

Title of Papers Presented at the 148th Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 Reference-based chromosome-scale assembly of Japanese barley (*Hordeum vulgare* ssp. *vulgare*) cultivar "Hayakiso 2"

○Tanaka, T.¹, Y. Haraguchi², T. Todoroki², D. Saisho³, T. Abiko⁴, H. Kai² (1.NAAC, NARO, 2.Fukuoka Agriculture and Forestry Research Center, 3.Okayama University, 4.Kyushu University)

102 *De novo* genome assembly of wild emmer wheat using nanopore sequencing

☆Nishimura, K.¹, K. Ushijima¹, Y. Yasui², N. Takano¹, R. Nakano², Y. Monden¹, K. Kato¹, H. Nishida¹ (1.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ., 2.Grad. Sch. Agr., Kyoto Univ.)

103 Identification of early-heading genes in wild emmer wheat by repeated QTL analysis using F₂ populations

☆Takano, N.¹, K. Nishimura¹, Y. Chang², M. Okuma¹, K. Murata², R. Nakano², T. Nakazaki^{2,3}, K. Kato¹, Y. Monden¹, H. Nishida¹ (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. of Agri., Kyoto Univ., 3.Office of Institutional Adv. and Comm., Kyoto Univ.)

104 High-Resolution Genomic Assembly of Hops (*Humulus*) to Unveil Sex Determination Factor

☆Segawa, T.¹, T. Akagi^{2,3}, R. Uchida², H. Tanaka⁴, K. Shirasawa⁵, N. Yamagishi⁶, H. Yaegashi⁶, S. Natsume⁷, H. Takagi⁷, A. Abe⁷, M. Okuno⁴, A. Toyoda⁸, K. Sato⁹, Y. Honniden², C. Zhang², K. Ushijima², J. Patzak¹⁰, L. Horáková¹¹, V. Bacůvský¹¹, R. Hobza¹¹, D. Charlesworth¹², T. Itoh⁴, E. Ono¹ (1.Res. inst. SIC Ltd., 2.Okayama Univ., 3.Nihon BioData Co., Ltd., 4.Inst. Sci. Tokyo, 5.Kazusa DNA Res. Inst., 6.Univ. Iwate, 7.Iwate Bio. Res. Cen., 8.Natl. Inst. Genet., 9.Univ. Toyama, 10.Hop Res. Inst. Co. Ltd., 11.Institute of Biophysics, Czech Acad. Sci., 12.Inst. Ecol. Evol., Univ. Edinburgh)

105 Assembling autotetraploid genomes only by nanopore sequencing

○Naito, K.¹, K. Akai² (1.Res. Cntr. Genet. Resour., NARO, 2.Hokkaido Agr. Res. Cntr., NARO)

106 New strategy for allele identification in autopolyploid sweet potato by Nanopore sequencing using allele-specific k-mer

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107 Comparative genomic analysis of Koshihikari-related varieties based on the telomere-to-telomere sequence of Koshihikari genome

○Yoshida, H.¹, H. Takahashi^{1,2}, T. Akagi³, D. Saisho^{4,7}, M. Suganami¹, G. Tamiya^{5,6,7}, E. Yamamoto⁸, A. Kobayashi⁹, M. Matsuoka¹ (1.IFeS, Fukushima Univ., 2.Fac. Food Agric. Sci., Fukushima Univ., 3.Nihon BioData Corp., 4.IPSR, Okayama Univ., 5.Grad. Sch. Med., Tohoku Univ., 6.ToMMo, Tohoku Univ., 7.AIP Center, RIKEN, 8.Grad. Sch. Agri., Meiji Univ., 9.Fukui Agri. Exp. Stn.)

108 A Paradigm Shift in Genetics Driven by Complete Genomes: Mutation Biases in Genic and Non-genic Regions

Akagi, T.¹, ○D. Saisho^{2,7}, H. Yoshida³, H. Takahashi^{3,4}, Y. Ikeda², T. Matsuda^{3,4}, G. Tamiya^{5,6,7}, A. Kobayashi⁸, M. Matsuoka³ (1.Nihon BioData Corp., 2.IPSR, Okayama Univ., 3.IFeS, Fukushima Univ., 4.Fac. Food Agric. Sci., Fukushima Univ., 5.Grad. Sch. Med., Tohoku Univ., 6.ToMMo, Tohoku Univ., 7.AIP Center, RIKEN, 8.Fukui Agric. Expt. Stn.)

109 Extension and Evaluation of Graphite for Genotype Imputation and Error Correction Using Pedigree Structure

○Inamori, M.¹, M. Minamikawa², T. Shimizu³, M. Kuniyoshi³, K. Nonaka³, S. Moriya³, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ., 3.NIFTS, NARO)

112 Identification of QTL for photosynthesis and yield in bread wheat chromosome 6A and elucidation of the surrounding genes

☆Hina, K.¹, T. Ishii², K. Nishimura³, Y. Matsuoka⁴, H. Tsujimoto², R. Mega¹ (1.Grad. Sch. Sci. Tech. Innov., Univ. Yamaguchi, 2.ALRC., Univ. Tottori, 3.Grad. Sch. Sci. Environ. Life Sci., Univ. Okayama, 4.Grad. Sch. Agri., Univ. Kobe)

113 Effectiveness of Targeted Sequencing in QTL Mapping of Mutant Barley Lines: Insights from Heading Time Analysis

☆Takeda, S., M. Okuma, A. Mandozai, K. Nishimura, K. Ushijima, Y. Monden, K. Kato, H. Nishida (Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

114 Identification of a candidate miRNA for sex determination in the staple crop white Guinea yam (*Dioscorea rotundata*)

☆Kudoh, A.¹, Y. Sugihara², K. Iseki³, R. Matsumoto⁴, K. Minoji¹, K. Onai¹, A. Abe⁵, S. Natsume⁵, T. Sakai¹, K. Oikawa⁵, M. Shimizu⁵, K. Itoh⁵, H. Adachi⁶, K. Honda¹, S. Yamanaka³, P. Adebola⁴, A. Asfaw⁴, R. Terauchi¹ (1.Grad. Agri., Kyoto Univ., 2.The Sainsbury Laboratory, 3.JIRCUS, 4.IITA, 5.IBRC, 6.Adv. Life Sci., Hokkaido Univ.)

115 Considerations on Crossing and Selection Strategies in Citrus Breeding Informed by Progeny Segregation Forecasts Based on Genomic Prediction Models

☆Kimura, S.¹, M. Minamikawa², K. Nonaka³, T. Shimizu³, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ, 3.NIFTS, NARO)

116 Genomic Predictions and genome wide association studies of first sprouting time in tea plant.

○Aoshima, C.¹, J. Kawaki¹, Y. Ishiguro², A. Nagano^{3,4}, T. Ikka^{2,5,6,7}, H. Yamashita^{2,5,6,7} (1.Tea Res. Cent., Shizuoka Pref., 2.The United Graduate School of Agricultural Science, Gifu Univ., 3.BBC, Nagoya Univ., 4.Institute for Advanced Biosciences, Keio Univ., 5.Grad. Agr., Shizuoka Univ., 6.Res. Inst. Green Sci. Tech., Shizuoka Univ., 7.Res. Inst. Tea Sci. Tech., Shizuoka Univ.)

117 Validating genomic prediction models of the first sprouting time for genomic selection in tea plant breeding population

○Kawaki, J.¹, C. Aoshima¹, Y. Ishiguro², A. Nagano^{3,4}, T. Ikka^{2,5,6,7}, H. Yamashita^{2,5,6,7} (1.Tea Res. Cent., Shizuoka Pref., 2.The United Graduate School of Agricultural Science, Gifu Univ., 3.BBC, Nagoya Univ., 4.Institute for Advanced Biosciences, Keio Univ., 5.Grad. Agr., Shizuoka Univ., 6.Res. Inst. Green Sci. Tech., Shizuoka Univ., 7.Res. Inst. Tea Sci. Tech., Shizuoka Univ.)

118 Comparative analysis of genome-wide genotyping techniques in peanut

○Shirasawa, K.¹, T. Tsugane² (1.Kazusa DNA Res. Inst., 2.Chiba Pref. Agric. Forest Res. Center)

119 Genomic breeding research on fruit traits in persimmon cultivars

☆Horiuchi, A.^{1,2}, N. Onoue³, R. Matsuzaki³, K. Nishimura², K. Shirasawa⁴, Y. Kubo², K. Ushijima², T. Akagi², M. Minamikawa⁵ (1.Grad. Sch. Hort., Chiba Univ., 2.Grad. Sch. Environ. Life

120 Genome-wide association study of leaf morphological traits in leafy amaranth

○Asri, S.¹, K. Shirasawa³, Y. Yoshioka² (1.Grad. Sch. Sci. & Tech., Univ. Tsukuba, 2.Inst. Life & Env. Sci., Univ. Tsukuba, 3.Kazusa DNA Research Institute)

121 Genetic and epigenetic changes associated with ancient allopolyploidization of *Oryza coarctata*, the only halophyte in the genus *Oryza*

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122 Mapping of novel QTLs that promote coleoptile elongation under oxygen deprivation in rice using GRAS-Di.

☆Hirano, H.¹, S. Hirata², M. Fukuda², T. Fukao¹ (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.Dept. Biosci. Biotech., Fukui Pref. Univ.)

123 Activated Mutator transposon in IR24 derivatives

○Ishikawa, R.¹, R. Kanbe¹, K. Ichitani^{2,3}, エ. エレワラ カンカナンギ³, E. Fukai⁴, Y. Fukuta⁵, L. Dinh Thi¹ (1.Fac. Agri. and Life Sci., Hirosaki Univ., 2.Fac. Agri., Kagoshima Univ., 3.United Grad. Sch. Agri. Sci., Kagoshima Univ., 4.Fac. Agri., Niigata Univ., 5.Fac. Agri., Ryuku Univ.)

201 Regulation of chromatin accessibility in the shoot apical meristem of rice by florigen activation complex

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202 Development of PHYTOmap for rice shoot apical meristem II

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203 Development of super resolution expansion microscopy for rice shoot apical meristem

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204 Chromatin state analysis of the rice shoot apical meristem using ATAC-seq imaging

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205 The first developmental changes in rice shoot apical meristem during the transition

☆Honda, M.¹, M. Tanaka¹, W. Tanaka², H. Tsuji^{1,3} (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 3.Biosci. Biotechnol. Center, Nagoya Univ.)

206 Functional analysis of *ASP1* and *TAB1* during axillary bud development in rice

☆Ohyama, A.¹, T. Toriba², M. Sato³, H. Tsuji^{3,4}, W. Tanaka¹ (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ., 3.Kihara Inst. Biol. Res., Yokohama City Univ., 4.Biosci. Biotechnol. Center, Nagoya Univ.)

207 Functional analysis of strigolactone-related genes in rice shoot formation

☆Aimori, S.¹, A. Ohyama¹, T. Toriba², W. Tanaka¹ (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ.)

208 Expression analysis of tillering-related genes in ectopic meristems of *adaxial bipolar leaf* mutants

☆Chiba, K.¹, M. Kikuchi¹, K. Yashima³, T. Yamazaki³, R. Okamoto³, M. Watanabe³, H. Sunohara², N. Nagasawa³, N. Satoh-Nagasawa³ (1.Grad. Sch. Biores. Sci., Akita Pref. Univ., 2.Fac. Sci., Univ. Kumamoto, 3.Fac. Biores. Sci., Akita Pref.)

