Title of Papers Presented at the 145th Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 Development of "Pedigree Tracer (PEDIT)", a Web-Database system to support crop breeding in Hokkaido Research Organization (HRO)

☆Adegawa, S.[1], K. Horikawa[2], Y. Tanaka[1], T. Suzuki[3] (1.Central Agr. Exp. Stn., HRO, 2.Kamikawa Agr. Exp. Stn., HRO, 3.Agr. Res. Dept., HRO)

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102 Improvement of Plant GARDEN, a portal site for plant genome information (FY2023, Q4 ver): Development of tools to use evolutionary information.

☆Ichihara, H.[1], M. Yamada[1], Y. Toda[1], A. Nakaya[2], S. Yamashita[1], T. Shimizu[1], S. Shirasawa[1], M. Kohara[1], H. Hirakawa[1], Y. Nakamura[1,3], T. Tanabata[1], S. Tabata[1], S. Isobe[1] (1.Kazusa DNA Res. Inst., 2.Grad. Sch. Front. Sci., Univ. Tokyo, 3.Nat. Inst. Genet.)

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103 A mutation database for 2,000 tobacco EMS lines by whole genome sequencing

○UDAGAWA, H., T. TAKEUCHI, Y. TAKAKURA (JAPAN TOBACCO INC. Leaf Tobacco Research Center)

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104 Development of a novel alignment-free approach for investigating past hybridizations

☆Minoji, K.[1], T. Sakai[1], A. Ohta[1], Y. Sugihara[2], A. Kudoh[1], R. Terauchi[1,3] (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.IBRC)

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105 Development of KASP markers for the potato virus Y resistance gene *Rychc* using whole-genome resequencing data.

○Asano, K.[1,2], J. Endelman[2] (1.HARC, NARO, 2.University of Wisconsin–Madison)

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106 DNAMarkMaker: developing ARMS and CAPS marker development from resequencing data with NGS short reads

☆Saiga, S.[1], T. Segawa[1], M. Takata[1], R. Kumazawa[1], M. Hara[1], H. Yamakawa[2], H. Takagi[1] (1.Ishikawa Prefectural University, 2.NICS,NARO)

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107 QTL analysis for petal length using interspecific crosses among *Eustoma* species.

○Kawakatsu, K.[1], A. Nagano[2], N. Fukuta[1], T. Kawakatsu[3] (1.NIVFS, NARO, 2.Fac. Agr., Ryukoku Univ., 3.Inst Agrobiological Sci, NARO)

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108 Identification of the pigment and causative gene for reddish seed coat in soybean

☆Suganami, M.[1], S. Kojima[2], H. Yoshida[1], H. Takahashi[1,3], N. Nihei[1,3], T. Matsuda[1,3], M. Watanabe[4], M. Matsuoka[1] (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Graduate School of Agricultural Science, Tohoku University, 3.Department of Agriculture, Fukushima University, 4.Graduate School of Life Sciences, Tohoku University)

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109 Identification of QTLs associated with good eating quality in Dadachamame and estimation of responsible genes for these QTLs

☆Shioya, N.[1], S. Yokoyama[2], Y. Takagi[1], A. Miyagi[1,2], M. Kawai-Yamada[3], E. Ogiso-Tanaka[4], T. Hoshino[1,2] (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ., 3.Grad. Sch. Sci. Eng., Saitama Univ., 4.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci.)

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110 MSH1 is involved in Mitochondrial Genome Repair through Introduction of Double-Strand Breaks around Mismatched Base Pairs.

☆zhou, c., N. Tsutsumi, S. Arimura (Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo)

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111 Does gene dosage compensation occur in Arabidopsis chromosomes?

Ikoma, T.[1], R. Nishijima[2], M. Ikeda[1,2], A. Nagalla[3], T. Abe[3], ○Y. Kazama[1,2,3] (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.Dep. Biosci. Biotech., Fukui Pref. Univ., 3.RIKEN Nishina Cent.)

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113 Identification of novel QTLs for heading date and lodging resistance using a population derived from a cross between temperate *japonica* rice in Japan

☆Chigira, K.[1], M. Yamasaki[2], S. Adachi[1], T. Ookawa[1] (1.Graduate School of Agriculture, Tokyo University of Agriculture and Technology, 2.Graduate School of Science and Technology, Niigata University)

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114 QTL analysis for aphid resistance in sorghum

☆Inui, R., M. Ishimori, H. Tanaka, A. Makino, J. Yamada, N. Tsutsumi, H. Takanashi (The University of Tokyo / Graduate School of Agricultural and Life Sciences)

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115 Mapping of genes controlling prostrate trait of barley using high-density linkage map

☆Nishimura, K.[1], M. Okuma[2], N. Fukushima[2], Y. Monden[1], H. Nishida[1], K. Kato[1] (1.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ., 2.Grad. Sch. Environ. Life Sci., Okayama Univ.)

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117 Comparative genomic context analysis for the somaclonal evolution of Satsuma mandarin (Citrus unshiu)

☆Matsuda, T.[1], K. Masuda[1], I. Henry[2], L. Comai[2], T. Akagi[1] (1.Graduate School of Environmental, Life, Natural Science and Technology, Okayama University, 2.Department of Plant Biology and Genome Center, University of California Davis)

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118 Evolutionary dynamics of giant sex chromosomes in the genus *Silene*

○Akagi, T.[1], N. Fujita[1], K. Masuda[1], K. Shirasawa[2], K. Nagaki[3], A. Horiuchi[1], E. Kuwada[1], R. Kunou[1], K. Nakamura[3], Y. Ikeda[3], K. Ushijima[1], D. Charlesworth[4] (1.Grad. Sch. Environ. Life Nat. Sci., Okayama Univ., 2.Kazusa DNA Res. Inst., 3.Inst. Plant Sci. Res., Okayama Univ., 4.Inst. Ecol. Evol., Univ. Edinburgh)

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119 "Tokoro": A rhizomatous crop cultivated in Tohoku-machi, Aomori Prefecture

☆Natsume, S.[1], Y. Sugihara[2], A. Kudoh[3], K. Oikawa[1], M. Shimizu[1], Y. Ishikawa[3], M. Nishihara[1], A. Abe[1], H. Innan[4], R. Terauchi[1,3] (1.Iwate Biotechnology Research Center, 2.The Sainsbury Laboratory, University of East Anglia, 3.Crop Evolution Laboratory, Kyoto University, 4.Research Center for Integrative Evolutionary Science, The Graduate University for Advanced Studies)

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120 Genome analysis of allotetraploid wasabi (*Eutrema japonicum*)

○Tanaka, H.[1], N. Masahiro[1], A. Toyoda[2], K. Yamane[3], T. Itoh[1] (1.Tokyo Inst. Tech. LST., 2.Nat. Inst. of Gen. Comp. Genome., 3.Gifu U. App. Bio. Sci.)

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121 Population structure analysis of *Oryza rufipogon* using large-scale sequencing

○Yoshikawa, T., Y. Sato (Nat. Inst. Genet.)

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122 Population Geonmics on the Origin of Azuki Bean

○Naito, K.[1], C. Chih-Cheng[2], C. Muto[1], C. Lee[2] (1.Res. Cntr. Genet. Resour., NARO, 2.Inst. Ecol. Evol. Biol., Natl. Taiwan Univ)

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123 Painting the genome.

Watanabe, S.[1], H. Yoshida[2], ○A. Kobayashi[1], N. Saka[3], M. Suganami[2], M. Matsuoka[2] (1.Fukui Agri. Exp. Stn., 2.Fukushima Univ., 3.Nagoya Univ.)

