Using Marker-Assisted Selection and Conventional Breeding Methods.. **2022**, 23, 1-11 0
- 135 Closing the gap between phenotyping and genotyping: review of advanced, image-based phenotyping technologies in forestry. **2022**, 79, 1-11 0
- 134 Nanotechnology-enabled biofortification strategies for micronutrients enrichment of food crops: Current understanding and future scope. **2022**, 100407 1
- 133 Analysis of the genes controlling cotton fiber length reveals the molecular basis of plant breeding and the genetic potential of current cultivars for continued improvement. **2022**, 111318 0
- 132 Cadmium Toxicity in Rice: Tolerance Mechanisms and Their Management. **2022**, 833-850 0
- 131 Virulence Structure and Genetic Diversity of *Blumeria graminis* f. sp. *avenae* from Different Regions of Europe. **2022**, 11, 1358 0

130	Phenotypic variation and quantitative trait loci for resistance to southern anthracnose and clover rot in red clover.	
129	A meta analysis of low temperature tolerance QTL in maize. 2022,	0
128	Marker-Assisted Backcross Breeding for Improving Bruchid (<i>Callosobruchus</i> spp.) Resistance in Mung Bean (<i>Vigna radiata</i> L.). 2022, 12, 1271	0
127	Breeding and Omics Approaches to Understand Abiotic Stress Response in Rice. 2022, 341-404	
126	Molecular Breeding and Marker-Assisted Selection for Crop Improvement. 2022, 129-164	
125	Breeding Methods: Population Improvement and Selection Methods. 2022, 83-96	
124	Genetic Improvement of Wheat for Drought Tolerance: Progress, Challenges and Opportunities. 2022, 11, 1331	2
123	Development and validation of an optimized marker set for genomic selection in southern U.S. rice breeding programs.	0
122	Mapping of QTL and candidate genes associated with powdery mildew resistance in triticale (<i>Triticosecale</i> Wittm.).	1
121	Development of Superior Fibre Quality Upland Cotton Cultivar Series Bavnaq Using Marker-Assisted Selection. 2022, 13,	1
120	QTL Analysis of Grain Yield-Related Traits for Terminal Heat Stress Tolerance in Wheat Using SSR Markers. 2022, 25, 516-530	
119	Next-Generation Sequencing Technologies: Approaches and Applications for Crop Improvement. 2022, 31-94	1
118	Exploration of Modern Biotechnology Trends in Functional Foods. 2022, 15-42	
117	QTL Mapping for Resistance to Bacterial Wilt Caused by Two Isolates of <i>Ralstonia solanacearum</i> in Chili Pepper (<i>Capsicum annuum</i> L.). 2022, 11, 1551	0
116	Validity Control of Markers Used in Molecular Marker Assisted Selection in Tomato. 300-309	
115	Identification of Gene Biomarkers for Tigilanol Tiglate Content in <i>Fontainea picrosperma</i> . 2022, 27, 3980	0
114	Contribution of IR20 and IR64 in Developing Three Bangladeshi Popular Rice Cultivars. 2022, 10, 81-93	
113	Genome edited wheat- current advances for the second green revolution. 2022, 60, 108006	0

- 112 Current trends in genetic enhancement of legumes in the genomics era for a sustainable future. **2022**, 533-552 0
- 111 Omics Technology: Revolution in Plant Biology. **2022**, 197-212
- 110 DNA Markers: An Essential Tool for Cis-genic Improvement of Rice. **2022**, 183-211
- 109 Physiological and Molecular Approaches for Developing Thermotolerance in Vegetable Crops: A Growth, Yield and Sustenance Perspective. 13, 1
- 108 Quantitative Trait Locus Mapping of Marsh Spot Disease Resistance in Cranberry Common Bean (*Phaseolus vulgaris* L.). **2022**, 23, 7639 0
- 107 Thirty Years of Mungbean Genome Research: Where Do We Stand and What Have We Learned?. 13,
- 106 Data mining of transcriptional biomarkers at different cotton fiber developmental stages.
- 105 QTLs Controlling Physiological and Morphological Traits of Barley (*Hordeum vulgare* L.) Seedlings under Salinity, Drought, and Normal Conditions. **2022**, 11, 26 0
- 104 Investigation of the association between goat DNMT3B gene polymorphism and growth traits. 1-7
- 103 Using Genomic Selection to Develop Performance-Based Restoration Plant Materials. **2022**, 23, 8275 2
- 102 IN VITRO SELECTION OF PATHOGEN RESISTANT GENOTYPES AMONG SOLANUM WILD SPECIES USING DNA MARKERS. **2020**, 28, 57-63
- 101 Molecular Breeding to Overcome Biotic Stresses in Soybean: Update. **2022**, 11, 1967 3
- 100 TaGSNE, a WRKY transcription factor overcomes the tradeoff between grain size and grain number and associates with root development in common wheat.
- 99 Capsicum: Breeding Prospects and Perspectives for Higher Productivity.
- 98 Validation of Molecular Markers Significant for Flowering Time, Plant Lodging, Stem Geometry Properties, and Raffinose Family Oligosaccharides in Pea (*Pisum sativum* L.). **2022**, 12, 1125 0
- 97 From Evolution to Revolution: Accelerating Crop Domestication Through Genome Editing. 0
- 96 Does the paradigm of genotype-environment associations need to be re-assessed? The paradox of adaptive phenotypic clines with non-clinal patterns in causal alleles. 0
- 95 Identification of single major QTL and candidate gene(s) governing hull-less seed trait in pumpkin. 13, 0