209 Functional analysis of spinach *CONSTANS* homologs using transgenic *Arabidopsis thaliana*

☆Hatsukade, M.¹, R. Ishikawa¹, K. Yamano¹, H. Hirakawa², Y. Onodera¹ (1.Grad. Ach. Agr., Hokkaido Univ., 2.Grad. Ach. Agr., Kyusyu Univ.)

210 *BoFLC2* Introgression Alters the Vernalization Response through Epigenetic Memory in *Brassica rapa*

☆Chowdhury, A.¹, S. Yano¹, K. Tonasaki², R. Fujimoto¹ (1.Graduated School of Agricultural Science, Faculty of Agriculture, Kobe University, 2.Kihara Inst. Biol. Res.)

211 Functional analysis of *FLOWERING LOCUS C* homologs and identification of vernalization-responsive regions in *Brassica rapa*.

☆Yamada, M.¹, A. Chowdhury¹, K. Osabe², K. Tonosaki³, R. Fujimoto¹, D. Buzas⁴ (1.Grad. Sch. Agric., Kobe Univ., 2.Plant Epigenetics Unit, Okinawa Inst. Sci. Technol., 3.Grad. Sch. Sci., Yokohama City Univ., 4.Grad. Sch. Life Environ. Sci., Univ. Tsukuba)

212 Study on floral meristem identity genes and morphological modification in German Chamomile

○Kurogi, K.¹, Y. Takahara² (1.Grad. Sch. Materials Science and Bioengineering., Nagaoka University of Technology, 2.Materials Science and Bioengineering., Nagaoka University of Technology)

213 Identification of the headings-related gene *TaBBX-A19* through the genetic analysis of a wheat early heading mutant

☆Komura, S.^{1,2}, F. Kobayashi², Y. Oono², H. Handa³, M. Kishi-Kaboshi⁴, F. Abe⁵, Y. Inoue¹, K. Yoshida¹ (1.Grad. Sch. Agr., Kyoto U., 2.NICS, 3.Grad. Sch. Life Env. Sci., Kyoto Pref. U., 4.Kazusa DNA Res. Inst., 5.NIAS)

214 Estimation of rice cultivating condition based on results of QTL analyses for heading date in Zambia

☆Yonamine, K.¹, H. Kobayashi¹, S. Komatsubara², R. Mulenga³, G. Munkombwe³, P. Mabuto³, M. Chinji³, E. Musabla³, N. Museta³, L. Kamguya³, j. Njobvu³, Y. Fukuta¹ (1.Univ. Ryukyus., 2.JICA, 3.ZARI)

215 Identification of the Genetic region Responsible for Extremely Late Bolting in the Turnip Variety 'Tokinashikokabu'

☆Yano, S.¹, A. Chowdhury¹, M. Hara², M. Sakemoto², M. Shimizu³, H. Takagi², R. Fujimoto¹, K. Tonosaki⁴ (1.Grad. Sch. of Agri. Sci., Kobe Univ., 2.Faculty of Bioproduction Sci., Ishikawa Prefectural Univ., 3.Iwate Biotechnology Res. Center, 4.Kihara Inst. Biol. Res., Yokohama City Univ.)

216 Substitution of vernalization requirement allele in the diversification of cultivated beet

☆Oishi, M., R. Hayakawa, E. Taniguchi, K. Kitazaki, T. Kubo (Grad. Sch. Agr., Hokkaido Univ)

217 Changes in cytokinin content and sensitivity in frill mutants of *Trenia*

☆Mayuzumi, T.¹, K. Ishi², M. Hatashita³, K. Takagi³, M. Kojima⁴, Y. Takabayashi⁴, H. Sakakibara^{4,5}, T. Higashiyama⁶, T. Abe⁷, Y. Kazama^{1,7} (1.Fac. Biosci. Biotech., Fukui Pref. Univ, 2.NIRS, QST, 3.Wakasa-wan Ener. Cent, 4.RIKEN Center for Sustainable Resource Science, 5.Department of Applied Biosciences, Graduate School of Bioagricultural Sciences, Nagoya Univ,, 6.Department of Biological Sciences, Graduate School of Science, Tokyo Univ, 7.RIKEN Nishina Center)

218 Improving rice lateral root development through understanding its auxin-dependent and independent regulatory pathways

☆DONG, Y.¹, S. Kushida¹, M. Kanao¹, C. Wainaina², P. Lipio¹, Y. Inukai³ (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Dept. Hort. Food Sec., JKUAT, 3.ICREA, Nagoya U.)

219 Genetic analysis of two kinds of asymmetric divisions during stomatal development in rice

☆Miya, M.¹, H. Takanashi², Y. Sato¹, J. Itoh² (1.Natl. Inst. Genet., 2.Grad. Sch. Agri. & Life Sci., Univ. Tokyo)

220 Left-right asymmetry-driven physical interaction causes twisting in rice (*Oryza sativa*) leaves

☆Hikichi, K.¹, S. Okada¹, Y. Tokuyama², S. Miura¹, M. Taguchi¹, Y. Kishima¹, I. Takamure¹, Y. Koide¹ (1.Graduate school of Agriculture, Hokkaido University, 2.National Institute of Genetics)

221 Quantification of barley stems and leaves spatial arrangement using 3D imaging and its application to genetic analysis

☆Kikkawa, D., K. Nishimura, Y. Monden, K. Kato, H. Nishida (Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ.)

222 Regulation of germination by site-directed mutagenesis of *HvMFT1* gene in barley

○Hisano, H.¹, N. Yamaji¹, M. Hamaoka¹, K. Sato² (1.IPSR, Okayama Univ., 2.Grad, Sch. Agr. Setsunan U.)

223 QTL analysis for shattering in recombinant inbred lines derived from a cross between Miliyang 23 and Akihikari

☆TOMARI, H.¹, S. KOMATSUBARA², R. MULENGA³, P. MABUTO³, M. CHINJI³, E. MUSABULA³, N. MUSETA³, L. KAMGUYA³, J. NJOBVU³, Y. FUKUTA¹ (1.Univ. Ryukyus, 2.JICA, 3.ZARI)

224 Why was the single grain per spikelet selected for einkorn wheat?

○Sakuma, S.¹, K. Nakamura¹, C. Koiso¹, S. Takenaka², S. Nasuda³ (1.Fac. Agr. Tottori U., 2.Fac. Agr. Ryukoku U., 3.Grad. Sch. Agr. Kyoto U.)

301 A mutant allele in *qSOR1*, rice gravitropism QTL, confers deeper rooting, resulting in enhanced drought resistance

○Uga, Y.¹, Y. Kitomi¹, R. Kuroda¹, R. Nakata¹, M. Iba^{1,2}, F. Soma¹, S. Teramoto¹, K. Sugimoto¹, T. Kawai¹ (1.Inst. Crop Sci., NARO, 2.Tokyo Univ. Agri.)

302 Estimation of Genetic Regions Associated with Waterlogging-Inducible Soil-Surface Root in the Wild Rice *Oryza glumaepatula*

☆Tamaru, S.^{1,2}, T. Miyashita¹, K. Katayama¹, T. Kimoto¹, H. Tokuo¹, Y. Uga³, K. Shiono¹ (1.Grad. Sch. Biosci. Biotech., Fukui Pred. Univ., 2.JSPS Research Fellow, 3.Inst. Crop Sci., NARO)

303 Development of Culture Conditions for Genetic Transformation in the Sweetpotato Cultivar 'J-Red'

☆Kobayashi, H.¹, M. Otani², H. Matui¹, H. Tabuchi³, K. Nishimura¹, H. Nishida¹, K. Kato¹, Y. Monden¹ (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Res. Inst. Biore. Biotech., Ishikawa Pref. Univ., 3.KARC/NARO)

304 Establishment of a genetic transformation system in *Echinochloa phyllopogon*

☆Sugahara, M.¹, S. Iwakami², K. Yasuda³, T. Gondo⁴ (1.Grad. Sch. Agr., Univ. Miyazaki, 2.Tokyo Univ. Of. Agr. Tech, 3.Agr. Bior. Sci., Akita. Pre. Univ, 4.FSRC, Univ. Miyazaki)

305 Development of a highly efficient genome editing technique in melon by iPB and creation of a long shelf-life melon ripened by exogenous ethylene

○Sasaki, K.¹, K. Urano¹, N. Mimida², S. Nonaka³, H. Ezura^{2,3}, R. Imai¹ (1.NIAS, NARO, 2.Sanatech Life Science Co., Ltd., 3.Fac. Life Environ. Sci., Univ. Tsukuba)

306 Genome editing of the *S-locus EARLY FLOWERING3* gene in 'Kitawasesoba' via iPB-RNP method.

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307 Biochemical and molecular biological characterization of *bas1* mutant in soybean seed

☆Asa, H.¹, H. Morita², H. Seki², K. Matsumoto³, R. Shigeta³, K. Fujii³, T. Yamamoto³, Y. Masuda³, T. Yamada¹ (1.Grad. Sch. Agric., Hokkaido Univ., 2.Grad. Sch. Eng., Univ. of Osaka, 3.Kanematsu Corp.)

308 Generation and characterization of lipoxygenase-deficient soybean mutants by site-directed mutagenesis

☆Tamamoto, Y.¹, K. Okada¹, Y. Haga², Y. Takata¹, K. Matsumoto³, R. Shigeta³, K. Fujii³, T. Yamamoto³, Y. Masuda³, H. Matsuura¹, T. Yamada¹ (1.Grad. Sch. Agric., Hokkaido Univ., 2.Fac. Agric., Hokkaido Univ., 3.Kanematsu Corp)

309 Targeted mutagenesis of soybean *IFS2* gene by CRISPR-Cas3

○Saika, H., N. Hara, M. Endo (Inst. Agrobiol. Sci., NARO)

310 Alternative splice acceptor site in *MSH4* gene is responsible for male sterility conferred by *ms5* in soybean

Nagayama, T.¹, H. Yamatani², N. Yamaguchi³, H. Igarashi⁴, M. Tsuda^{5,6}, S. Kato¹, K. Takahashi¹, ○A. Kaga¹ (1.Inst. Crop Sci., NARO, 2.QST, Takasaki, 3.Central Agr. Exp. Sta., HRO, 4.Tokachi Agr. Exp. Sta., HRO, 5.T-PIRC, Tsukuba Univ., 6.Fac. Food Nutr. Sci., Toyo Univ.)

311 Functional analysis of the *WOX4* gene regulating secondary meristem formation in soybean

☆Goto, M.¹, F. Hasegawa¹, Y. Baba¹, A. Kaga², A. Agata¹, M. Nakazono¹, H. Takahashi¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Inst. Crop Sci., NARO)

312 Impact of loss-of-function of DNA maintenance methyltransferase on the phenotype of the C24 accession of *Arabidopsis thaliana*

☆Kawamoto, Y.¹, M. Yamashita¹, T. Murakami¹, K. Matsuo¹, S. Shiraki¹, M. Shimizu², R. Fujimoto¹ (1.Grad. Sch. Agri. Sci., Kobe Univ, 2.Iwate Biotechnology Res. Center)

313 Secondary siRNA production of *CHS-A* cosuppression in petunia originates from multiple mRNA cleavage sites

☆Oguri, K., M. Yuhazu, M. DwiYanti, A. Kanazawa (Res. Fac. Agr., Hokkaido Univ.)