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201 Development of multi-wavelength image analysis method for objective evaluation of seed quality of soybean

○Yamada, T.[1], Y. Nanjo[1], J. Sun[2], E. Aoki[1], K. Hirata[1], S. Kato[1], R. Yamazaki[1], J. Yonemaru[2], H. Nakamura[1], G. Ishikawa[1], A. Kaga[1] (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)

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202 Estimation of amylose content of white rice flour by near-infrared spectroscopy

○Araki, E.[1], T. Umemoto[1], K. Hori[2] (1.Inst. Food Res., NARO, 2.Inst. Crop. Sci., NARO)

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203 Cloning of *MP3* gene from a rice cultivar "Koshihikari" that forms an ideal plant architecuture and improves grain yield under climate change

○Takai, T.[1], Y. Taniguchi[2], M. Takahashi[2], H. Nagasaki[6], E. Yamamoto[5], S. Hirose[2], N. Hara[2], H. Akashi[3], J. Ito[3], Y. Arai (Sanoh)[2], K. Hori[2], S. Fukuoka[2], H. Sakai[2], T. Tokida[2], Y. Usui[2], H. Nakamura[7], K. Kawamura[1], H. Asai[1], T. Ishizaki[1], K. Maruyama[1], K. Mochida[4], N. Kobayashi[1,2], M. Kondo[2,8], H. Tsuji[3,8], Y. Tsujimoto[1], T. Hasegawa[2], Y. Uga[2] (1.JIRCAS, 2.NARO, 3.Yokohama City Univ., 4.RIKEN, 5.Meiji Univ., 6.Kazusa DNA Research Institute, 7.Taiyo Keiki Co. Ltd., 8.Nagoya Univ.)

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204 Characteristics of paddy rice lines introduced with the DENSE AND ERECT PANICLE 1 (*DEP1*) gene in Hokkaido.

○Kinoshita, M.[1], K. Douman[2], K. Horikawa[1], Y. Yamashita[2], S. Adegawa[2], C. Souma[2] (1.Kamikawa Agr. Exp. Stn., HRO, 2.Central Agr. Exp. Stn., HRO)

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205 Field trial test of *Gn1a* knockout rice line aiming enlarged sink capacity by genome-editing. II. When “IR64” is used as the original variety.

○Komatsu, A.[1], M. Ohtake[1], M. Nagata[1], H. Kato[2], M. Kondo[3] (1.Institute of Agrobiological Sciences, NARO, 2.Institute of Crop Science, NARO, 3.Graduate School of Bioagricultural Sciences, Nagoya University)

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206 Genetic characterization of an Indica Group rice variety Supa in Zambia

○Fukuta, Y.[1], T. Sato[2], K. Toriyama[2], H. Kobayashi[1], N. Nagano[1], R. Mochizuki[1] (1.University of the Ryukyus, 2.Tohoku University)

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207 Detection of QTLs controlling internode elongation pattern using rice dwarf mutants *d1* (No.1)

☆Moe, S.[1], T. Ha[1], V. Reyes[1], K. Doi[1], K. Miura[2], A. Maeno[3], K. Tsuda[3,4], K. Nagai[5], M. Ashikari[5] (1.Graduate School of Bioagricultural Sciences, Nagoya University, 2.Faculty of Biotechnology, Fukui Prefectural University, 3.National Institute of Genetics, 4.Graduate University for Advanced Studies, 5.Bioscience and Biotechnology Center, Nagoya University)

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208 Detection of QTLs controlling internode elongation pattern using rice dwarf mutants *d1* (No.2)

☆Ha, T.[1], S. Moe[1], V. Reyes[1], K. Doi[1], K. Miura[2], A. Maeno[3], K. Tsuda[3,4], K. Nagai[5], M. Ashikari[5] (1.Graduate School of Bioagricultural Sciences, Nagoya University, 2.Faculty of Biotechnology, Fukui Prefectural University, 3.National Institute of Genetics, 4.Graduate University for Advanced Studies, 5.Bioscience and Biotechnology Center, Nagoya University)

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209 Genetic differentiation of safflower genetic resources revealed by variation analysis in chloroplast *trn*F region

☆Hosono, K.[1], S. Kimura[2], H. Suzuki[2], T. Sasanuma[1,2] (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ.)

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210 Is NEKODE in foxtail millet caused by transposon-insertion into the *YABBY* gene?

○Fukunaga, K.[1], N. Abe[1], A. Abe[2], M. Hamashita[1], I. Watanabe[1] (1.Faculty of Bioresource Sci.,　Pref. U. Hiroshima, 2.Iwate Biotech.Res.Center)

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213 A loss-of-function mutation in the ortholog of soybean maturity gene E3 detected in early maturing cultivars of common beans

○Yamaguchi, N.[1], K. Tanaka[2], A. Hosoi[3], K. Nakagawa[4], H. Sato[4] (1.Central Agr. Exp. Sta., HRO, 2.Tokyo Univ. of Info. Sci., 3.Genome Research Center, Tokyo Univ. of Agri., 4.Tokachi Agr. Exp. Sta., HRO)

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214 Genome-wide association study of resistance to Phytophthora stem rot of Adzuki bean, using phenotyping data obtained by breeding programs

☆Horikawa, K.[1], M. kayamori[1], K. Shirasawa[2], N. Yamaguchi[3], C. Souma[3], K. Sato[3], M. Nagahama[1], R. Ogura[4], O. Fujine[5], K. Todai[6], n. Murata[6], H. Nagasawa[6], Y. Horiuchi[6] (1.Kamikawa Agri. Exp. Stn., HRO, 2.Kazusa DNA Res. Inst., 3.Central Agri. Exp. Stn., HRO, 4.Kitami Agri. Exp. Sta., HRO, 5.Ornamental plant & Veg. Res. Ctr., HRO, 6.Tokachi Agri. Exp. Sta., HRO)

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215 Application of Genome-Wide Association studies and Genomic selection to potato breeding.

○Shinada, H.[1], N. Yamaguchi[2], K. Shirasawa[3] (1.Kitami Agr. Exp. Sta., HRO, 2.Central Agr. Exp. Sta., HRO, 3.Kazusa DNA Res. Inst.)

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216 Design and validation of genomic prediction models for fruit traits to improve the efficiency of the sweet cherry breeding program

☆Shimada, N.[1], K. Shirasawa[2], N. Yamaguchi[1], M. Sato[1], M. Yoshida[1] (1.Central Agr. Exp. Sta., HRO, 2.Kazusa DNA Res. Inst.)

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217 Mutant alleles in the *SSII* gene that causes low-temperature gelatinization properties of starch in sweetpotato revealed by WGS using Nanopore long reads

☆Nakahara, T.[1], I. Kataoka[1], K. Shimo[1], K. Tada[2], M. Tanaka[3], A. Kobayashi[3], M. Izumitani[4], K. Naito[5], K. Nishimura[4], H. Nishida[4], K. Kato[4], Y. Monden[4] (1.Fac. Agri., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.KARC/NARO, 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 5.NGRC/NARO)

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218 Identification of genetic region related to the anthocyanin accumulation in sweetpotato storage roots and sequence analysis of the candidate gene

☆Horita, N.[1], Y. Okada[2], H. Kanzaki[1], M. Kurihara[3], K. Nishimura[1], H. Nishida[1], K. Kato[1], Y. Monden[1] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Sci., Okayama Univ.)

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219 QTL analysis of shoot morphology traits in RIL population of green foxtail and coastal green foxtail

Hira, D.[1], K. Fukunaga[2], ○T. Ohsako[3] (1.Fac. Life Env. Sci., Kyoto Pref. Univ., 2.Fac. Bioresource Sci., Pref. Univ. Hiroshima, 3.Grad. Sch. Life Env. Sci., Kyoto Pref. Univ.)

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220 Genetic study on the search for the gene responsible for the amaranth shattering trait

☆Fujihara, R.[1], F. Kondo[2,3], T. Mikoshiba[4], K. Matushima[5], K. Nemoto[5] (1.Fac. Agric., Univ. Shinshu, 2.Grad. Sch. Med. Sci. Tech, 3.JSPS Research Fellowship for Young Scientists, 4.Grad. Sch. Sci. Tech., Shinshu U, 5.Inst. Agric. Acad. Assy. Fac., Shinshu U)

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221 Search for strawberry powdery mildew race1 resistance loci using genome wide association studies.

Ebihara, Y., ☆N. Inubushi (CAFRC)

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222 Genome-wide association study for flowering time using small spray-type chrysanthemum varieties.

○Inazaki, F.[1], K. Shirasawa[2], S. Kurihara[1,3], T. Gounai[1] (1.Plant Biotech. Inst., Ibaraki Agri. Cent., 2.Kazusa DNA Res. Inst., 3.Hitachiomiya Dist. Agri. Dev. Ext. Cent.)

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223 Production and indentation of an interspecific hybrid between *Artemisia princeps* and *A. vulgaris*

☆Xu, T., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)

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301 Development of a predicting model for heading time and yield of a rice progeny population based on genomic information, meteorological and spatial effect.