- 94 Mapping of genomic regions linked to stemphylium blight (*Stemphylium botryosum* Wallr.) resistance in lentil using linkage mapping and marker-trait association analysis.
- 93 Integrated Approach in Genomic Selection to Accelerate Genetic Gain in Sugarcane. **2022**, 11, 2139 2
- 92 Screening a collection of local and foreign varieties of *Solanum lycopersicum* L. in Kazakhstan for genetic markers of resistance against three tomato viruses. **2022**, 8, e10095 0
- 91 Identification of two new QTLs of maize (*Zea mays* L.) underlying kernel row number using the HNAU-NAM1 population. **2022**, 23,
- 90 A genome-wide association study identifies SNPs and candidate genes associated with nacre color of pearl oyster *Pinctada fucata martensii*. **2022**, 561, 738743 0
- 89 Recent Advances in Omics Approaches for Mungbean Improvement. **2022**, 181-200 0
- 88 Omics research for crop improvement in spices. **2022**, 467-500 0
- 87 Marker-Assisted Selection for Value Addition in Crop Plants. **2022**, 23-39 0
- 86 Recent Genetic Tools for the Management of Stored Product Pests. **2022**, 559-567 0
- 85 *Diospyros Lotus* Genome. **2022**, 65-74 0
- 84 Genomics-Enabled Breeding for Heat and Drought Stress Tolerance in Crop Plants. **2022**, 299-321 0
- 83 Genomic Designing for Abiotic Stress Tolerant in Potato. **2022**, 49-75 0
- 82 Marker-assisted introgression of bacterial blight resistance gene xa13 into improved CO43. **2022**, 218, 0
- 81 Evaluation of Models for Utilization in Genomic Prediction of Agronomic Traits in the Louisiana Sugarcane Breeding Program. **2022**, 12, 1330 0
- 80 Quantitative trait loci identification and breeding value estimation of grain weight-related traits based on a new wheat 50K single nucleotide polymorphism array-derived genetic map. 13, 0
- 79 Advances in integrated genomic selection for rapid genetic gain in crop improvement: a review. **2022**, 256, 1
- 78 Dissecting the genetic basis of bioactive metabolites and fruit quality traits in blueberries (*Vaccinium corymbosum* L.). 13, 1
- 77 Phenotypic variation and quantitative trait loci for resistance to southern anthracnose and clover rot in red clover. 0