314 The petunia vein clearing virus genome encodes a suppressor against cosuppression

☆Kitagawa, T.¹, H. Sobue¹, K. Oguri¹, M. Yuhazu¹, T. Fukuhara², A. Kanazawa¹ (1.Res. Fac. Agr., Hokkaido Univ., 2.Dept. Appl. Biol. Sci., Tokyo Univ. Agr. Tech.)

315 Study of tissue-specific expression of pATPase in Phalaenopsis orchid

☆Tashiro, R.¹, Y. Takahara² (1.Grad.Sch.Materials Science and Bioengineering.,Nagaoka University of Technology, 2.Materials Science and Bioengineering.,Nagaoka University of Technology)

316 Two *Stabiliser* loci in *Antirrhinum* suppress Tam3 transposition via a novel mechanism

☆Wang, S.¹, T. Yoshida², K. Nakahara¹, Y. Kishima¹ (1.Research Faculty of Agriculture, Uni. Hokkaido, 2.Grad. Sch. Agriculture, Univ. Hokkaido)

317 The analysis of genes related Endornavirus replication in *Oryza sativa*

☆Masu, T., H. Naramoto, H. Moriyama (TUAT)

318 Identification of Candidate Genetic Loci Associated with the Frequency of Chromosomal Mutations in an *Nicotiana* Interspecific Hybrid

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319 Investigation of *Rf^{multi}* and the corresponding the cytoplasmic male sterility gene in *Triticum-Aegilops* alloplasmic lines

○TsujiMura, M.¹, Y. Oshikawa¹, M. Takenaka², T. Terachi³, S. Takenaka¹ (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Sci., Kyoto Univ., 3.Fac. Life Sci., Kyoto Sangyo Univ.)

320 PHENOTYPIC AND METABOLIC EFFECT OF HYBRID MITOCHONDRIA OF WHEAT AND MAIZE OR PEARL MILLET IN IN VITRO FERTILIZATION-DERIVED WHEAT CYBRIDS

☆IKPA-AGODO, K.¹, R. SUGIURA¹, N. ONDA², A. SATOH², T. MARYENTI^{2,3}, N. MOHAMED^{4,5}, T. OKAMOTO², T. ISHII^{4,6,7} (1.Graduate School of Sustainability Science, Tottori University, 2.Grad. Sch. Sci., Univ. Tokyo Metro., 3.Grad. Sch. Math., Univ. Indonesia, 4.IPDRE, Univ. Tottori, 5.Agri. Res. Corp. Sudan, 6.ALRC, Univ. Tottori, 7.Ch. Eng. Res. Univ. Tottori)

321 Identification of Mitochondrial Genome Factors Controlling the Phenotype of Rice-Wheat Cybrid Plant

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322 Complementation test of candidate genes responsible for dominant genic male sterility gene derived from rice cultivar Lebed.

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323 High-Precision Reassembly of the RT98-Type Mitochondrial Genome and Transcriptomic Analysis of CMS-Associated ORFs

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324 Comparison of PPR genes and the fertility restoration effect on WA-type cytoplasmic male sterile rice among three fertility restorer lines from *O. rufipogon*

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401 Development of multimodal generative AI agents harnessing breeders' insights

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402 Breeding support system enhancing use of breeding data

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403 Demonstrating a breeding strategy using genomic prediction based on a NAM population

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404 Integrative Analysis of Drought Response Using Multi-Omics Data in a Soybean RIL Population

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405 Selection and crossing of soybean RILs based on ionomic and genomic data for improving drought tolerance across distinct controlled environments

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406 Strategic crossing using genome data to improve genetic potential in soybean RIL population

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407 Single-step genomic best linear unbiased predictions in sugarcane

○Morota, G.¹, M. Goncalves², L. Peternelli² (1.Grad. Sch. Agr. Life Sci. Univ. Tokyo, 2.Federal Univ. of Vicosa)

408 Validation of genomic selection efficiency in Perilla via crossing experiments

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409 Development of R package gpyramid for optimization of major gene pyramiding

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410 Assessment of Crop Interactions in Soybean–Sorghum Intercropping Using Time-Series UAV Data

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411 New planar oxygen optode: New planar oxygen optode: New methods enable high-resolution and wide-area observation of oxygen dynamics in rice root systems

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412 Accumulation of starch characteristic data in the 'Breeding Information Infrastructure' being developed by NARO.

○Araki, E.¹, E. Kimura¹, T. Umemoto¹, K. Hori², T. Ikegaya², N. Suzuki², K. Matsushita², A. Goto², M. Kuroki² (1.Inst. Food Res., NARO, 2.Inst. Crop Sci., NARO)

413 Estimation for milling performance of wheat grains using image analysis

☆Tani, M.¹, T. Yamada², G. Ishikawa³, S. Nishiuchi¹ (1.Grad. Sch. Bioagr. Sci., Nagoy Univ., 2.RCAIT, NARO, 3.NICS, NARO)

414 Trials to isolate the mutants from the plastid genome random-mutagenized populations

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415 QTL-seq GUI: A user-friendly tool for QTL-seq analysis with click-based operation.

☆Sakemoto, M.¹, M. Takata¹, T. Segawa¹, M. Oishi¹, M. Yoshizumi¹, Y. Machi¹, T. Shiraya², H. Takagi¹ (1.Ishikawa Prefectural University, 2.Niigata Prefectural Agricultural Research Institute)

416 A study on the development of hybrid progeny in Helleborus

☆Miyakawa, R.¹, K. Koizumi², K. kawamura², S. Bang¹, T. Ohnishi¹ (1.Grad. Reg. Cre. Sci., Univ. Utsunomiya, 2.Giardino Kawamura Co.,Ltd.)

417 Effects of Seed Tuber Production Methods on Sprouting Stability in Double Cropping of the Potato Cultivar 'Shimaakari' and Its Breeding Significance

○Tanaka, Y.¹, M. Sato², S. Kashiwagi¹ (1.Kagoshima Pref. Inst. for Agri., 2.Kagoshima Pref. College of Agri.)

418 Effect of combing *SD1* and *SPIKE* genes under unfavorable environmental conditions in rice (*Oryza sativa* L.)

☆SEKIMATA, G., R. MOCHIZUKI, Y. FUKUTA (Univ. Ryukyus,)

419 A methodology of genetic analysis for phenotypic plasticity using unstable climate of the northern-limit regions of rice cultivation

○Ito, Y. (Green Evolution Lab.)

501 Identification of the rice resistance locus *Pi-eTO5* consisting of four NLR genes

○Shimizu, M.¹, S. Asuke², A. Abe¹, H. Takata², H. Adachi³, T. Fujiwara³, T. Sakai⁴, Y. Tosa², R. Terauchi^{1,4} (1.IBRC, 2.Grad. Sch. Agric. Sci., Kobe Univ, 3.Fac. Adv. Life Sci., Hokkaido Univ, 4.Grad. Sch. Agric., Kyoto Univ.)

502 Mapping of a wheat blast resistance gene possessed by the Japanese wheat accession R3

☆Sota, K.¹, S. Asuke², Y. Tosa², H. Handa¹ (1.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ.)

503 Development of DNA markers and discovery of novel alleles for tan spot of wheat resistance genes

☆Taro, S.¹, G. Ishikawa², H. Nakamura³, A. Kurono¹, T. Touyama¹ (1.Aichi Agri. Res. Cent., 2.NICS,NARO, 3.HARC,NARO)

504 GWAS-based identification of genomic regions conferring root-knot nematode resistance derived from the black oat (*Avena strigosa*) cultivar 'Terara'

○UWATOKO, N.¹, K. Uesugi², T. Mizubayashi¹, G. Murata², H. Yamakawa¹, M. Katsura³ (1.Institute of Crop Science, NARO, 2.Institute for Plant Protection, NARO, 3.Kyushu Okinawa Agricultural Research Center, NARO)

505 Genetic linkage analysis between the genes for seed coat color and resistance to Bean Common Mosaic Virus using DNA markers in common bean.

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506 Identificaion of Candidate Regions for Tolerance in the Turnip Mosaic Virus Tolerance Mustard Cultivar 'BIAN GAN QING'

☆Hoshino, H.¹, R. Kuwahara², O. Kim², K. Komatsu³, S. Yoshida³, K. Irie⁴, K. Wakui³ (1.Grad. Sch. Agri., Tokyo Univ. of Agri., 2.Dept. of Agri., Tokyo Univ. of Agri., 3.Dept. of Biores. Dev., Tokyo Univ. of Agri., 4.Dept. of Int. Agri. Dev., Tokyo Univ. of Agri.)

507 Selection and evaluation of herbicide-tolerant adzuki bean lines derived from callus of 'Benidainagon'

☆Adegawa, S.¹, N. Yamaguchi¹, C. Souma¹, H. Nagasawa², M. Oonami^{1,2}, T. Maruta^{1,3}, K. Shirasawa⁴ (1.Central AES, HRO, 2.Tokachi AES, HRO, 3.Donan AES, HRO, 4.Kazusa DNA Research Institute)

508 Imaging of the dynamics of root growth and radial oxygen loss during the seedling stage of rice using a planar oxygen optode

○Shiono, K.¹, S. Tamaru^{1,2}, N. Fujiwara¹, H. Shiba^{1,2} (1.Grad. Sch. Biosci. Biotech., Fukui Pred. Univ., 2.JSPS Research Fellow)

509 Analysis of the regulatory mechanism of ABA response in the region of aerenchyma formation induced by moisture damage in rice roots.

☆Kojima, M., A. Shinozawa, K. Izawa, S. Nakamura (Dept. Bioscience, Tokyo Univ. Agric.)

510 Evaluation of waterlogging tolerance in maize introduced traits for formation of constitutive aerenchyma and radical oxygen loss barrier from *Zea nicaraguensis*

☆Okada, T.¹, F. Omori², Y. Mano², A. Agata¹, H. Takahashi¹, M. Nakazono¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Inst. Livest. Grassl. Sci., NARO)

511 The Role of Absciscic Acid in Low Oxygen Stress Response

☆Yokouchi, N.¹, H. Tamai¹, H. Takahashi², M. Nakazono², K. Izawa¹, S. Nakamura¹, A. Shinozawa¹ (1.Dept. Bioscience, Tokyo Univ. Agric., 2.Grad. Sch. Bioagric. Sci., Univ. Nagoya)

512 Search for genes involved in varietal differences in the accumulation of protein aggregates under high-temperature stress in rice seedlings

☆Inushima, A., T. Yamada (Grad. Sch. Agr., Tokyo Univ. Agr. Tech.)

513 Estimating the impacts of 21st-century warming trends on the percentage of first-grade rice and the effectiveness of heat-tolerant cultivars in Japan

○HASEGAWA, T., H. WAKATSUKI (National Agriculture and Food Research Organization (NARO))

514 An approach to classifying heat tolerance ranks in rice cultivars using a model for estimating chalky grain percentage and field trials

○Wakatsuki, H.¹, Y. Suzuki², M. Hirayama², H. Ishikawa², T. Nakano², T. Hasegawa¹ (1.Institute for Agro-Environmental Sciences, NARO, 2.Plant Biotechnology Institute, Ibaraki Agricultural Center)

515 Quantitative evaluation of heat tolerance of rice based on re-analysis of nationwide field experiment data collected through systematic review

○Toda, Y., H. Wakatsuki, Y. Ishigooka, T. Hasegawa (Inst. Agro-Env. Sci., NARO)

516 Flour quality studies using candidate lines for heat stress tolerance.

○Tanaka, H.¹, Y. Shikoro¹, M. Tsuboi¹, Y. Gorafi^{2,3}, I. Tahir^{3,4}, H. Tsujimoto⁴ (1.Fac. Agr., Tottori Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.ARC, Sudan, 4.ALRC, Tottori Univ.)