○Goto, A.[1,2], S. Taniguchi[2], T. Hayashi[2], S. Yabe[1], K. Matsushita[1], H. Kajiya-Kanegae[2], M. Yano[2], J. Yonemaru[2] (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)

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302 Estimating growth curves from fragmented time series measurements: application to citrus growth assesment

☆Kimura, S.[1], M. Minamikawa[2], K. Nonaka[3], T. Shimizu[3], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ, 3.NIFTS, NARO)

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303 Genomic prediction of fruit shape using elliptic Fourier descriptors in pepper

☆Kumanomido, Y.[1], K. Matsushima[2], M. D'Andrea[3], V. Palombo[3], K. Nemoto[2], F. Kondo[3,4,5] (1.Grad. Sch. Sci. Tech., Univ. Shinshu, 2.Inst. Agric. Acad. Assay. Fac., Univ. Shinshu, 3.Fac. Agric., Univ. Molise, 4.Grad. Sch. Med. Sci. Tech., Univ.Shinshu, 5.JSPS Research Followship for Young Scientists)

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304 Development of a sweet potato spoilage risk detection system trained from 3D data

○Taguchi, K.[1], K. Kodama[2], M. Nishinaka[1], H. Inoue[3], W. Guo[2], Y. Nishiba[3] (1.NARO CARC, 2.Univ. Tokyo, 3.NARO KARC)

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305 Image Selection of Planted seedlings from Strawberry Crossbreeding seedlings through Machine Learning

○Yamada, H.[1], T. Kawata[1], S. Mochizuki[1], Y. Nomura[2], H. Mineno[2] (1.Shizuoka Pref. Res. Inst. Agri. Forest . Station, 2.Fac. Inform., Dept. Comp. Sci., Shizuoka Univ.)

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306 Selection method of a high milling yield soft wheat by multispectral imaging analysis of cross-sections of wheat grains.

○Kato, K., T. Ikeda, Y. Ban, K. Kawaguchi, M. Ito (Western Region Agricultural Research Center, NARO)

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307 Breeding selection criteria for grain size of high-yielding indeterminate Soybeans in Hokkaido, Japan.

☆Igarashi, H.[1], A. Kaga[2], N. Yamaguchi[3] (1.Tokachi Agr. Exp. Stn., HRO, 2.Inst. Crop Sci., NARO, 3.Central Agr. Exp. Stn., HRO)

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308 Evaluating the suitability for mechanical harvesting of adzuki beans and consideration of ideal plant architecture

☆Hosokawa, Y.[1], K. Yoshida[1], K. Sekiguch[1], H. Nagasawa[1], K. Shirasawa[2], N. Yamaguchi[3] (1.Tokachi Agr. Exp. Stn., HRO, 2.Kazusa DNA Res. Inst., 3.Central Agr. Exp. Stn., HRO)

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309 Genome region associated with resistance to brown stem rot in adzuki bean derived from "Akamame"

○Sato, K.[1], H. Nagasawa[2], S. Adegawa[1], C. Souma[1], T. Suzuki[1,3] (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO, 3.Agr. Res. Dept., HRO)

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310 Useful wheat leaf rust resistance genes in Hokkaido and evaluation of near-isogenic lines carrying the resistance gene *Lr34*

☆Doman, K.[1], S. Ohnishi[2], H. Jinno[1,2], S. Maeno[1], C. Souma[1], T. Sonoda[2], H. Ito[3], A. Nakamaru[3], S. Ikenaga[3], K. Hatta[4,5] (1.Central AES, HRO, 2.Kitami AES, HRO, 3.TARC, NARO, 4.HARC, NARO, 5.NICS, NARO)

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311 Evaluation and genetics of bacterial blight resistance of rice mutant lines induced by ion beam irradiation

☆Takahashi, R.[1], K. Kato[1], Y. Maeda[1], Y. Shibata[1], Y. Gatayama[2], S. Taura[3], K. Ichitani[4] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.KIAD Tokunoshima, 3.Inst. Gene Res., Kagoshima Univ., 4.Fac. Agr., Kagoshima Univ.)

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312 Breeding of cracked tolerant rice and added valuable traits as giant embryo and high content of saturated fatty acid

○Ishikawa, R., L. Dinh Thi (Fac. Agri. and Life Sci.m Hirosaki Univ.)

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313 "Maitebo", a new otebo bean variety with resistance to lodging and less leaf retention at maturity

○Nakagawa, K.[1], Y. Horiuchi[1], H. Sato[1], H. Nagasawa[1], M. Okuyama[1], H. Sato[2], S. Hagihara[1], N. Yamaguchi[2], Y. Saito[3] (1.Tokachi Agri. Exp.Sta., HRO, 2.Central Agri. Exp.Sta., HRO, 3.Kamikawa Agri. Exp.Sta., HRO)

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314 Breeding of a new sweetpotato cultivar for table use, “Benihinata”, with strong resistance to sweetpotato foot rot, and selecting of its virus-free lines

○Kawata, Y.[1], T. Sakaigaichi[1], K. Suematsu[1], Y. Kai[1], T. Sakai[1], Y. Takahata[1], M. Enomoto[2], A. Kobayashi[1] (1.KARC, NARO, 2.Kaneko Seeds Co., Ltd.)

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315 Identification of sweetpotato cultivar 'Benihinata' using DNA markers based on cultivar-specific InDels

○TANAKA, M., Y. Kawata, A. Kobayashi (Kyushu Okinawa Agr. Res. Cent., NARO)

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316 Genome analyses of Japanese Azuki beans

○Ota, T.[1], H. Nasu[2] (1.RCIES, SOKENDAI, 2.Ctr. Fund. Edu., Okayama Univ. Sci.)

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317 Breeding of [Sadowa] egg plant of a Miyazaki original vegetable ~ A new variety of [NANKYU SENSA No.4 GO] created by crossing between varieties and selection~

○Chen, L., N. Emoto, T. Hiejima, S. Yoshizaki, N. Iwakiri, T. Oonishi, R. Nozaki, K. Takane, Y. Matsushita (Fac. Envir. Hort. Sci., Minami Kyushu U.)

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318 Characteristics of intergeneric hybrids between marguerite and Roman chamomile, and breeding of a new variety: 'New Summer Stella'.

○Katsuoka, H.[1], T. Fujii[1], C. Kato[1], F. Baba[2], M. Taneishi[1], T. Sasaki[3] (1.Izu Agri. Res. Center, Shizuoka Pref. Res. Inst. Agri. Forest., 2.Kamo Agri. Forest. Office, 3.Fruit Tree Res. Center, Shizuoka Pref. Res. Inst. Agri. Forest.)

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319 Hiroshige Utagawa had drown the original Someiyoshino tree 193 years ago

○Nakamura, I. (Grad. Sch. Hortic., Chiba Univ.)

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320 Confectionery suitability of soft wheat lines carrying crab wheat-derived glutenin subunit genes with different combinations of *SSIIa* gene mutations

○Tougou, M.[1], K. Hatta[1], T. Okada[1], H. Kojima[1], M. Fujita[2], M. Yamamori[1], H. Matsunaka[3], K. Nakamura[2], T. Ikeda[4] (1.Inst. Crop Sci., NARO, 2.HQ, NARO, 3.HARC, NARO, 4.WARC, NARO)

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321 Is the cytoplasm of *Aegilops mutica* useful for wheat breeding?

○Murai, K., Y. Watanabe, H. Tada (Dep. Sus. Agri., Fukui Pref. U.)

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322 Exploration of introgressed regions between *O. sativa* ssp. *Japonica* and AA-genome species of the genus *Oryza* based on comparative genome analysis

○KOYANAGI, K.[1], Y. Kotoku[2], Y. Kishima[3] (1.Faculty of Information Science and Technology, Hokkaido University, 2.Graduate School of Agriculture, Hokkaido University, 3.Research Faculty of Agriculture, Hokkaido University)

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323 An early heading gene with *indica* genetic background widens rice cultivation area in Japan

○Dinh, T.[1], Y. Ueda[2], H. Saito[2], R. Ishikawa[1] (1.Faculty of Agriculture and Life Science, Hirosaki University, 2.JIRCAS)

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401 Resistance to the herbicide metribuzin conferred to *Arabidopsis thaliana* by targeted base editing of the chloroplast genome

☆Nakazato, I.[1], W. Yamori[1], H. Matsumura[2], M. Okuno[3], N. Tsutsumi[1], S. Arimura[1] (1.Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo, 2.Col. of Life Sci., Ritsumeikan Univ., 3.Sch. of Med., Kurume Univ.)