- 76 Mapping of genomic regions linked to stemphylium blight (*Stemphylium botryosum* Wallr.) resistance in lentil using linkage mapping and marker-trait association analysis. 0
- 75 Designing Tobacco Genomes for Resistance to Biotic Stresses. **2022**, 441-581 1
- 74 The Lablab Genome: Recent Advances and Future Perspectives. **2022**, 229-253 0
- 73 Abiotic Stress Resistance in Tobacco: Advances and Strategies. **2022**, 329-427 0
- 72 Transgenics and Crop Improvement. **2022**, 131-347 0
- 71 Marker assisted improvement for leaf rust and moisture deficit stress tolerance in wheat variety HD3086. 13, 0
- 70 Validation of KASP-SNP markers in cassava germplasm for marker-assisted selection of increased carotenoid content and dry matter content. 13, 0
- 69 Legume Breeding: From Conventional Method to Modern Technique. 0
- 68 Role of Biotechnology in Climate-Resilient Agriculture. **2022**, 78-94 0
- 67 Development of breeder chip for gene detection and molecular-assisted selection by target sequencing in wheat. 0
- 66 Multi-environment genomic selection in rice elite breeding lines. 0
- 65 Developing Genetic Engineering Techniques for Control of Seed Size and Yield. **2022**, 23, 13256 0
- 64 Identification of QTL and candidate genes associated with biomass yield and Feed Quality in response to water deficit in alfalfa (*Medicago sativa* L.) using linkage mapping and RNA-Seq. 13, 0
- 63 Development of New Drought Tolerant Breeding Lines for Vietnam Using Marker-Assisted Backcrossing. 59, 1-13 0
- 62 OMICS in Fodder Crops: Applications, Challenges, and Prospects. **2022**, 44, 5440-5473 1
- 61 Introgression of *tsv1* improves tungro disease resistance of a rice variety BRR1 dhan71. **2022**, 12, 0
- 60 Novel Single-Nucleotide Variants for Morpho-Physiological Traits Involved in Enhancing Drought Stress Tolerance in Barley. **2022**, 11, 3072 0
- 59 Editorial: Genetics and molecular breeding in aquaculture animals. 13, 0

58	Identification and validation of quantitative trait loci for chlorophyll content of flag leaf in wheat under different phosphorus treatments. 13,	0
57	Molecular breeding for drought and heat stress in maize: Revisiting the progress and achievements. 2023 , 57-74	0
56	Nutritional quality improvement in maize (<i>Zea mays</i>): Progress and challenges. 2019 , 89,	1
55	In vitro selection of chili (<i>Capsicum annuum</i>) varieties tolerant to reduced nitrogen supplements.	0
54	Polymorphism within the GATA binding protein 4 gene is significantly associated with goat litter size. 1-10	0
53	Fine Mapping and Identification of a Candidate Gene of Downy Mildew Resistance, RPF2, in Spinach (<i>Spinacia oleracea</i> L.). 2022 , 23, 14872	0
52	SNP-based bulk segregant analysis revealed disease resistance QTLs associated with northern corn leaf blight in maize. 13,	0
51	Transgenic Improvement for Biotic Resistance of Crops. 2022 , 23, 14370	0
50	QTL mapping of yield components and kernel traits in wheat cultivars TAM 112 and Duster. 13,	1
49	Linking genetic markers with an eco-physiological model to pyramid favorable alleles and design wheat ideotypes.	0
48	Biodiversity and ecosystem stability based on molecular and genetic technologies in plant breeding. 2022 , 1112, 012102	0
47	Resistance to <i>Pythium</i> root rot and anthracnose among Kenyan common bean genotypes and marker-assisted introgression of resistance genes. 1-21	0
46	Sustainable Agriculture Through Technological Innovations. 2023 , 223-239	0
45	Advances in Lettuce (<i>Lactuca</i> spp.) Molecular Breeding Strategies. 2023 , 251-277	0
44	Molecular Markers for Detecting Inflorescence Size of <i>Brassica oleracea</i> L. Crops and <i>B. oleracea</i> Complex Species (n = 9) Useful for Breeding of Broccoli (<i>B. oleracea</i> var. <i>italica</i>) and Cauliflower (<i>B. oleracea</i> var. <i>botrytis</i>). 2023 , 12, 407	2
43	Plant growth promoting microorganisms mediated abiotic stress tolerance in crop plants: a critical appraisal.	1
42	Assessment of genetic diversity and population structure in wild <i>Ziziphus</i> species from northwest India using SSR marker technique. 2023 , 21,	0
41	Big Data Revolution and Machine Learning to Solve Genetic Mysteries in Crop Breeding. 2023 , 83-101	0