517 Identification of Heat Stress-Related Genes Using Selfed Lines of Buckwheat

☆Mochizuki, R.^{1,2}, K. Fujino², H. Shimura² (1.KARC, NARO, 2.Res. Fac. Agr., Univ. Hokkaido)

518 Identification of salt tolerant maize-wheat (^{Zea}Wheat) and pearl millet-wheat (^{Cenchrus}Wheat) cybrid lines produced through in vitro fertilization system

☆Nowroz, F.¹, N. Onda¹, A. Satoh¹, T. Ishii², T. Okamoto¹ (1.Dept. Biol., TMU, 2.ALRC., Univ. Tottori)

519 Elucidating the Na⁺ influx mechanism into the uppermost fully expanded leaf in *Vigna luteola*

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601 Development of maize transformation system using leaf primordia

☆Kojima, T.¹, K. Tanaka¹, Y. Mano², T. Furuta³, M. Ashikari⁴, H. Tsuji⁴, A. Agata¹, H. Takahashi¹, M. Nakazono¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Inst. Livest. Grassl. Sci., NARO, 3.IPSR, Okayama Univ., 4.Biosci. Biotechnol. Center, Nagoya Univ.)

602 Variation on crossabilities of bread wheat with Triticeae species

☆Ryu, A., S. Sakuma (Fac. Agr. Tottori U.)

603 Time-course single pollen RNA-seq analysis for elucidating a gametocidal gene in wheat

☆Yamamori, K.^{1,2}, K. Murata¹, H. Kakui³, T. Yoshikawa¹, S. Nasuda¹ (1.Grad. Sch. Agric., Kyoto Univ., 2.IPSR, Okayama Univ., 3.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

604 Evaluation of the self-incompatibility inhibitor gene from cultivated potatoes

☆Yamashita, M., I. Asai, A. Yasuga, K. Suzuki, K. Hosaka, R. Sanetomo (Obihiro University of Agriculture and Veterinary Medicine)

605 Knockout of mitochondrial gene, *orf352*, in Wild Abortive-cytoplasmic male sterile rice

☆Mon, H.^{1,2}, S. Arimura³, T. Kazama¹ (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Dept. Agri. Biotech, Yezin Agri. Univ., 3.Grad. Schl. Agri. Life Sci., The Univ. of Tokyo)

606 Production of neo-tetraploid and -diploid hybrids between *Oryza sativa* and *O. rufipogon/longistaminata* exhibiting high salt tolerance by in vitro fertilization

☆Wongla, W.¹, S. Ono¹, Y. Sato², T. Okamoto¹ (1.Dept. Biol., TMU, 2.Plant Gen., NIG)

607 Mode of inheritance for the fertility restoration found in near isogenic lines of the F₁ pollen sterility gene *S21* from *Oryza rufipogon* and *O. meridionalis*

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608 Allelic divergence of hybrid sterility gene *S13* found between African wild rice *O. longistaminata* and Asian cultivated rice *O. sativa*

☆Shiozaki, K., M. Zin Mar, W. Takanishi, Y. Kishima, Y. Koide (Grad. Sch. Agriculture, Hokkaido Univ.)

609 New strategy to enhance soybean pod shattering resistance with quadruple *GmMYB26* mutations

○Takahashi, Y.¹, R. Takeshima², A. Kaga², R. Nakata², K. Naito¹, M. Ishimoto² (1.Research Center of Genetic Resources, NARO, 2.Institute of Crop Science, NARO)

610 Chromosome-scale genome assembly of Dadachamame using long-read technology and estimation of candidate genes for good taste QTLs

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611 High-throughput QTL detection for good taste in Dadachamame using near-infrared spectroscopy

☆Abe, H.¹, N. Shioya², E. Ogiso-Tanaka³, T. Hoshino^{1,4} (1.Grad. Sch. Agr., Yamagata Univ., 2.Grad. Sch. Agr., Iwate Univ., 3.Grad. Sch. Agr., Tokyo Univ. of Agr. & Tech., 4.Fac. Agr., Yamagata Univ.)

612 Selection of high-sucrose soybean lines derived from EMS mutagenesis and crossbreeding for improvement of tofu taste

☆Takahashi, H.¹, H. Igarashi², S. Kobayashi³, N. Yamaguchi³ (1.Kamikawa Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO, 3.Central Agr. Exp. Sta., HRO)

613 Effects of high temperatures on sucrose content of soybean seeds in Hokkaido.

☆Igarashi, H.¹, H. Takahashi², Y. Hosokawa³, M. Kawahara⁴, S. Koyano³, K. Nakamichi³, S. Kobayashi³, N. Yamaguchi³ (1.Tokachi Agr. Exp. Stn., HRO, 2.Kamikawa Agr. Exp. Stn., HRO, 3.Central Agr. Exp. Stn., HRO, 4.Tokachi Foundation)

614 Variation in carotenoid composition among yellow-fleshed potato varieties

☆Ishizu, Y.¹, A. Endo¹, H. Sasaki², T. Igarashi², T. Yamada¹ (1.Res. Fac. Agr., Hokkaido Univ., 2.Calbee Potato, Inc.)

615 Analysis of Vascular Browning and Differential Gene Expression in Japanese Pear ‘Rinka’ During Cold Storage

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616 Analysis of regulatory mechanism of gene expression associated with heterosis for low-pH tolerance during early growth in sugar beet.

☆Yamada, K.¹, H. Ogawa¹, Y. Hiragori¹, H. Matsuhira², K. Kitazaki¹ (1.Graduate School of Agriculture, Hokkaido University, 2.NARO, HARC)

617 Pyramiding root QTLs *DRO1* and *qRL6.1* maintains photosynthesis and increases rice yield in paddy fields

☆Iba, M.^{1,2}, Y. Arai-Sanoh¹, R. Tanaka¹, Y. Kitomi¹, S. Teramoto¹, K. Irie², Y. Uga¹ (1.NICS, NARO, 2.Tokyo Univ. Agr.)

618 Genetic analysis of pre-harvest sprouting resistance by using backcross population from bread wheat × spelt wheat

☆Diaz Suarez, L., S. Kamizawa, K. Yoshikawa, K. Inoshita, K. Onishi (Obihiro U. Agric. & Vet. Med.)

619 Alterations in growth patterns following polyploidization of diploid wild strawberry

☆Tomioka, H., S. Bang, T. Kurokura, T. Ohnishi (Grad. Reg. Cre. Sci., Utsunomiya U.)

701 Developmental stage-specific genotype-by-environment interactions for grain quality in Etsunan rice lines.

○Kobayashi, A.¹, E. Yamamoto², H. Yoshida³, S. Watanabe¹, Y. Machida¹, G. Chaya¹, F. Nakaoka¹, M. Matsuoka³ (1.Fukui Agri. Exp. Stn., 2.Meiji Univ., 3.Fukushima Univ.)

702 Population structure analysis of Indochinese rice landraces preserved as seed specimens collected over 60 years ago

○Numaguchi, K.¹, L. Sathya¹, O. Chhoun², Y. Higashikubo³, H. Saito⁴, Y. Sato⁵, R. Gutaker⁶ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodia Agr. Res. Dev. Inst., 3.Fucl. Agr., Kobe Univ., 4.Trop. Agr. Res. Front, JIRCAS, 5.Natl. Inst. Genet., 6.Royl. Bot. Gard., Kew)

703 Genetic variation of grown root angle in rice (*Oryza sativa* L.) germplasm from Zambia

☆Fujiwara, N.¹, K. Ohshiro¹, S. Komatsubara², P. Mabvuto³, Y. Fukuta¹ (1.Univ. Ryukyus, 2.JICA, 3.ZARI)

704 Evaluation of salinity tolerance in Bangladesh rice varieties under soil and two hydroponic cultivation conditions

☆Inoue, Y.¹, Y. Yamagata², H. Yasui² (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Fac. Agr., Kyushu Univ.)

705 Production of prebreeding lines from crosses between wild species *Aegilops umbellulata* Zhuk. lines encompassing genetic diversity and *ph2* mutant bread wheat.

☆Son, I.¹, K. Yoshida², Y. Matsuoka¹ (1.Grad. Sch. Agr. Sci., Kobe U., 2.Grad. Sch. Agr., Kyoto U.)

706 Rice and wheat hybrid mitochondrial genome changes rice - wheat root system architecture

○Ubi, B.^{1,2}, R. Sugiura³, K. Ikpa-agodo³, N. Onda⁴, A. Satoh⁴, T. Maryenti^{4,5}, T. Okamoto⁴, T. Ishii^{1,6,7} (1.IPDRE, Tottori Univ., 2.Dept. of Biotech., Ebonyi State Univ., Nigeria, 3.Grad. Sch. Sustainability Sci., Tottori Univ., 4.Grad. Sch. Sci., Tokyo Metro. Univ., 5.Bio, Fac. of Math. and Nat. Sci., Univ., Indonesia, 6.ALRC, Tottori Univ., 7.Ch. Eng. Res., Tottori Univ.)

707 Analysis of genetic diversity and population structure of Himalayan wheat landraces

☆Li, Y.¹, Z. Meng¹, M. Nitta¹, A. Ohta¹, K. Nemoto², S. Gorafi¹, S. Nasuda¹ (1.Grad. Sch. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Shinshu Univ.)

708 Breeding of the Japanese two-row hulless waxy barley variety 'Fuhei 1103' for Hokkaido.

○Kihara, M., R. Kanatani, T. Hoki (Crop Research Laboratories, SAPPORO BREWERIES LTD.)

709 Contribution of variety development to recent wheat yield increases in Japan

○Yanagisawa, A.^{1,2} (1.HRO Fellow, 2.Calbee Potato, Inc.)

710 Mutation breeding of the Satsuma mandarin 'Harushizuka' using heavy-ion beam irradiation and development of a DNA marker for cultivar identification

☆Ishii, K.^{1,2}, T. Okubo^{3,4}, Y. Shirakawa¹, K. Tomura³, M. Kato^{3,5}, T. Abe¹ (1.Nishina Cent., RIKEN, 2.IRS, QST, 3.Fruit Tree Res. Cent., Shizuoka Pref. Inst. of Agr. and For., 4.Agr. Strategy Div., Agr.

711 Breeding of Miyazaki's native vegetable "Itomaki-Daikon" using mass selection ~
Cultivation of "Nankyu Spool No. 7" ~

○Chen, L.^{1,2}, T. Ochi¹, S. Sugiura¹, S. Mandai¹, S. Yagi¹, Y. Kimura¹, F. Abe¹, C. Sarugaku¹ (1.Fac. Envir. Hort. Sci., Minami Kyushu U., 2.Grad. Sch. Hort. & Food Sci., Minami Kyushu U.)

712 Development of Tomato Mutant Resources and Public Release of Exome Sequencing Database

☆Kuya, N.¹, K. Sugimoto^{1,2}, S. Kawamoto³, N. Fukuda¹, H. Ezura^{1,4} (1.Tsukuba-Plant Innovation Research Center, Univ. Tsukuba, 2.Research Center for Advanced Analysis, NARO, 3.Department of Informatics, National Institute of Genetics, 4.Sanatech Life Science Co., Ltd.)