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402 Rice lipid-related gene family, *OsGELP*, differentiated latitude-adapted haplotypes

☆LUBBA, K.[1], K. YAMAMORI[2], Y. KISHIMA[1] (1.Grad. Sch. Agriculture, Univ. Hokkaido, 2.Grad. Sch. Agriculture, Univ. Kyoto)

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403 Genetic progress for anther and stigma morphology under different nitrogen fertilization regimes of cultivars released during past 109 years in Japan

○Shimono, H.[1,2], R. Sato[1], A. Abe[3], H. Nishio[4,5], H. Kudoh[5] (1.Fac.Agric., Iwate Univ., 2.Agri.Innov.Center, Iwate Univ., 3.Iwate Biotech. Res. Center, 4.Data Sci. AI Innov.n Res.Prom. Cent., Shiga Univ., 5.Cent. Ecol. Res., Kyoto Univ.)

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404 Field trials of barley core collections in stressed soils with different pH

○Hisano, H., H. Shirato (IPSR, Okayama University)

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405 Analysis of the regulatory mechanism of *Ghd7* expression using rice with upstream deletion by genome editing

○Ogo, Y.[1], H. Itoh[2], K. Naito[3], T. Izawa[4] (1.NIVFS, 2.NICS, 3.NGRC, 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

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406 Transcriptional control of a floral repressor gene *Ghd7* by distal *cis*-regulatory elements

☆Kawauchi, T.[1], Y. Ogo[2], M. Mimura[3], T. Izawa[3] (1.Faculty of Agriculture, Univ. Tokyo, 2.NIVFS, 3.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

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407 Understanding of molecular mechanisms on lateral root development by *our1* mutation and its application to further root system improvement in rice

☆Dong, Y.[1], M. Kanao[1], C. Wainaina[2], P. Lipio[1], Y. Inukai[3] (1.Grad. Sch. Bioagr., Nagoya U., 2.Dept. Hort. Food Sec., JKUAT, 3.ICREA, Nagoya U.)

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408 Do microspores of rice anther have the callus formation ability?

☆Xu, M.[1], N. Kudo[1], C. Nachilima[1], K. Miyamoto[1], J. Kim[2], Y. Kishima[1] (1.Grad. Sch. Agriculture., Univ. Hokkaido, 2.Grad. Sch. Agricultural and Life Sci., Univ. Tokyo)

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409 Functional analysis of *Trehalose-6-Phothphate Synthase 1* during rice embryogenesis

☆Homma, D.[1], T. Tezuka[3], M. Nosaka-Takahashi[2,3], M. Okada[1], K. Okazaki[1], Y. Sato[2,3], E. Fukai[1] (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Plant Genet., Natl. Inst. Genet., 3.Sch, Life Sci.,Grad. Univ. Adv. Study/SOKENDAI)

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410 Analysis of transcription factors and downstream genes involved in the regulation of tomato fruit set

☆Nomura, Y.[1], Y. Lu[2], K. Harada[1], Y. Shinozaki[2], H. Enomoto[3], R. Yano[4], M. Kojima[5], Y. Takebayashi[5], H. Sakakibara[6], H. Ezura[2,7], T. Ariizumi[2,7] (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Dept. Biosci., Univ. Teikyo, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)

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411 Producing transformants for identifying a yet-to-be discovered gene associated with southern root-knot nematode resistance in sweetpotato

☆Izumitani, M.[1], M. Otani[2], O. Nakayachi[2], H. Tabuchi[3], H. Nishida[1], K. Kato[1], K. Nishimura[1], Y. Monden[1] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 2.Res. Inst. Biore. Bioen., Ishikawa Pref. U., 3.KARC/NARO)

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412 Development of transformation method and tissue culture system toward gene editing in sweetpotato cultivar J-Red

☆Nakamura, S.[1], M. Izumitani[2], M. Otani[3], H. Matsui[2], H. Tabuchi[4], K. Nishimura[2], H. Nishida[2], K. Kato[2], Y. Monden[2] (1.Fac. Agri., Okayama Univ., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 3.Res. Inst. Biore. Bioen., Ishikawa Pref. Univ., 4.KARC/NARO)

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413 A frame-shift mutation of *InCO* presumed to be necessary for Japanese morning glory to spread over temperate Asia

Katsuyama, H.[1,5], K. Ezura[1,6], A. Hoshino[2,3], E. NItasaka[4], ○T. Kuboyama[1] (1.Col. Agr. , Ibaraki U., 2.National Inst. Basic Biol., 3.SOKENDAI, 4.Grad. Sch. Sci., Kyushu U., 5.Fac. Life Environ. Sci., U. Tsukuba, 6.Pref. Gov., Ibaraki Pref.)

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414 Developmental analysis of rice shoot apical meristem by microtubule imaging and depolymerization

☆Takata, R.[1], M. Tanaka[1], H. Takeuchi[2], D. Maruyama[1], J. Ito[1], H. Tsuji[1,3] (1.KIBR, Yokohama City Univ., 2.ITbM, Nagoya Univ., 3.BBC, Nagoya Univ.)

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415 Epigenetic modification analysis using single-cell resolution 3D immunostaining for rice shoot apical meristem

☆Morishita, Y.[1], R. Takata[2], A. Yoshida[2], A. Higo[2], H. Tsuji[3] (1.Sch Agri, Nagoya Univ., 2.KIBR, Yokohama City Univ., 3.BBC, Nagoya Univ.)

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416 Cell biological analysis of stem cell activity and cell death during abortion of the barley inflorescence

☆Matsumoto, H.[1], J. Ito[1], Y. Nomura[1], M. Wakazaki[2], M. Sato[2], N. Takeda-Kamiya[2], D. Saisho[3], K. Toyooka[2], H. Tsuji[1,4] (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Bioscience and Biotechnology Center, Nagoya Univ.)

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417 Genetic variation in caryopsis types in the genus *Triticum·Aegilops* －comparisons to the genus *Hordeum*

○Taketa, S. (Institute of Plant Science and Resources, Okayama University)

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418 Exploration of heading-time mutant genes by exome sequencing analysis in barley mutant lines

☆Takeda, S.[1], M. Okuma[2], C. Ibuki[1], A. Mandozai[3], K. Nishimura[3], Y. Monden[3], K. Kato[3], H. Nishida[3] (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

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419 Relationship of heading time-related genotype and heading-time instability in a barley RIL population

☆Okuma, M.[1], K. Nishimura[2], Y. Monden[2], K. Kato[2], H. Nishida[2] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

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420 Identification of major loci involved in forming a constitutive barrier to radial oxygen loss in wild rice, Oryza glumaepatula

○Shiono, K.[1], M. Ejiri[1], R. Nishijima[1], M. Baba[1], H. Shiba[1], Y. Yamagata[2], K. Miura[1] (1.Dept. Bioscience. Biotech., Fukui Pref. Univ., 2.Grad. Sch. Bioresouce Bioenviron. Sci.,

Kyushu Univ.)

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421 Role of Jasmonic acid during secondary aerenchyma formation in soybean

☆Watanabe, K.[1], Y. Baba[1], A. Agata[1], A. Toyoda[2], Y. Sato[2], M. Nakazono[1], H. Takahashi[1] (1.Grad.Sch.Bioagric.Sci., Univ. Nagoya, 2.National Institute of Genetics)

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501 Variations in the novel fertility restorer gene, *Rfs*, of Ogura cytoplsmic male sterility in radish.

○Yamagishi, H.[1], A. Fukunaga[2], M. Takenaka[3], T. Terachi[2] (1.Professor Emeritus of Kyoto Sangyo Univ., 2.Fac. Life Sci., Kyoto Sangyo Univ., 3.Grad. Sch. Sci., Kyoto Univ.)