- 40 Genetic control of morphological traits useful for improving sorghum. **2023**, 1
- 39 Quantitative Trait Loci Associated with Agronomical Traits in Strawberry. 0
- 38 Genotyping by sequencing and a newly developed mRNA-GBS approach to link population genetic and transcriptome analyses reveal pattern differences between sites and treatments in red clover (*Trifolium pratense* L.). 10, 0
- 37 Identification of Genomic Regions Associated with High Grain Zn Content in Polished Rice Using Genotyping-by-Sequencing (GBS). **2023**, 12, 144 0
- 36 Dissecting the genetic architecture of leaf morphology traits in mungbean (*Vigna radiata* (L.) *Wizcek*) using genome-wide association study. **2023**, 6, 0
- 35 Advances in genomics for diversity studies and trait improvement in temperate fruit and nut crops under changing climatic scenarios. 13, 0
- 34 Breeding techniques to dispense higher genetic gains. 13, 0
- 33 Digitalizing breeding in plants: A new trend of next-generation breeding based on genomic prediction. 14, 0
- 32 Contributions of plant breeding to soil carbon storage: Retrospect and prospects. 0
- 31 Mitigation of abiotic stress tolerance in wheat through conventional breeding. **2023**, 15-32 0
- 30 Recent advances in marine biotechnology. **2023**, 187-217 0
- 29 Marker-trait association analyses revealed major novel QTLs for grain yield and related traits in durum wheat. 13, 0
- 28 Morphophysiological and Molecular Diversity in Mung Bean (*Vigna radiata* L.). **2023**, 115-147 0
- 27 Molecular Characterization and Mapping of Stress Resistance Genes Using SNP Platform in Legumes. **2023**, 149-188 0
- 26 Phenotyping drought tolerance and yield performance of barley using a combination of imaging methods. **2023**, 209, 105314 0
- 25 Genetic linkage map construction and QTL mapping of blade length and width in *Saccharina japonica* using SSR and SNP markers. 10, 0
- 24 Molecular mapping of two recessive genes controlling resistance to bacterial leaf pustule disease in soybean (*Glycine max*). **2023**, 142, 184-194 0
- 23 Backcrossing with Marker Assistance to Introduce Broad-Spectrum Bacterial Leaf Blight Resistance in the Malaysian Elite Variety MR297. **2023**, 13, 372 0

- 22 Multi-environment Genomic Selection in Rice Elite Breeding Lines. **2023**, 16, ○
- 21 Development of breeder chip for gene detection and molecular-assisted selection by target sequencing in wheat. **2023**, 43, ○
- 20 Modified High-Resolution Melting (HRM) Marker Systems Increasing Discriminability Between Homozygous Alleles. **2023**, 351-363 ○
- 19 Identification and validation of novel genomic SSR markers for molecular characterization of guava (*Psidium guajava* L.). **2023**, 155, 79-89 ○
- 18 Pyramiding Rice Blast Resistance Gene Pi2 and Fragrance Gene badh2. **2023**, 13, 589 ○
- 17 Development of bread wheat (*Triticum aestivum* L) variety HD3411 following marker-assisted backcross breeding for drought tolerance. 14, ○
- 16 Temperature response of plants and heat tolerance in Rice: A review. **2023**, 135-203 ○
- 15 Genome-wide association mapping for pre-harvest sprouting in European winter wheat detects novel resistance QTL, pleiotropic effects, and structural variation in multiple genomes. ○
- 14 Food Production and Ecosystem Protection. **2023**, ○
- 13 IP4GS: Bringing genomic selection analysis to breeders. 14, ○
- 12 Marker-Assisted Selection of Male-Sterile and Maintainer Line in Chili Improvement by Backcross Breeding. **2023**, 9, 357 ○
- 11 Meta-QTL s and haplotypes for efficient zinc biofortification of rice. ○
- 10 Pyramiding QTLs using multiparental advanced generation introgression lines enhances salinity tolerance in rice. **2023**, 45, ○
- 9 State of the Art of the Molecular Biology of the Interaction between Cocoa and Witches' Broom Disease: A Systematic Review. **2023**, 24, 5684 ○
- 8 Perceptions of plant breeding methods from phenotypic selection to genetic modification and new breeding technologies [1-49] ○
- 7 Molecular dissection of connected rice populations revealed important genomic regions for agronomic and biofortification traits. 14, ○
- 6 From Transgenesis to Genome Editing in Crop Improvement: Applications, Marketing, and Legal Issues. **2023**, 24, 7122 ○
- 5 Breeding and Genomic Approaches towards Development of Fusarium Wilt Resistance in Chickpea. **2023**, 13, 988 ○

- 4 Marker-assisted selection and use of molecular markers in sunflower breeding for resistance to diseases and parasites. **2022**, 14-29
- 3 Smart breeding driven by advances in sequencing technology. **2023**, 1, 43-56
- 2 Marker-assisted selection for the improvement of cereals and pseudocereals. **2023**, 253-283
- 1 Are There Adequate Incentives for Research and Innovation in the Plant Breeding Supply Chain?.