713 Development of restorer of fertility lines and elucidation of fertility restoration mechanisms toward efficient F₁ seed production in tomato

☆Kuwabara, K.¹, R. Nakajima², A. Van Bosstraeten³, K. Ezura^{4,5}, K. Toriyama¹, T. Arizumi⁵, K. Shirasawa⁶ (1.Grad. Sch. Agric. Sci., Tohoku Univ., 2.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 3.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 4.JIRCAS, 5.Fac. Life Env. Sci., Univ. Tsukuba, 6.Kazusa DNA Res. Inst.)

714 Breeding of a new potato cultivar, "Kiyominori" for starch production with slightly strong resistance to *Globodera pallida*

○Akai, K.¹, H. Nakajima¹, I. Sakata¹, S. Okamoto^{1,2}, S. Tamiya^{1,3}, K. Katayama¹, E. Shimosaka¹, K. Asano¹ (1.Hokkaido Agricultural Research Center, NARO, 2.Center for Seeds and Seedlings, NARO, 3.Tohoku Agricultural Research Center, NARO)

715 An in-house cultivar identification method and its application to local varieties of unknown origin

☆SANETOMO, R., A. Oriyama, K. Hosaka (Obihiro University of Agriculture and Veterinary Medicine)

716 Chloroplast pangenomics traces back to the origin of domesticated melon

☆Shigita, G.¹, M. Okuma², N. Sogo³, T. Seiko⁴, C. Muto⁴, K. Tanaka⁵, K. Shimomura⁶, M. Sugiyama⁶, Y. Kawazu⁶, H. Ezura¹, K. Naito⁴, N. Tomooka⁴, K. Kato² (1.Life Environ. Sci., U. Tsukuba, 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 3.Grad. Sch. Environ. Life Sci.,

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717 Is there still native mulberry variety in Japan?

○Matsumura, H.¹, K. Hirauchi², S. Yoshinobu², R. Shimizu², M. Suzuki², A. Mizoguchi² (1.Gene Res. Ctr, Shinshu Univ., 2.Grad. Sch. Sci. Tech., Shinshu Univ)

718 Genetic diversity analysis of Taro (*Colocasia esculenta* Schott) with a focus on Japanese cultivars

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719 Evaluation of adaptability and quality characteristics of sweetpotato varieties in cold region

○Ishiguro, K.¹, T. Kuranouchi², Y. Kai³, T. Hara¹, S. Otsuka¹, M. Nishinaka⁴, K. Taguchi⁴ (1.Hokkaido Agric. Res. Cent., NARO, 2.Inst. Crop Sci., NARO, 3.Kyushu Okinawa Agric. Res. Cent., NARO, 4.Cent. Reg. Agric. Res. Cent., NARO)

Poster Presentations

P101 Production and analysis of multiple genome editing rice using an original plasmid set and a method for high-density crop hydroponics in a plant incubator

○Kuroda, M., H. Park, M. Chiba, T. Oikawa (Inst. Agrobiol. Sci. NARO)

P102 Examining conditions in rice seeds for the development of a new mutation breeding method using the boron neutron capture reaction.

○Segami, S.¹, T. Kinouchi², Y. Hattori³, M. Kiriata³ (1.Res. Inst. Env. Agr. Fish., Osaka Pref., 2.KURNS, 3.Osaka Metro. Univ. Res. Cent. for BNCT)

P103 Production of polyphenol mutants using heavy-ion beam irradiation on sweet potato (*Ipomoea batatas* [L.] Lam.)

○Narasako, Y.^{1,2}, M. Yamamura³, Y. Setoguchi¹, M. Takeshita³, T. Abe⁴, T. Hirano^{3,4}, M. Otani⁵, H. Kunitake³ (1.Interdiscip. Grad. Sch. Agric. Eng., Univ. Miyazaki, 2.Kushima Aoifarm Co., Ltd.,

3.Facul. Agric., University of Miyazaki, 4.RIKEN Nishina Center, 5.Res. Inst. Agric. Resour., Ishikawa Pref. Univ.)

P104 Examination of Training Datasets in the Development of a Deep Learning-Based Detection Model for *Rumex obtusifolius*

○Kuwata, K.¹, K. Kurogi¹, M. Makishima¹, T. Yagi², M. Miyaji², Y. Sanada², Y. Takahara³, Y. Akiyama² (1.Grad. Sch. Materials Science and Bioengineering., Nagaoka University of Technology, 2.Hokkaido Agric. Res. Ctr., NARO, 3.Materials Science and Bioengineering., Nagaoka University of Technology)

P105 Analysis of dormancy to bud-break transition in tea winter buds using transcriptome and temperature data

☆UEDA, T.¹, M. Onuki¹, J. Kawaki², A. Nagano^{3,4}, T. Ikka^{1,5,6}, H. Yamashita^{1,5,6} (1.Grad.Agr., Shizuoka Univ., 2.Shizuoka Tea Res. Cent., 3.Biosci. and Biotech. Center, Univ. Nagoya, 4.Inst. Adv. Biosci., Keio Univ., 5.Shizuoka Univ. Res. Inst. Green Sci. Tech., 6.Shizuoka Univ. Res. Inst. Tea Sci.)

P106 An Attempt at Gene Discovery Using Phenotypic Measurement of Chinese Cabbage via Deep Learning

☆Kanbayashi, Y.¹, Y. Kobayashi¹, H. Matsumura², N. Hayashida³ (1.Graduate School of Science and Technology, Shinshu University, 2.Gene Research Center, Shinshu University, 3.Faculty of Textile Science and Technology, Shinshu University)

P107 NGS-ACT: A Tool for allele determination using short reads from Next-Generation Sequencing

☆Oishi, M., M. Takata, M. Sakemoto, M. Yoshizumi, M. Hara, H. Takagi (Ishikawa Prefectural University)

P108 Comparing methods for imputing missing phenotypes and predicting breeding values in multi-trait and multi-environment data

☆Kinami, A., A. Onogi (Grad. Sch. of Agri., Ryukoku Univ.)

P109 Establishment of emasculation method using TFMSA: male sterility induction via inhibition of proline transport and phenylpropanoid biosynthesis

☆Sekiguchi, Y.^{1,2}, K. Terada³, G. Yan¹, N. Kamal^{4,5}, T. Ishii^{5,6,7} (1.United Grad. Sch. Agricultural Sci., Tottori U., 2.JSPS Research Fellow DC, 3.Grad. Sch. Sus. Sci. Tottori U., 4.ARC., Sudan,

5.International Platform for Dryland Research and Education (IPDRE), Tottori U., 6.ALRC, Tottori U., 7.Chromosome Engineering Research Center, Tottori U.)

P110 The effect of Ca ions on double-strand break repair in plant DNA

☆Emori, Y.¹, A. Sanjaya¹, M. Sakaguchi¹, K. Takagi², Y. Kazama¹ (1.Fac.Biosci.Biotech.Fukui Pref.Univ, 2.Wakasa-wan Ener.Cent)

P111 Development of semi-glutinous, high-yielding Inbred variety "Yumiharizuki" and its improved NIL with non-photosensitivity.

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

P112 Improvement of Tocopherol Composition in Soybean by Accumulation of Genes Related to Tocopherol Biosynthesis

☆PARK, C., D. Xu (Japan International Research Center for Agricultural Sciences (JIRCAS))

P113 Identification of the 'Sanuki no Yume 2023' cultivar using DNA markers

☆Ueta, S., Y. Tada (Kagawa Pref. Agric. Exp. Stn.)

P114 Feasibility Study on the Development of Winter Two-row Malting Barley Varieties in Hokkaido

○TOKIZONO, Y.¹, Y. NAKANO², M. SHIBAMURA¹, K. KOIE¹, T. NAGAMINE², T. HOKI¹ (1.Crop Research Laboratories, Sapporo Breweries Ltd., 2.Central Region Agricultural Research Center, NARO)

P115 Genetic variation in the ionome of a Barley line population

☆Niwa, Y.¹, A. Kiyota¹, T. Ikka^{1,2}, Y. Nakano³, H. Yamashita^{1,2} (1.Grad. Agr., Shizuoka Univ., 2.Shizuoka Univ. Res. Inst. Green Sci. Tech., 3.CARC, NARO)

P116 Project introduction for future development of wheat genetic resources maintained by NBRP-Wheat

○Ohta, A., M. Nitta, S. Nasuda, K. Yoshida, T. Sakai, R. Terauchi (Graduate School of Agriculture, Kyoto University)

P117 Exploring the Genetic Diversity and Population Patterns in Asian Cowpea (*Vigna unguiculata* (L.) Walp.)

☆Ofem, N.¹, N. Kamal^{2,3}, S. Pearson⁴, T. Shatte⁵, D. Jordan⁴, E. Mace⁴, T. Ishii^{2,6,7} (1.Grad. Sch. Agric. Sci., Tottori Univ., 2.Int. Platf. Dryl. Res. & Educ., Tottori Univ., 3.Biotechnol. & Biosaf. Res. Cent., Agric. Res. Corp., Sudan, 4.Qld. Alliance Agric. & Food Innov., Univ. Qld., Hermitage Res. Facil., Australia, 5.Qld. Dept. Prim. Ind., Hermitage Res. Facil., Australia, 6.Arid Land Res. Cent., Tottori Univ., 7.Chromosome Eng. Res. Cent., Tottori Univ.)

P118 Phylogenetic analysis on Japanese ramie (*Boehmeria nivea*) based on chloroplast DNA sequencing

Ogata, R.¹, K. Saito¹, ☆K. Yamada¹, H. Murakami², T. Sasanuma¹ (1.Fac. Agr., Yamagata Univ., 2.Aoso Rivival Dreaming Corps)

P119 Genetic characterization of Nikkokisuge (*Hemerocallis dumortieri*) indigenous to Anan town, Nagano Prefecture

☆Okada, K.¹, N. Saito², K. Tamagawa^{1,2}, Y. Sato², Y. Osafune³, T. Sugawara³, S. Kishimoto^{3,4}, T. Sasanuma^{1,2} (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ., 3.Mt. Chokai and Tobishima island Geopark Promotion Council, 4.Fac. Life Design, Tohoku Inst. Tech.)

P120 Development of an efficient intermediate line enabling introgression of late-flowering alleles in *Brassica rapa*

☆Shimizu, S., M. Hara, K. Miyaki, M. Yoshizumi, H. Takagi (Ishikawa Prefectural University)

P121 Examination for applying the U.S. maturity indicator to Japanese Soybean cultivars

☆Nakashima, K.^{1,2}, R. Takeshima², K. Hirata², R. Yamazaki², T. Wada², S. Kato² (1.Kyushu Okinawa Agricultural Research Center, NARO, 2.Institute of Crop Science, NARO)

P122 Evaluating the Accuracy of Rice Phenotype Prediction Using Large Language Models: Leveraging Breeding and Agricultural Insurance Data

☆Fukumoto, Y.¹, S. Isomichi¹, C. Sato², A. Abe³, T. Sato¹, C. Kim^{4,5}, T. Nakatani¹, H. Shimono⁴, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ., 2.Ifur-Rinrin, 3.Iwate Biotechnology Research Center, 4.Iwate University, 5.Sky Ocean Technology Co., Ltd.)