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502 Identification of a Temperature-Sensitive Male Sterility Factor

○Kawagishi-Kobayashi, M.[1], A. Nishizawa-Yokoi[1], M. Endo[1,4], T. Nunome[2], H. Kato[1,5], Y. Tozawa[3] (1.Inst. Agrobiol. Sci., NARO, 2.Inst. Vegetable Floriculture Sci., NARO, 3.Grad. Sch. Sci. Eng., Saitama Univ., 4.present address: Takii co, 5.present address: Tokyo Univ. Agriculture)

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503 Protein analysis of temperature-sensitive male sterility factor

☆Tozawa, Y.[1], Y. Takani[1], T. Tezuka[1], H. Suda[1], K. Atsuzawa[2], A. Nishizawa-Yokoi[3], Y. Kaneko[4], M. Toyota[1], M. Kawagishi-Kobayashi[3] (1.Grad.Sch.Sci.&Eng., Saitama Univ., 2.Comprehensive Anal. Centr. for Science, 3.Inst. Agrobiol. Sci., NARO, 4.Fac. Liberal Arts)

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504 The gene responsible for cytoplasmic male sterility in *Oryza glaberrima* with the cytoplasm of Taichung 65 is *orf288*

☆Igarashi, K.[1], Y. Iwai[1], A. Takatsuka[1], T. Kazama[2], S. Arimura[3], K. Toriyama[1] (1.Grad.Sch. Agri. Sci., Tohoku Univ., 2.Fac. Agri. Sci., Kyusyu Univ., 3.Grad.Sch. Agri. Life Sci., Univ. Tokyo)

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505 Identification of hybrid sterility gene *S13* detected in African wild rice, *Oryza longistaminata*

☆Takanishi, W., Z. Mar Myint, Y. Kishima, A. Kanazawa, Y. Koide (Graduate School of Agriculture, Hokkaido University)

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506 *SDV1* and *SDV2*, duplicate genes involved in the seed development in the AA genome *Oryza* species.

☆Shibata, Y.[1], D. Toyomoto[2], M. Uemura[3], S. Taura[4], T. Sato[5], R. Henry[6], R. Ishikawa[7], K. Ichitani[2,8] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.United Grad. Sch. Agr. Sci., Kagoshima Univ., 3.Grad. Sch. Agr., Kagoshima Univ., 4.Inst. Gene Res., Kagoshima Univ., 5.Grad. Sch. Agr., Tohoku Univ., 6.QAAFI, Univ. of Queensland, 7.Fac. Agr. and Life Sci., Hirosaki Univ., 8.Fac. Agr., Kagoshima Univ.)

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507 Overcoming the hybridization barrier in interspecific hybrid seeds from a cross between *Oryza sativa* and *O. officinalis* using the *Osemf2a* mutant.

☆Sakurai, F.[1], K. Tonosaki[1], H. Furuumi[2], Y. Sato[2], T. Kinoshita[1] (1.KIBR, Yokohama City Univ., 2.NIG)

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508 Phylogenetic analysis of *Capsicum* using SSR markers and investigation of reproductive isolation including hybrid weakness in interspecific hybridization.

☆Seko, S., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)

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509 Genetic mapping of the *HLA1* locus*,* a gene causing hybrid lethality, in *Nicotiana* interspecific hybrids by bulked segregant RNA-Seq

☆Nagai, S., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)

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510 Cell biotechnology utilizing developmental and reproductive regulators.

○Igawa, T.[1,2,3], Y. Sato[1], B. Pratama[1], S. Koyama[1], A. Yoshimura[1] (1.Grad. Sch. Hort., Chiba Univ., 2.Plant Mol. Sci. Cent., Chiba Univ., 3.Res. Cent. Space Agr. Hort., Chiba Univ.)

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511 Involvement of plasma membrane H^+-ATPase in female papilla cells in the control of pollen hydration in Brassicaceae.

☆Hayashi, M.[1], K. Fukushima[1], H. Masuko-Suzuki[1], T. Kinoshita[2,3], S. Inoue[2], S. Takayama[4], Y. Takada[1], M. Watanabe[1] (1.Grad. Sch. Life Sci., Tohoku Univ., 2.Grad. Sch. Sci., Nagoya Univ., 3.ITbM, Nagoya Univ., 4.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

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512 Modification of W14 medium for wheat anther culture and validation of its applicability to wheat breeding in Hokkaido.

○Maruta, T.[1], K. Satou[2], K. Tomita[2], C. Souma[2], M. Okuyama[3], T. Suzuki[4] (1.Donan AES , HRO, 2.Central AES, HRO, 3.Tokachi AES, HRO, 4.Agri. Res. Dept, HRO)

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513 Effect of loci related to below-ground tuber pigmentation in the turnip cv. 'Akamaru' on the phenotype of progeny crossed with non-pigmented below-ground turnip

☆Segawa, T.[1], K. Miyaki[1], K. Tonosaki[2], R. Kumazawa[1], M. Hara[1], S. Saiga[1], M. Takata[1], H. Takagi[1] (1.Ishikawa Prefectural University, 2.Yokohama City University)

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514 Functional characterization of Stach Synthase in Cassava tuberous root

☆Utsumi, Y.[1], C. Utsumi[1], M. Tanaka[1,2], T. Tsuchihashi[3], H. Fujihara[3], M. Seki[1,2,4] (1.RIEKN CSRS, 2.RIKEN CPR, 3.Matsutani Chemical Industry Co., Ltd., 4.KIBR, Univ. Yokohama City)

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515 Natural variation in rice mitogen-activated protein kinase 4 contributes to improve photosynthesis rate in the field.

☆Ueda, T.[1], S. Adachi[2], K. Sugimoto[1], Y. Taniguchi[1], T. Hirasawa[2], T. Yamamoto[1,3], J. Tanaka[1,4] (1.NARO, 2.Tokyo University of Agriculture and Technology, 3.Okayama University, 4.University of Tsukuba)

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516 Genetic interactions of starch-related mutations differ between endosperm and pollen

○Matsushima, R.[1], H. Hisano[1], M. Rose[2], ジ. キム[1,3], F. Brendan[2], N. Oitome[4], S. David[2], N. Fujita[4], K. Sato[1] (1.Institute of Plant Science and Resources, Okayama University, 2.John Innes Centre, 3.RIKEN Center for Sustainable Resource Science, 4.Faculty of Bioresource Sciences, Akita Prefectural University)

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517 Alterations in DNA methylation during rice endosperm development

☆Uechi, M., K. Tonosaki, A. Ono, T. Kinoshita (Yokohama City University Kihara Institute for Biological Research)

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518 Intraspecific comparison of *ddm1* mutants in *Arabidopsis thaliana*

Nishimura, K., K. Kunita, Y. Kamiya, ○R. Fujimoto (Grad. Sch. Agric. Sci.)

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519 Exploration of CpG Methylation in Plant Mitochondrial DNA

☆ZHONG, Y.[1], M. Okuno[2], N. Tsutsumi[1], S. Arimura[1] (1.Grad. Sch. of Agri., Univ. Tokyo, 2.Kurume Univ. Sch. of Med.)

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520 Attempted excision of 641Kb Nuclear Mitochondrial DNA (NUMT) sequence in Arabidopsis thaliana chromosome 2

☆ITO, Y., Y. Zhong, I. Nakazato, N. Tsutsumi, S. Arimura (Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo)

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521 Development of a technology for induction of plant-organelle-genome-specific random mutagenesis by artificially-fused proteins. Evaluation of T_1 plants.

☆Kosaka, N.[1], Y. Harada[1], I. Nakazato[1], M. Okuno[2], T. Itoh[3], N. Tsutsumi[1], S. Arimura[1] (1.Grad. Sch. Agri. and Life Sci., Univ. Tokyo, 2.Sch. Med., Univ. Kurume, 3.Sch. Life Sci. and Tech., Tokyo Inst. Tech.)

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522 Mutation in a novel soybean isoflavone O-methyltransferase (*IOMT*3) gene cause a accumulation of 6-hydroxydaidzein isoflavones.

○Watanabe, S.[1], M. Horitani[1], R. Yamada[1], K. Taroura[1], T. Anai[2] (1.Fac. Agri., Saga Univ., 2.Fac. Agri., Kyushu Univ.)

Poster Presentations

P001 Optimizing progeny allocation strategies in breeding programs while updating genomic prediction models

☆Hamazaki, K.[1], K. Tsuda[1,2], H. Iwata[3] (1.Adv. Int. Proj., RIKEN, 2.Grad. Sch. Fro. Sci., Univ. Tokyo, 3.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P002 Crossing strategy considering segregation of later generations in a plant breeding program

☆Sakurai, K.[1], K. Hamazaki[2], M. Inamori[1], A. Kaga[3], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.RIKEN Ctr. for Advanced Intelligence Project, 3.Inst. Crop Sci., NARO)

P003 An Efficient training image dataset creation pipeline for sweet potato spoilage risk diagnosis model using 3D data

☆Kodama, K.[1], K. Taguchi[2], M. Nishinaka[2], W. Guo[1] (1.Univ. Tokyo, 2.NARO CARC)

P004 Field Phenotyping in Wheat and Barley Breeding: Head Detection Through Consecutive Video Frames

☆Nakamura, H.[1], G. Ishikawa[1], W. Guo[2], T. Yamada[1], M. Tougou[1], A. Takahashi[1], K. Hatta[1], H. Kojima[1], T. Okada[1], J. Yonemaru[3] (1.Inst. Crop Sci., NARO, 2.Grad. Sch. of Agri. and Life Sci., Univ. of Tokyo, 3.Res. Cent. Agric. Info. Tech., NARO)

P005 Effects of Variety Breed Groups, Gene Sets, and Regression Methods on the Versatility and Accuracy of Genetic-based Growth Prediction Models in Soybean.

☆Mori, T.[1], K. Nishimura[2], S. Nakano[3], H. Kokaji[4], K. Motoki[2], E. Kumagai[3], A. Kaga[3], H. Iwata[5], Y. Iwahashi[1], K. Nagasaka[1], K. Murata[1], Y. Kinoshita[1], T. Maki[1], H. Inoue[1], R. Nakano[1], H. Nakagawa[3], T. Nakazaki[1] (1.Grad. Sch. Agr., Kyoto Univ, 2.Grad. Sch. Environ.Life. Sci. and Tech., Okayama Univ, 3.NARO, 4.GRA&GREEN Inc., 5.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P006 Variation in flowering traits in Taro (*Colocasia esculenta* Schott) cultivars in relation to vegetative traits and ploidy.

☆Iijima, Y.[1], Y. Mitsui[1], T. Konishi[2] (1.Dept. Bioresour. Dev., Tokyo Univ. Agri., 2.Res. Inst. Evol. Biol.)

P007 Genetic characteristics of Japanese wild sugarcane with smut disease resistance

☆Umeda, M., T. Hattori, Y. Tarumoto (Kyushu Okinawa Agr. Res. Ctr., NARO)

P008 Study of QTLs associated with hybrid vigor in Kasalath genome using BC_1F_1 of Taichung 65 x Kasalath

☆Nakamura, Y.[1], S. Ogihara[1], K. Ichitani[2], T. Kuboyama[1] (1.Col. Agr. , Ibaraki U., 2.Fac. Agr. , Kagoshima U.)

P009 Evaluation of Genetic Diversity in 'Hodairakabu', a Local Turnip Variety of Nagano Prefecture

☆Kohara, R.[1], K. Matsushima[2], K. Nemoto[2] (1.Grad. Sch. Sci and Tec., Univ. Shinshu, 2.Inst. Agric. Acad. Assy. Fac., Univ. Shinshu)

P010 Genetic diversity analysis of diverse variant rice (*Oryza sativa* L.)

○Takenaka, S.[1], T. Seo[1], F. Okada[1], M. Takatani[1], K. Nagaoka[1], T. Itani[2] (1.Ryukoku Univ. Fac. Agri., 2.Ryukoku Univ. Res. Ctr. Satoyama Studies)

P011 Development of new F1 hybrid varieties “HYBRID TOGO 44 GO / 44 GO” that overcomes multiple issues faced by current varieties

○Jinushi, K., K. Iwatsuki (Research Institute of Rice Production &Technology Co., Ltd.)

P012 Production of a new type of vegetable, "Komina", by intergeneric hybridization between *Brassica rapa* var. *laciniifolia* and *Diplotaxis tenuifolia*

○Oyama, K.[1], W. Hashimotu[2], T. Suzuki[3], S. Bang[1], T. Ohnishi[1] (1.Grad. Reg. Cre. Sci., Utsunomiya U., 2.Sch. Agr., Utsunomiya U., 3.Center for Bioscience Research and Education, Utsunomiya U.)

P013 NBRP-Wheat: Development of large-scale mapping populations of wheat genetic resources for future research

○Ohta, A.[1,2], M. Nitta[1,2], S. Nasuda[1,2], K. Yoshida[1,2], T. Sakai[1,2], S. Takenaka[3], Y. Matsuoka[4], N. Mori[4], R. Nishijima[5], R. Terauchi[1,2] (1.Grad. Sch. Agri., Kyoto Univ., 2.NBRP-Wheat, 3.Fac. Agri, Ryukoku Univ., 4.Grad. Sch. Agri. Sci., Kobe Univ., 5.Fac. Biosci. Biotech., Fukui Pref. Univ.)

P014 Production of interspecific hybrid progenies by embryo rescue and testing of clubroot resistance during acclimation

○Ogura, T., T. Ohnishi, S. Bang (Grad. Reg. Cre. Sci., Utsunomiya U.)

P015 “Sorakirari”, a new rice cultivar for Hokkaido with high yield and blast resistance

○Yamashita, Y.[1], T. Nishimura[1], M. Ikenaga[1], H. Sato[2], H. Ozaki[3], S. Munekata[4], M. Kinoshita[3], T. Maruta[5], K. Sato[1], Y. Urushibata[6], T. Abe[1] (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO, 3.Kamikawa Agr. Exp. Stn., HRO, 4.Kitami Agr. Exp. Stn., HRO, 5.Donan Agr. Exp. Stn., HRO, 6.Orn. Plant Veg. Res.Cent., HRO)

P016 Study on trait changes in bread wheat-*Leymus racemosus* chromosome addition lines

Ono, T.[1], M. Kishii[2], M. Sato[3], M. Hirai[3], H. Tsujimoto[4], ○M. Okamoto[1,3,5] (1.Utsunomiya Univ., 2.JIRCAS, 3.CSRS・RIKEN, 4.Tottori Univ., 5.Yokohama City Univ.)

P017 Potential for breeding new energy crops using the robustness of Johnson grass (*Sorghum halepense*)

○Okada, S.[1,5], S. Hashimoto[2,5], C. Yamada[3], S. Araki-Nakamura[1], K. Ohmae-Shinohara[1], S. Kasuga[4], T. Sazuka[1] (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Grad. Sch. Agric. Life Sci., U. Tokyo., 3.Grad. Sch. Bioagri., Nagoya Univ., 4.AFC, Fac. of Agri. Shinshu Univ., 5.equally contributed author)

P018 A Practical Guide to Genome Assembly with Varied Levels of Heterozygosity

☆Mochizuki, T.[1], M. Sakamoto[1], Y. Tanizawa[1], T. Nakayama[2], G. Tanifuji[3], R. Kamikawa[4], Y. Nakamura[1] (1.Genome Informatics Lab., NIG, 2.Center for Computational Sciences, Univ. of Tsukuba, 3.Department of Zoology, National Museum of Nature and Science, 4.Graduate School of Agriculture, Kyoto Univ.)

P019 Development of various isogenic Koshihikari capable of stable production using the short-stem tillering gene *d65*

☆Fujita, K., M. Tomita (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

P020 Development of various isogenic Koshihikari capable of stable production under climate crisis

☆Nakayama, K., M. Tomita (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

P021 Exploration of chromosome regions that improve brown rice whiteness among *japonica* and *indica* varieties of rice

☆Otsuka, R.[1], J. Tanaka[2,3], M. Tsuda[4] (1.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 2.Faculty Life & Env. Sci., Univ. Tsukuba, 3.NICS/NARO, 4.T-PIRC., Univ. Tsukuba)

P022 Development of various isogenic Koshihikari capable of stable production using the robust stem and tillering gene

☆Sugihara, H., M. Tomita, T. Okada (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

P023 Genome-wide association study of cooked rice characteristics and screening for candidate genes.

☆Ono, K.[1], M. Shenton[2], K. Motizuki[2,3], Y. Tsujii[3], K. Hori[1,2] (1.Grad. Sch. Frontier Sci., Univ. Tokyo, 2.NARO, 3.Tokyo Univ. Agric)

P024 Improving the heading date of 'Yumemizuho': An early flowering rice cultivar from Ishikawa prefecture.