P123 Genetic variation of dry matter production in rice (*Oryza sativa* L.) germplasm from Zambia

Ohshiro, K.¹, T. Sato², K. Toriyama², S. Komatsubara³, R. Mulenga⁴, G. Munkombwe⁴, P. Mabvuto⁴, M. Chinji⁴, E. Musabula⁴, N. Museta⁴, L. Kamguya⁴, J. Njobvu⁴, ○Y. Fukuta¹ (1.Univ. Ryukyu, 2.Tohoku Univ., 3.JICA, 4.ZARI)

P124 Histological observation on abscission layer inhibition leading to non-seed-shattering trait in rice domestication

☆Matsubara, N.¹, S. Sugiyama¹, M. Sakuta¹, Y. Tsujimura¹, C. Inoue¹, T. Htun¹, K. Numaguchi¹, H. Nasu², T. Ishii¹, R. Ishikawa¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Fac. Bios.-Geos. Sci., Okayama Univ. Sci.)

P125 Role of seed pigments in wild rice, *Oryza rufipogon*

☆Furuta, Y., H. Iwamoto, K. Numaguchi, R. Ishikawa, T. Ishii (Grad. Sch. Agr. Sci., Kobe Univ.)

P126 Characterization of γ irradiated Yacon cv. 'Andesu no otome' in the M₁V₅ generation

Akagi, M.¹, G. Okuno¹, K. Ooe², M. Hirata², T. Murata¹, S. Yasuda^{1,2}, Y. Masuda^{1,2}, ○Y. Matsuda^{1,2} (1.Graduate School of Agriculture, Tokai University, 2.School of Agriculture, Tokai University)

P127 Mutations in the flavonoid 3'-hydroxylase gene in sweetpotato varieties containing pelargonidin-type anthocyanins

○Tanaka, M., T. Sakaigaichi, R. Kurata, K. Suematsu, T. Sakai, Y. Takahata (Kyushu Okinawa Agr. Res. Cent., NARO)

P128 Research on contribution of traditional crop Aoso (*Boehmeria nivea*) to regional revitalization in Oe town, Yamagata Prefecture

Ogata, R.¹, ☆E. Nagasawa¹, H. Murakami², T. Sasanuma¹ (1.Fac. Agr., Yamagata Univ., 2.Aoso Rivival Dreaming Corps)

P129 A large-scale screening population for enhanced CO₂ fixation in rice.

☆Suganami, M.¹, Y. Tobita², S. Ishizaki³, S. Honda², K. Nakajima⁴, S. Mori⁵, H. Ishida⁵, M. Matsuoka¹, S. Adachi², Y. Tanaka⁴ (1.Inst. Ferment. Sci., Fukushima Univ., 2.Grad. Sch. Agr., Tokyo Univ. Agri. Tech., 3.Fac. Afri., Okayama Univ., 4.GSES, Okayama Univ., 5.Grad. Sch. Agr. Sci., Tohoku Univ.)

P130 Pangenome study on Japanese soybean cultivars and development of genome database "Daizu-net"

○Yano, R.¹, F. Li², S. Hiraga², R. Takeshima², M. Kobayashi³, A. Kaga², M. Ishimoto² (1.NAAC, NARO, 2.Inst. Crop Sci., NARO, 3.NIAS, NARO)

P131 Whole genome resequencing of a high-density mutant library of the Japanese soybean cultivar Enrei, and development of a gene mutation search platform

○Hiraga, S.¹, R. Yano², R. Nakata¹, F. Li¹, A. Kaga¹, T. Anai³, M. Ishimoto¹ (1.Inst. Crop Sci., NARO, 2.Res. Cntr. Adv. Anal., NARO, 3.Grad. Sch. Agric., Kyushu Univ.)

P132 Development of a functional genomics platform for spinach based on a high-quality reference genome and VIGS system.

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P133 Draft genome sequence of Japanese traditional *Cannabis sativa*

☆Madambashi, M.^{1,3}, F. Nagaya^{1,3}, K. Ohira^{2,3}, A. Okamoto^{2,3}, Y. Nagaya^{2,3}, A. Ohyama^{1,3}, K. Suwabe^{1,3} (1.Grad. Sch. Reg., Mie Univ., 2.Grad. Sch. Bio., Mie Univ., 3.CIMC)

P134 DNA Marker Development for Plant Height in Grain Amaranth (*Amaranthus hypochondriacus*)

☆Zaelani, A.¹, Y. Yoshioka² (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.Inst. Life & Env. Sci., Univ. Tsukuba)

P135 Genetic analysis of resistance to highly virulent strains of *Corynespora cassicola* in cucumber

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P136 Enhanced Drought Resilience in Rice Through Post-Drought Root Emergence

Krusenbaum, L.¹, R. Sakusabe², R. Ishikawa², M. Wissuwa¹, ○T. Dinh² (1.Institute of Crop Science and Resource Conservation (INRES), University of Bonn, 2.Faculty of Agriculture and Life Science, Hirosaki University)

P137 Fine-mapping of QTL regulating plant height in azuki bean (*Vigna angularis*)

☆Nguyen, T.¹, Y. Horiuchi², H. Nagashawa², C. Wainaina³, P. Bethke⁴, M. Mori¹ (1.Obihiro Univ. Agr. Vet. Med., 2.Tokachi Agri. Exp. Sta., HRO, 3.Jomo Kenyatta Univ. Agr. Tec., 4.USDA, USA)

P138 Evaluation of genetic loci for stolon production ability in wild rice, *Oryza rufipogon*

P139 Characterization and genetic analysis of culm length using wild *Oryza* species

☆Suzuki, R.¹, M. Kato², H. Takahashi¹, M. Nakazono¹, T. Yoshikawa³, Y. Sato⁴, A. Agata¹ (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Fac. Agr., Nagoya U., 3.Grad. Sch. Agric., Kyoto Univ., 4.National Institute of Genetics.)

P140 Search for causative loci related to female flowering using Japanese larch mutant lines.

○Mishima, K.¹, K. Shirasawa², T. Iki¹, H. Hirakawa³, T. Hirao¹, K. Konagaya⁴, Y. Fukuda¹ (1.Forest Tree Breeding Center, FFPRI, 2.Inst.KAZUSA DNA Res, 3.Fac.Agr., Univ.Kyushu, 4.Forest Bio-Reseach Breeding Center, FFPRI)

P141 Genetic analysis of resistance to rice stink bugs in the rice variety 'Milyang 44'

○Nakamura, M.¹, M. Tsuzuki¹, H. Kokaji², H. Yamaguchi¹, K. Sugiura¹, T. Yoshida³, S. Kato¹, K. Mori¹, H. Ohashi¹, U. Yamanouchi⁴, S. Fukuoka⁴, A. Shomura⁴, S. Fukuta¹, Y. Mizukami^{1,5} (1.Aichi Agri. Res. Cent., 2.GRA&GREEN Inc., 3.Mount. Reg. Agri. Inst., Aichi Agri. Res. Cent., 4.NARO, 5.Aichi Agri. Promotion Div.)

P142 QTL analysis of watercore in Japanese pear and selection of DNA markers for risk of severe symptoms.

Tanabe, T.¹, K. Kajiyama¹, K. Shirasawa², ○T. Gonai¹ (1.Plant Biotech. Inst., Ibaraki Agri. Ctr., 2.Kazusa DNA Res. Inst.)

P143 Genetic study on nitrogen use efficiency of *Aegilops tauschii*-derived wheat populations under combined heat and nitrogen deficiency stress

☆EMAM, A.^{1,2}, I. Tahir^{2,3}, N. Kamal^{2,3}, Y. Gorafi^{2,4}, H. Tsujimoto⁵, T. Ishii^{3,5,6} (1.United Graduate School of Agricultural Sciences, Tottori University, 2.Agricultural Research Corporation (ARC), P.O. Box 126, Wad Medani, Sudan, 3.International Platform for Dryland Research and Education (IPDRE), Tottori University, 4.Graduate School of Agriculture, Kyoto University, 5.Arid Land Research Center (ALRC), Tottori University, 6.Chromosome Engineering Research Center, Tottori University)

P144 Objective Image-Based Evaluation of Perilla Leaf Curling and Subsequent QTL and GWAS for Gene Association Analysis

☆Chen, T.¹, S. Kinoshita¹, K. Sakurai¹, T. Tsusaka², M. Sakurai^{2,3}, K. Shirasawa⁴, S. Isobe^{1,4}, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.TSUMURA & CO., 3.LAO TSUMURA CO.,LTD,

P145 Genetic analysis of growth abnormalities observed in the S₁ generation of synthetic hexaploid wheat

☆Nakanishi, S.¹, K. Nishimura¹, T. Nakazaki^{2,3}, Y. Monden¹, K. Kato¹, H. Nishida¹ (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.IAC, Kyoto Univ.)

P146 Improvement of a GWAS for pearl millet by imputing missing genotypes

☆Kambara, K.¹, G. Shashi Kumar², D. Tsugama¹ (1.Grad. Sch. Agr., Univ. Tokyo, 2.ICRISAT)

P147 Generation of Male-Sterile *Chrysanthemum seticuspe* by Genome Editing

○Matsushita, S.¹, M. Nakano², S. Choukyuu¹, M. Kurao¹, A. Fujita¹ (1.Agr. Tech. Res. Cent., HiTRI, 2.Fac. Agr. Mar. Sci., Kochi Univ.)

P148 Construction of a new homologous recombination evaluation system in *Arabidopsis thaliana*

☆Asakawa, T.¹, M. Endo², S. Toki^{1,3,4}, H. Saika² (1.Grad. Sch. Agr., Univ. Ryukoku, 2.Inst. Agrobiol. Sci., NARO, 3.Grad. Sch. Nanobio., Yokohama City Univ., 4.Kihara Inst. Res., Yokohama City Univ.)

P149 Transportation of Protein from Agrobacterium to Plant Cell via Type III Secretion System

☆Fujihara, K.¹, I. Mitsuhashi², M. Endo², M. Kiran³, S. Toki^{1,4,5} (1.Grad. Sch. Agr., Univ. Ryukoku, 2.Inst. Agrobiol. Sci., NARO, 3.Dept. Biochem. Molbiol., Oklahoma State Univ., 4.Kihara Inst. Biol. Res., Yokohama City Univ., 5.Grad. Sch. Nanobio., Yokohama City Univ.)

P150 Construction of a genomic breeding database for the realization of digital breeding

☆Yumiya, M., H. Bono (Grad. Sch. Int. Sci., Hiroshima Univ.)

P151 Population structure analysis of Japanese sorghum landrace for genetic analysis of 'Amakibi'

☆Okada, S.¹, K. Kuga², S. Araki-Nakamura¹, K. Ohmae-Shinohara¹, T. Sazuka¹ (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Grad. Sch. Bioagri., Nagoya Univ.)

P152 Genomic prediction-based evaluation of trait segregation in the progenies populations of tea plants

☆Shibata, M.¹, Y. Ishiguro², J. Kawaki³, A. Nagano^{4,5}, H. Yamashita^{1,2,6,7}, T. Ikka^{1,2,6,7} (1.Grad. Agr., Shizuoka Univ., 2.Uni. Agr., Gifu Univ., 3.Shizuoka Tea Res. Cent., 4.Biosci. and Biotech. Center, Univ. Nagoya, 5.Inst. Adv. Biosci., Keio Univ., 6.Shizuoka Univ. Res. Inst. Green Sci. Tech., 7.Shizuoka Univ. Res. Inst. Tea Sci.)