☆Takata, M.[1,2], K. Kontani[2], M. Sakemoto[2], M. Ino[1], H. Hatanaka[1], K. Nakamura[1], K. Okada[1], H. Takagi[2] (1.Ishikawa Agriculture Research Center, 2.Ishikawa Prefectural University)

P025 Exploration and comparative analysis of nematode resistance loci in hexaploid sweetpotato with GWAS, QTL mapping, and k-mer based bulk segregation analysis

☆Kurihara, M.[1], H. Tabuchi[2], K. Nishimura[3], H. Nishida[3], K. Kato[3], Y. Monden[3] (1.Grad. Sch. Environ. Life Sci., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ.)

P026 Genome sequencing analysis of Japanese mulberry (Morus spp.) resources

○Matsumura, H.[1], S. Yoshinobu[2], R. Shimizu[2], M. Suzuki[2], A. Mizoguchi[2] (1.Gene Res. Ctr., Shinshu Univ., 2.Grad. Sch. Sci. Tech, Shinshu Univ.)

P027 Genome-wide association studies of leaf shape in mulberry

☆Gye, H.[1], S. Yoshinobu[3], M. Suzuki[3], R. Simizu[3], A. Mizoguchi[3], H. Matsumura[2] (1.Fac. Textile Sci. Tech, Shinshu Univ., 2.Gene Res. Ctr., Shinshu Univ., 3.Grad. Sch. Sci. Tech)

P028 Identification of regions involved in sex determination in mulberry

☆Suzuki, M.[1], R. Shimizu[1], H. Gye[2], R. Atsumi[1], H. Matsumura[3] (1.Grad. Sch. Sci. Tech., Shinshu Univ, 2.Fac. Textile Sci. Tech, Shinshu Univ., 3.Gene Res. Ctr., Shinshu Univ.)

P029 ptpTALEN-mediated double-strand break in chloroplast genome of*Arabidopsis thaliana*

○Suefuji, S., I. Nakazato, N. Tsutsumi, H. Takanashi, S. Arimura (Grad. Sch. Agri., Univ. Tokyo)

P030 Identification of a genetic locus for seed shattering in Italian ryegrass (*Lolium multiflorum* Lam.)

○Tamura, K.[1], T. Mizubayashi[2], H. Yamakawa[2] (1.NILGS, NARO, 2.NICS, NARO)

P031 Generation of major glutelin–deficient (GluA, GluB, and GluC) semi-dwarf Koshihikari rice line

○Wakasa, Y.[1], T. Kawakatsu[1], K. Ishimaru[2], K. Ozawa[1] (1.Inst. Agrobiol. Sci., NARO, 2.Inst. Crop Sci., NARO)

P032 Cross-species knowledge transfer driven by the genome-wide ortholog analysis

○Furuta, T. (IPSR, Okayama Univ.)

P033 Interaction between the gametocidal genes *Gc1* and *Gc5* in wheat

☆Murata, K., S. Nasuda (Grad. Sch. Agric., Kyoto Univ.)

P034 Analysis of seed development process of rice Orysa;KRP3 genome editing mutant

☆Chida, T., T. Ito, S. Oya, S. Miyakawa, R. Sugawara, Y. Saitoh (Fac.agri.,Univ.iwate)

P035 Search for aquaporins related to acquisition of environmental stress tolerance

☆Hikaru, M., W. Ahmadzai, S. Mohammad Taheb, R. Nakayama, Y. Kamiya, K. Kawaura (KIBR, Yokohama City Univ.)

P036 Method development and validation of simultaneous expression of two proteins and multiple organelle localization in Arabidopsis thaliana using P2A sequences.

☆Shiba, M., I. Nakazato, N. Tsutsumi, H. Takanashi, S. Arimura (Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo)

P037 Creating multiplex genome-edited wheat mutants using the arrayed tRNA-gRNA system

☆Komura, S.[1], F. Abe[2], M. Kishi-Kaboshi[2], K. Yoshida[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.NICS)

P038 Generation and analysis of fertilization-defective mutants eliminated the gene coding region by genome editing.

☆Yoshimura, A.[1], S. Kobayashi[1], T. Igawa[1,2,3] (1.Graduate School of Horticulture, Chiba University, 2.Plant Molecular Science Center, Chiba University, 3.Research Center for Space Agriculture and Horticulture, Chiba University)

P039 Effect of the developmental regulators from different plant species in inducing autonomous differentiation

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P040 Functional analysis of the abiotic stress-responsive SlWRKY6, SlWRKY9 and SlWRKY45 transcription factors in tomato

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P041 Investigation of novel male sterility genes in alloplasmic lines of wheat

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P042 Screening of a gene that determines saccharification yields from rice straws by overexpression of the candidates

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P043 Evaluation of the yield-related traits and drought stress response in rice through phenomics and transcriptomics analyses

☆Wei, S.[1], R. Kuroda[1], R. Tanaka[1], F. Soma[1], Y. Kitomi[1], N. Kanno[1], A. Hayashi[2], N. Kochi[2], M. Negishi[2], K. Tokuda[2], T. Tanabata[3], M. Endo[4], H. Saika[4], S. Yabe[1], Y. Uga[1] (1.NICS, NARO, 2.RCAR, NARO, 3.Kazusa DNA Res. Inst, 4.NIAS, NARO)

P044 Genetic analysis of the drought stress response of rice using time-series transcriptome data

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P045 Utilization of the Tobacco Mutation Database: Isolation and characterization of low alkaloid mutants

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P046 Effects of Na^+/H^+ antiporter HvSOS1 from barley on salt tolerance of Arabidopsis.

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P047 Toward the establishment of a separately phenotyping method of soybean shoot and root traits by grafting

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P048 Ion-gene co-expression analysis to explore the mechanism of phosphorus deficiency tolerance derived from wild rice

☆Matsunaga, S., Y. Ohmori, T. Fujiwara (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P049 Analysis of the mechanism regulating the number of cortical cell layers in rice roots under low-oxygen conditions

☆Minami, S.[1], K. Tsuda[2], T. Yamauchi[3] (1.Sch. Agr., Nagoya U., 2.Natl. Inst. Genet., 3.Biosci. Biotech. Center, Nagoya U.)

P050 Analysis of temporal changes in disease resistance-related genes and bioactive small molecules during infection process of powdery mildew in wheat

☆SATO, Y.[1,2], Y. WENG[2,3], T. SHIMAZAKI[1,2], K. NIHEI[4], K. YOSHIDA[5], M. OKAMOTO[1,2,6] (1.Grad. Sch. Reg. Dev.&Creat., Utsunomiya Univ., 2.Ctr. for Biosci. Res.&Educ., Utsunomiya Univ., 3.UGSAS, Tokyo Univ. of Agri.&Tech., 4.Sch. Agri., Utsunomiya Univ., 5.Grad. Sch. Agri., Kyoto Univ., 6.RIKEN, CSRS)

P051 Comparison of salt induced genes in synthetic hexaploid wheat derived from different tetraploid wheat

☆Yokota, A., H. Moriya, R. Watanabe, Y. Kamiya, K. Kawaura (KIBR, Yokohama City Univ.)

P052 Molecular and physiological analyses of abscisic acid receptor-mediated disease resistance in wheat

☆Weng, Y.[1,2], T. Shimazaki[2], R. Mega[3], F. Abe[4], J. Kim[5], K. Yoshida[6], K. Nihei[7], M. Okamoto[2,5] (1.UGSAS, Tokyo Univ. of A&T, 2.Bio., Univ. Utsunomiya, 3.Gra. Sch. Sci., Univ. Yamaguchi, 4.Inst. Crop Sci., NARO, 5.CSRS, Riken, 6.Agri., Univ. Kyoto, 7.Agri., Univ. Utsunomiya)

P053 Soil environment measurement toward elucidating the mechanism that soil surface roots reduce rice yield loss in saline paddy fields.