P153 Functional Analysis of Four Wax Biosynthesis Genes Involved in Rice Hydrophobicity

☆ZHU, T., A. HIRAIWA, S. AIGA, J. ITOH (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P154 Fine mapping of the causal genomic region for perpetual flowering and its genotypic effects during early growth stage in *Fragaria* × *ananassa*

☆Yoshizumi, M., Y. Machi, T. Nishitani, M. Hara, H. Takagi (Ishikawa Prefectural University)

P155 Modulation of Plant Height in Rice via Genome Editing of a Conserved Noncoding Sequence Near the Transcription Start Site of the *SD1* gene

○Kuroha, T.¹, H. Park¹, W. Iwasaki², S. Chechetka¹, M. Kimizu¹, Y. Kawahara³, K. Hayashi¹, Y. Hayano¹, T. Makino², H. Yoshida¹ (1.Inst. Agrobiological Sci., NARO, 2.Graduate School of Life Sciences, Tohoku University, 3.Research Center for Advanced Analysis, NARO)

P156 Identification of bHLH transcription factor regulating proanthocyanidin accumulation in barley testa layer

○Nakano, Y.¹, M. Nakata², H. Yamakawa³, T. Tonooka⁴, H. Maejima⁵, T. Nagamine¹ (1.CARC, NARO, 2.KARC, NARO, 3.Inst. Crop Sci., NARO, 4.Headquarters, NARO, 5.Nagano Agricultural Experiment Station)

P157 Shoot Apical Meristem Bombardment Enables Stable In Planta Transformation in Pearl millet (*Pennisetum glaucum* L.)

☆Arikpo, G.¹, Y. Kentaro², T. Ishii^{3,4,5} (1.United Graduate School of Agricultural Sciences (UGSAS) Tottori University, 2.Graduate School of Agriculture, Kyoto University, 3.International Platform for Dryland Research and Education (IPDRE), Tottori University Arid Land Research Center, 4.Tottori University, 5.Chromosome Engineering Research Center, Tottori University)

P158 Genome editing of *CAD* gene involved in lignin biosynthesis in bahiagrass—*k*-mer analysis in F1 null segregants and fixation of mutant loci in F2 generation—

○Gondo, T.¹, M. Yamada² (1.FSRC, Univ. Miyazaki, 2.Agr., Univ. Miyazaki)

P159 Molecular genetic analysis of the LHCI deficient mutant in rice

☆Yamatani, H.¹, S. Ozawa², T. Takami², W. Sakamoto², M. Kusaba³ (1.QST, Takasaki, 2.IPSR, Univ., Okayama, 3.Grad. Sch. Int. Sci. Life, Univ. Hiroshima)

P160 Creation of Soybean AGPase Mutants via iPB-RNP-based Genome Editing

☆Ogawa, T., K. Fujii, W. Achley, R. Imai (Inst. Agrobiol. Sci., NARO)

P161 Creation of genome-edited lines of transcription factor SHP in bread wheat

☆Sakurai, S., N. Kawano, S. Sakoguchi, Y. Kamiya, K. Kawaura (KIBR, Yokohama City Univ.)

P162 Isolation of six-rowed mutants derived from a two-rowed barley cultivar “Haruka Nijo” and pyramiding of the causal genes

○Nakata, M., M. Taira, M. Yanaka, H. Shimizu (KARC, NARO)

P163 Comparative Analysis of Genetic and Epigenetic Regulation of Light-Dependent Anthocyanin Differences in *Brassica rapa* Cultivars ‘Akamaru’ and ‘Hinona’

☆Miyaki, K., T. Segawa, M. Hara, M. Sakemoto, H. Takagi (Ishikawa Prefectural University)

P164 Mitochondrial morphology of mitochondrial fission mutants in *Arabidopsis thaliana*

☆Hashimoto, M., Y. Ito, I. Nakazato, H. Takanashi, S. Arimura (Graduate School of Agricultural and Life Sciences, The University of Tokyo)

P165 Characterization of the QTLs that control Na accumulation in leaf blades of rice

○Horie, T.¹, H. Sakagami¹, R. Ishikawa², Y. Ishii¹, H. Matsumura³, P. Amarasinghe⁴, M. Katsuhara⁵, T. Ishii² (1.Div. Appl Biol., FTST, Shinshu Univ., 2.Grad. Sch., Agric Sci., Kobe Univ., 3.Grad. Sch. Sci. Tech., Shinshu Univ., 4.GLORDC, Sri Lanka, 5.IPSR, Okayama Univ.)

P166 Exploration of candidate genes related to fruit peelability and hardness in citrus using RNA-seq analysis

☆Takada, K.¹, K. Nonaka², T. Shimizu^{2,3}, M. Minamikawa⁴ (1.Grad. Sch. Hort., Chiba Univ, 2.NIFTS, NARO, 3.Kazusa DNA Res. Inst., 4.IAAR, Chiba Univ.)

P167 Transcriptome analysis of ditelosomic lines in common wheat

☆Imoto, K., R. Nishijima (Grad. Sch. Biosci. Biotech., Fukui Pref. Univ.)

P168 Genome-wide identification of the *LOX* gene family in adzuki bean and identification of seed-specific *LOX* genes

☆Iwayama, D.^{1,2}, Y. Horiuchi³, S. Isobe¹, M. Mori², K. Kato² (1.Tokachi Daifuku Honpo, Inc., 2.Obihiro Univ. Agri. Vet. Med., 3.Tokachi. Agri.Exp.Stn.,HRO)

P169 Hormonome and transcriptome analysis in winter buds of tea cultivars with different bud-break timing

☆Yamada, M.¹, M. Onuki¹, J. Kawaki², M. Kojima³, Y. Takebayashi³, H. Sakakibara^{3,4}, A. Nagano^{5,6}, T. Ikka^{1,7,8}, H. Yamashita^{1,7,8} (1.Grad. Agr., Shizuoka Univ., 2.Shizuoka Tea Res. Cent., 3.Biosci. and Biotech. Center, Univ. Nagoya, 4.Inst. Adv. Biosci., Keio Univ., 5.CSRS, RIKEN, 6.Grad. Sci. Bioagr., Univ. Nagoya, 7.Shizuoka Univ. Res. Inst. Green Sci. Tech., 8.Shizuoka Univ. Res. Inst. Tea Sci.)

P170 Genomic regions associated with seed storage protein contents between *japonica* rice cultivars grown in Hokkaido

☆Yamaguchi, M.¹, K. Shishido¹, S. Iiduka¹, S. Yoshikawa¹, T. Wakabayashi¹, J. Kasuga¹, H. Ozaki², K. Kato¹ (1.Obihiro Univ. Agric. & Vet. Med., 2.Kamikawa Agri. Exp. Sta., HRO)

P171 Estimating the temporal origins of mutations associated with domestication and improvement in *Oryza sativa* ssp. *japonica*

○Koyanagi, K.¹, Y. Kawahara², Z. Zhou³, H. Watanabe¹ (1.Fac. Info. Sci. Tech., Hokkaido Univ., 2.Research Center for Advanced Analysis, NARO, 3.Grad. Sch. Info. Sci. Tech., Hokkaido Univ.)

P172 Comparative analysis of Homoeologous Recombination in synthetic and landrace *Brassic napus*

☆Hara, M.¹, K. Okazaki², T. Segawa¹, K. Miyaki¹, M. Yoshizumi¹, H. Takagi¹ (1.Ishikawa Prefectural University, 2.Faculty of Agriculture Niigata University)

P173 Relationship between polyphenol and foot rot resistance in sweet potato

☆Setoguchi, Y.¹, Y. Narasako^{1,2}, T. Hirano³, M. Otani⁴, H. Kunitake³ (1.Interdiscip. Grad. Sch. Agric. Eng., Univ. Miyazaki, 2.Kushima AoiFarm Co. Ltd., 3.Facul. Agric., Univ. Miyazaki, 4.Res. Inst. Agric. Resour., Ishikawa Pref. Univ.)

P175 Variation in blast resistance in wheat conferred by gene dosage effects.

Trinh, V., ○Y. Inoue, K. Yoshida (Grad. Sch. Agri., Kyoto U.)

P176 Evaluation of chilling tolerance in Hokkaido rice varieties and detection of quantitative trait loci for chilling tolerance after acclimation

○Sagehashi, Y. (Institute of Agrobiological Science, NARO)

P177 Analysis of occurrence factors for internal browning in sweet potato

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P178 Multi-omics investigation of protein phosphorylation control in a water-saving wheat line.

Hirata, S.¹, K. Yamashita², T. Umezawa², J. Kim³, A. Nieda¹, H. Tsujimoto⁴, ○R. Mega¹ (1.Grad. Sch. Sci. Tech. for Innovation, Yamaguchi U., 2.BASE, Tokyo U. Agr. Tech., 3.CSRS • RIKEN, 4.ALRC, Tottori U.)

P179 Stress Responses of *Arabidopsis thaliana* RBOHF Knockout Mutants to Heat, Drought, and Their Combination.

☆Furihara, M.¹, N. Suzuki² (1.Grad. Sch. Sci. Tech., Sophia Univ., 2.Fac. Sci. Tech., Sophia Univ.)

P180 Analysis of ROS regulation and chloroplast signaling in the *Arabidopsis* sid2-1 KO mutant under combined heat and drought stress conditions

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P181 Functional Analysis of *Arabidopsis* RBOHD in the Memory Response to Short-Term Heat Stress

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P182 Identification of phytohormones that regulate the pattern of passage cell formation in rice roots.

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P183 Change in aquaporin gene families through polyploid evolution of Triticeae

☆Moriya, H.¹, A. Ezoe², Y. Kamiya¹, K. Kawaura¹ (1.KIBR, Yokohama City Univ., 2.RIKEN CSRS)

P184 Roles of ubiquitination and heat response transcription factors in the regulation of heat-responsive systemic acquired resistance in Arabidopsis.

☆Ayana, M.¹, N. Suzuki² (1.Grad. Sch. Sci. Tech., Sophia Univ., 2.Fac. Sci. Tech., Sophia Univ.)

P185 Effects of different pH and low fertilizer soil conditions on the detection of QTLs associated with element accumulation in rice straw and grains

Zhang, Q.², T. Furuta¹, K. Kashiwara¹, D. Ogawa³, J. Yonemaru⁴, J. Ma¹, ○T. Yamamoto¹ (1.IPSR, Okayama U., 2.Grad. Sch. Environ. Life Nat. Sci., Okayama U., 3.NICS, NARO, 4.RCAIT, NARO)

P186 Response of Arabidopsis Deficient in Reactive Oxygen Species Producing Enzyme, RBOHD to Salt, Waterlogging, and Combined Stress

☆Taniguchi, Y.¹, N. Suzuki² (1.Grad. Sch. Sci. Tech., Sophia Univ., 2.Fac. Sci. Tech., Sophia Univ.)

P187 Investigating of the role of C group Raf kinase in aerenchyma formation in rice roots

☆Seimiya, Y., A. Shinozawa, K. Izawa, S. Nakamura (Dept.Bioscience, Tokyo Univ. Agric)

P188 Analysis of ethylene- and ABA-mediated hypoxic response in *Brassica napus*

☆Tamai, H.¹, N. Yokouchi¹, H. Takahashi², M. Nakazono², K. Izawa¹, S. Nakamura¹, A. Shinozawa¹ (1.Dept. Bioscience, Tokyo Univ. Agric., 2.Grad. Sch. Bioagric. Sci., Univ. Nagoya)

P189 Evaluation of mechanized cultivation suitability under narrow-row cultivation conditions for the new soybean cultivar "Soratakaku".