○Hanzawa, E.[1], M. Bamba[1], S. Hashimoto[1], Y. Oba[2], T. Sato[3], Y. Kitomi[4], T. Kawai[4], T. Tokida[5], S. Sato[1], Y. Uga[4] (1.Grad. Sch. LifeSci., Univ. Tohoku, 2.Murata Manufacturing Co., Ltd., 3.Grad. Sch. Agri. Sci., Univ. Tohoku, 4.Inst. Crop Sci., NARO, 5.Inst. Agro-Env. Sci., NARO)

P054 Novel allele at a reported QTL for resistance to Fusarium head bright contributed to develop wheat lines KK1932 and KK1976 resistant to Fusarium head bright

○Ohnishi, S.[1], K. Horikawa[2], K. Morita[1], C. Souma[2], Y. Sato[1], T. Sonoda[1] (1.HRO Kitami AES, 2.HRO Central AES)

P055 High temperature tolerance in grafted tomato: an analysis in the special netted-house

○Nishiguchi, M.[1], K. Hondo[2,3], S. Nakamura[1], Y. Shinozaki[4,5], T. Ariizumi[4,6], H. Ezura[4,6], K. Kobayashi[1] (1.Fac. Agri., Ehime University, 2.ADRES・愛媛大, 3.Fac. Sci. Tech., Tokyo Univ. Sci.,, 4.T-PIRC, Univ. Tsukuba, 5.Inst. Global Innov. Res, Tokyo Univ. Agri. Tech., 6.Grad. Sch. Life Environ. Sci., Univ. Tsukuba)

P056 Genetic differences in soil pH-dependent mineral accumulation in rice straw and grains

○Yamamoto, T.[1], K. Kashihara[1], T. Furuta[1], Q. Zhang[1], E. Yu[1,2], J. Ma[1] (1.IPSR, Okayama Univ., 2.College of Agronomy, Anhui Agriculture University)

P057 Development of flooding-tolerant F_1 hybrid by introgression of two teosinte QTLs into maize F1 cultivar “Yumesodachi” and evaluation of the pyramiding effect

○Imase, R.[1], H. Takahashi[2], F. Omori[1], Y. Mano[1] (1.Inst. Livest. Grassl. Sci., NARO, 2.Fac. Food Agric. Sci., Fukushima Univ.)

P058 Investigation of the suitability and optimal cultivation period for applicating cell nursery system to sweet potato

☆Nakajima, H.[1], M. Nishinaka[2], K. Taguchi[2] (1.HARC/NARO, 2.CARC/NARO)

P059 Heterosis observed in the methylation level of *18S rDNA* in seedlings of rice hybrids using bisulfite amplicon sequencing

☆Ohtsuki, H.[1], Y. Nakamura[1], K. Ichitani[2], T. Kuboyama[1] (1.Col. Agr., Ibaraki U., 2.Fac. Agr., Kagoshima U.)

P060 Effects of pollen parents on rutin content and related enzyme genes in buckwheat

☆Otsuka, S.[1,2], T. Hara[1], K. Ishiguro[1], K. Matsushima[3], Y. Yasui[4], K. Matsui[2,5] (1.Inst. HARC., NARO, 2.Grad. Sch. Lif., Univ. Tsukuba, 3.Inst. Agric. Acad. Assy. Fac., Shinshu U., 4.Grad. Sch. Agr., Kyoto U., 5.Inst. Crop Sci., NARO)

P061 Did SSIIa gene contribute to early heading rice breeding in Fukui Prefecture?

☆Makida, E.[1], A. Kobayashi[2], M. Suganami[3], H. Yoshida[3], S. Watanabe[2], Y. Machida[2], G. Chaya[2], F. Nakaoka[2], Y. Morinaka1[1], N. Sato[2], M. Matsuoka[3], K. Miura[1] (1.Fukui Pref. Univ., 2.Fukui Agri. Exp. Stn., 3.Fukushima Univ.)

P062 Identification of alleles from wild soybeans that increase protein content without decreasing oil content

☆Park, C.[1], T. NGUYEN[1,2], D. LIU[1,3], W. Qingyu[3], D. Xu[1] (1.Japan International Research Center for Agricultural Sciences (JIRCAS), 2.Agricultural Genetics Institute (Vietnam), 3.College of Plant Science, Jilin University (China))

P063 Impact of the semi-dwarfing gene *Rht8* at a wheat breeding program in Hokkaido

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P064 Identification of proteins that contribute to flour strength among elite breeding lines in a breeding program

○Kizawa, K.[1], N. Ashikaga[2], K. Hayashi[2], S. Ohnishi[2], K. Hayakawa[1] (1.Cereal Science Research Center of Tsukuba, Nisshin Flour Milling Inc., 2.Hokkaido Research Organization Kitami Agricultural Experiment Station)

P065 Analysis of seed coat cracking caused by steaming on soybean cultivars suitable for natto.

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Management Office, 3.Agriculture Technology Division, Ibaraki Prefecture Department of Agriculture, Forestry and Fisheries, 4.Agricultural Research Institute, Ibaraki Agricultural Center)

P066 Analysis of the locus controlling the grain width of brown rice near the region of rice brown spot resistance gene *bsr1*

○Matsumoto, K., Y. Honda (Mie Pref. Agri. Res. Inst.)

P067 Rice lines introduced mutated *spdt* gene, which reduce phosphorus accumulation in grains, into Momiroman improved absorption of calcium

○Mizobuchi, R.[1], M. Yamazaki[2], H. Ohmori[2], H. Ohtsu[2], F. Nanto-Hara[2], C. Tsuiki[1], U. Yamanouchi[1], A. Shomura[1], N. Yamaji[3], J. Ma[3], K. Yoshida[4] (1.Inst. Crop. Sci., NARO, 2.Institute of Livestock and Grassland Science, NARO, 3.Institute of Plant Science and Resources, Okayama University, 4.Graduate School of Agricultural and Life Sciences, The University of Tokyo)

P068 Effect of high spacing seeding of short stem soybean line to yield

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P069 Exploring the loci derived from *Oryza meridionalis* regulating panicle morphology

☆Agata, A.[1,2], H. Takahashi[1], M. Nakazono[1], Y. Sato[2] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.National Institute of Genetics)

P070 Search for the gene responsible for Frilly Petal Undulation 1 (fpu 1), a novel Torenia mutant.

☆Mayuzumi, T.[1], M. Hatashita[2], K. Takagi[2], K. Ishi[3], T. Abe[4], Y. Kazama[1,4] (1.Fac. Biosci. Biotech., Fukui Pref. Univ, 2.Wakasa-wan Ener. Cent, 3.NIRS, QST, 4.RIKEN Nishina Center)

P071 Diversity in the seed dormancy among the NARO Rice Core Collection of Japanese Landraces

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P072 Analysis of the function of the *qLTG3-1* gene product in controlling low-temperature germination of rice seeds

☆Yamamoto, M.[1], T. Yamaguchi[2], K. Murata[3], T. Yamada[1], M. Kanekatsu[1] (1.Grad. Sch. Agr., Tokyo U. Agr. Tec., 2.Toyama Pref. Tonami Agr. For. Prom. Cent., 3.Toyama Pref. Agr. Forest. Fish. Res. Cent.)

P073 Identification of the flowering time genes responsive to the environmental factors in the Dual-NAM populations.

○SAITO, H.[1], K. Doi[2], A. Abe[3], S. Ogawa[4] (1.JIRCAS, 2.Grad. Sch. Bioagr. Sci., Nagoya U., 3.Iwate Biotechnology Research Center, 4.Nosho Navi Co., Ltd.)

P074 Possible origin of new species from allodiploid hybrids between species with different chromosome numbers

☆Nakata, K., M. Kanekatsu, T. Yamada (United Grad. Sch. Agr. Tokyo U. Agr. Tech.)

P075 Proteomic analysis of soluble and insoluble proteins whose abundance varied in the cotyledons after inducing hybrid lethality in *Nicotiana* interspecific hybrids

☆Asai, A., M. Kanekatsu, T. Yamada (Grad. Sch. Agr., Tokyo U. Agr. Tech.)

P076 Search for genes related to pollen germination by transcriptome analysis in cytoplasmic male sterile tomato

☆Kuwabara, K.[1], T. Ariizumi[2] (1.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 2.Fac. Life Env. Sci., Univ. Tsukuba)

P077 Effect of closure of the Plasmodesmata between the central cell and the egg cell on DNA methylation in the egg cell

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P078 Difference and similarlity between two cytoplasmic male sterility in sugar beet

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