○Saruta, M.¹, H. Katoh¹, Y. Kawasaki², Y. Takada¹ (1.WARC, NARO, 2.Inst. Crop Sci., NARO)

P190 Varietal Differences in Sweet Potato Yield and Dried Sweet Potato Shirota Incidence under Hot and Dry Environments

☆Konosu, H.¹, M. Nishinaka², Y. Yoshioka³, K. Taguchi² (1.Grad. Sch. Sci., Univ. Tsukuba, 2.Carc., NARO, 3.Sci., Univ. Tsukuba)

P191 Varietal Differences of Rice Grain Quality at High Temperature during Ripening Period in Ibaraki

○Suzuki, Y., H. Ishikawa, T. Nakano, K. Akita, K. Okano, M. Hirayama (Plant Biotechnology Institute, Ibaraki Agricultural Center)

P192 Characterization of starch branching enzyme (SBE) for the ripening buckwheat grain with a low-temperature gelatinization trait

☆Katsuta, M., T. Suzuki, K. Katsu (Kyushu Okinawa Agricultural Research Center, NARO)

P194 Generation and analysis of mutants of promoters and coding sequences of lipase genes for enhanced production of rice bran oil

Kuwabara, K., M. Urakawa, K. Toriyama, ○Y. Ito (Grad Sch Agri Sci, Tohoku Univ)

P195 Heritability of medicinal compound levels in clonal lines of *Glycyrrhiza uralensis*

○Tsusaka, T.¹, M. Sakurai^{1,2} (1.Tsumura & Co., 2.LAO TSUMURA CO.,LTD)

P196 Trade-off relationship between grain yield and zinc concentration in rice

☆Kataoka, S.¹, N. Miyazaki¹, R. Takahashi¹, M. Ogasawara¹, K. Taniko¹, G. Monden¹, L. Sathya¹, M. Iwata¹, K. Numaguchi¹, T. Ishii¹, H. Maeda², J. Ma³, R. Ishikawa¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.NARO, 3.ISPR, Okayama Univ.)

P197 Genomic Loci Underlying Early Developmental Heterosis in Chinese Cabbage (*Brassica rapa* L. subsp. *pekinensis*)

☆SARKER, K., H. MEHRAJ, R. FUJIMOTO (Graduate School of Agricultural Science, Faculty of Agriculture, Kobe University)

P198 QTL analysis of hybrid vigor for early growth in rice BC₁F₁ derived from the cross between Taichung 65 as the donor parent and Asu as the recurrent parent

☆Ogihara, S.¹, Y. Nakamura¹, K. Ichitani², S. Taura³, T. Kuboyama¹ (1.Grad. Sch. Agr., Ibaraki U., 2.Fac. Agr., Kagoshima U., 3.Gene Res. Inst., Kagoshima U.)

P199 Analysis of growth traits and genetic factors associated with heterosis level in hybrids generated by crossing different parental lines in sugar beet.

☆Suda, M.¹, R. Iwahori¹, K. Hiroki¹, A. Naito¹, H. Matsuhira², K. Kitazaki¹ (1.Hokkaido University, Research Faculty of Agriculture, 2.NARO • HARC)

P200 Analysis of rice *abl2-d* mutant with a mutation in microRNA166 target sequence

☆Mikami, K.¹, M. Kobukai², K. Chiba¹, M. Kuwamura², N. Nagasawa², N. Satoh-Nagasawa² (1.Grad. Sch. Biores. Sci., Akita Pref. Univ., 2.Fac. Biores. Sci., Akita Pref.Univ.,)

P201 Development of an experimental system for single-nucleus RNA-seq and single-cell resolution 3D imaging analysis of barley shoot apex

☆Takeda, R.¹, J. Ito¹, Y. Nomura¹, N. Sato¹, A. Hirota², M. Hayashi², D. Shi², Y. Sasai², P. Kao², K. Sugimoto², D. Saisho³, H. Hisano³, T. Uchino⁴, S. Nasuda⁴, K. Tonosaki¹, T. Kinoshita¹, K. Amagai⁵, M. Kashima⁵, H. Tsuji^{1,6} (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.CSRS, RIKEN., 3.IPSR, Okayama Univ., 4.Grad. Sch. Agric., Kyoto Univ., 5.Fac. Sci., Toho Univ., 6.Biosci. Biotechnol. Center, Nagoya Univ.)

P202 Morphological characterization and identification of genes responsible for monogerm/multigerm seed formation in sugar beet and its relatives.

○Kuno, A.¹, K. Takayasu¹, K. Hiroki¹, T. Narihiro², H. Matsuhira², Y. Kuroda², T. Kubo¹, K. Kitazaki¹ (1.Hokkaido University, Research Faculty of Agriculture, 2.NARO • HARC)

P203 Exploration of genes involved in late heading in a barley *hy2* mutant via time-lapse Lasy-Seq

☆Okuma, M.¹, K. Nishimura¹, M. Kashima², Y. Monden¹, K. Kato¹, H. Nishida¹ (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 2.Fac. Sci., Toho U.)

P204 Single-cell resolution imaging of the development of three spikelet meristems from a triple spikelet meristem in barley inflorescence

☆Mitsuishi, R.¹, J. Ito¹, Y. Nomura¹, R. Takeda¹, H. Tsuji^{1,2} (1.Kihara Inst. Biol. Res., Yokohama City Univ, 2.Biosci. Biotechnol. Center, Nagoya Univ)

P205 Functional analysis of genes involved in branching and floral induction in cassava using genome editing

○Tokunaga, H.^{1,2}, Q. Do Thi Nhu⁴, M. Endo³, A. Nguyen Hai⁴, H. Le Huy⁴, M. Seki² (1.TARF, JIRCAS, 2.CSRS, RIKEN, 3.Institute of Agrobiological Sciences, NARO, 4.National Key Laboratory for Plant Cell Biotechnology, Agricultural Genetics Institute)

P206 Genome-wide association study reveals key loci controlling the timing of juvenile-to-adult vegetative transitions in rice

☆Shiragaki, K.^{1,2}, T. Okasaki³, M. Yamamoto³, T. Tezuka^{1,2}, S. Yokoi^{1,2} (1.Grad. Sch. Agri., Osaka Metro. Univ., 2.Edu. Res. Field, Sch. Agri., Osaka Metro. Univ., 3.Grad. Sch. Life Envi. Sci., Osaka Pref. Univ.)

P207 Characterization of photoperiod sensitivity of landraces in common buckwheat.

☆Nakano, A.¹, Y. Mizukami¹, K. Nemoto¹, A. Fukushima¹, j. Seino¹, N. Washizu¹, N. Hara¹, A. Toda², T. Kaizu², H. Nakayama², M. Oya², J. Aii¹ (1.NUPMLS, 2.Niigata City Agri. Dev. Res Cent.)

P208 Comparative growth and seed yield of *Lotus* experimental strains under fluorescent and LED lighting conditions

☆Ng, H.¹, H. Tanaka², T. Gondo³, R. Akashi⁴, M. Hashiguchi¹ (1.Fac. of Regional and Innov., Univ. of Miyazaki, 2.Fac. of Agr., Univ. of Miyazaki, 3.FSRC, Univ. of Miyazaki, 4.Univ. of Miyazaki)

P209 Inheritance of monoecious traits in XY spinach plants derived from germplasm resources.

☆Yajima, Y.¹, S. Maeda², Y. Onodera³ (1.Sch. Agr., Hokkaido Univ., 2.Grad. Sch. Agr., Hokkaido Univ., 3.Res. Fac. Agr., Hokkaido Univ.)

P210 Comparative analysis of cell morphology in glandular trichomes and phenolic compounds of polyploid strains obtained from crosses among Japanese *Drosera* species

○Hoshi, Y.¹, S. Funakoshi², K. Terasaki², T. Katogi³ (1.Sch. Agri., Univ. Tokai, 2.Grad. Sch. Agri., Univ. Tokai, 3.Res. Inst. Agr.)

P211 Detection of hybrid lethality alleles in *Nicotiana* species using agroinfiltration

○Nagai, S.^{1,2}, K. Kobayashi¹, M. Mino¹, Y. Tanaka³, K. Nakata⁴, T. Yamada⁴, S. Yokoi^{1,5}, T. Tezuka^{1,5} (1.Grad. Sch. Agr., Osaka Metro. Univ., 2.Res. Inst. Env. Agr. Fish., Osaka Pref., 3.Wakasa Wan Energy Res. Cent., 4.United Grad. Sch. Agr. Sci., Tokyo U. Agr. Tech., 5.Educ. Res. Field., Sch. Agr., Osaka Metro. Univ.)

P212 Transcription factors and internal plant hormones during secondary somatic embryogenesis of tea plant (*Camellia sinensis*).

☆Mikami, K.¹, S. Hirata^{1,2}, H. Yamashita³, T. Ikka³, M. Kojima⁴, Y. Takebayashi⁴, H. Sakakibara^{4,6}, s. Koshimizu⁵, M. Arita⁵, K. Furukawa¹ (1.KOSEN Numazu college, 2.Grad. Sch.

P213 Analysis of potassium ion transporters involved in pollination in *Arabidopsis thaliana*

☆Naoe, A., K. Yokota, M. Hayashi, M. Watanabe (Grad. Sch. Life Sci., Tohoku Univ.)

P214 Analysis of the molecular mechanism in the female papilla cells regulating self-incomaptibility in Brassicacea plants.

Harada, Y.¹, A. Nozawa², T. Sawasaki², ○M. Hayashi¹, M. Watanabe¹ (1.Grad. Sch. Life Sci., Tohoku Univ., 2.PROS, Ehime Univ.)

P215 Genetic analysis of the UI region responsible for intraspecific unilateral incompatibility in *Brassica rapa*.

○Takada, Y.¹, M. Shimizu², G. Suzuki³, M. Watanabe¹ (1.Grad. Sch. Sci., Tohoku Univ., 2.IBRC, 3.Osaka kyoiku Univ.)

P216 Which Shaplotypes are utilized in Japanese radish F₁ varieties?

Ji, J., R. Kato, M. Yamashita, Y. Wang, S. Miyashita, M. Yamamoto, ○H. Kitashiba (Grad. Sch. Agr. Sci., Tohoku U.)

P217 Multiomics analysis aiming for self seed production of anther indehiscence-type cytoplasmic male sterile rice

☆Takatsuka, A.^{1,2}, T. Kazama¹, K. Toriyama² (1.Grad. Sch. Biores. Bioenviron. Sci., Kyushu Univ., 2.Grad. Sch. Agri. Sci., Tohoku Univ.)

P218 Candidate genomic regions of pollen and spikelet sterility genes at *qSG11* for F₁ sterility between *Oryza sativa* and *O. glumaepatula*

☆Amano, H.¹, T. Kawata¹, A. Umebara¹, H. Yasui², Y. Yamagata² (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Fac. Agr., Kyushu Univ.)

P219 Genetic analysis of fertility restorer genes for Taichung 65/O. glaberrima (TG)-type cytoplasmic male sterile rice

☆Oniki, M., Y. Yamagata, H. Yasui, T. Kazama (Fac. Agr., Kyushu Univ.)

P220 QTL analysis of grain quality related traits on chromosome 6 including *THB1* in rice.

☆Wakabayashi, T.¹, H. Ozaki², K. Kato¹ (1.Obihiro Univ. of Agri. & Vet. Med., 2.Kamikawa Agri. Exp. Sta., HRO)
