

Title of Papers Presented at the 141st Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 V-primer: A new application for designing large-scale primers from NGS data

☆Natsume, S., K. Oikawa, K. Ito, H. Utsushi, M. Shimizu, A. Abe (Iwate Biotechnology Research Center)

102 Development of chromosome specific SNP markers in strawberry

○Isobe, S.¹, K. Shirasawa¹, S. Kataoka², T. Sueyoshi³, Y. Noguchi², H. Monden³, T. Wada^{3,4} (1.Kazusa DNA Res. Inst., 2.NARO, NIVFS, 3.Fukuoka Agric. For. Res. Ctr., 4.Present address: TAKII & CO.,LTD.)

103 The root of flowering cherry 'Somei-Yoshino' revealed by genome sequencing analysis

○Shirasawa, K.¹, T. Esumi², G. 京府大生命科学³, K. Hatakayama⁴, T. Takashina⁵, T. Yakuwa⁶, K. Sumitomo⁷, T. Kurokura⁸, E. Fukai⁹, K. Sato¹⁰, T. Shimada¹¹, K. Shiratake¹², M. Hosokawa¹³, Y. Monden¹⁴, M. Kusaba¹⁵, H. Ikegami¹⁶, S. Isobe¹ (1.KDRI, 2.Acad. Assem. Inst. Agr. Life Sci., Shimane U., 3.Grad. Sch. Life Environ. Sci, Kyoto Pref. U., 4.Fac. Agri., Iwate U., 5.Hort. Res. Inst., Yamagata Integrated. Agri. Res. Cent., 6.Yamagata Nishi High Sch., 7.NIVFS, NARO, 8.Sch. Agri., Utsunomiya U., 9.Fac. Agri., Niigata U., 10.Yamanashi Kofu Minami High Sch., 11.NIFTS, NARO, 12.Grad. Sch. Bioagri. Sci., Nagoya U., 13.Fac. Agri., Kindai U., 14.Fac. Agri., Okayama U., 15.Grad. Sch. Integrated Sci. Life, Hiroshima U., 16.Fukuoka Resident)

104 Whole genome sequence of cucumbers and eggplants.

☆Seiko, T.¹, C. Muto¹, K. Shimomura², K. Miyatake³, K. Kato⁴, R. Yano⁵, K. Naito¹ (1.Genetic Resources Center, NARO, 2.Inst. Vegetable and Floriculture Sci., NARO, 3.Inst. Vegetable and Floriculture Sci., NARO, 4.Grad. Sch. Environmental and Life Sci., Okayama Univ., 5.Advanced Analysis Center, NARO)

105 Estimating quantitative trait loci and QTL analysis related fruit traits in Japanese netted melon

☆Sato, N.¹, Y. Akashi², R. Ishikawa¹, K. Tanaka¹, H. Nishida², K. Kato² (1.Fac. Agr. Life Sci., Hirosaki U., 2.Grad. Sch. Environ. Life Sci., Okayama U.)

106 Genetic basis of the maturity time independent of the flowering time of common buckwheat (*Fagopyrum esculentum*)

☆Takeshima, R., S. Yabe, K. Matsui (Inst. Crop. Sci., NARO)

107 Various response to the fertilization in 120 rice cultivars

☆Hasegawa, K.¹, T. Mori¹, M. Amano¹, S. Nishiuchi¹, H. Yoshida², J. Murase¹, M. Matsuoka², M. Nakazono¹, H. Takahashi¹ (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.IFes., Fukushima Univ.)

108 Identification of additional QTLs for flowering time by removing the effect of the major photoperiod sensitive gene *FD1/VaE1* in adzuki bean

☆Oka, T.¹, Y. Horiuchi², K. Kato¹ (1.Obihiro Univ.Agr. & Vet. Med., 2.Tokachi Agr. Exp. Sta., HRO)

109 Identification of QTLs for yield related traits using chromosome segment substitution lines in adzuki bean

☆Takamitsu, A.¹, Y. Horiuchi², T. Oka¹, S. Murayama¹, K. Kata¹ (1.Obihiro Univ. Agr. & Vet. Med., 2.Tokachi Agr. Exp. Sta., HRO)

110 Detection of chromosomal regions affecting adzuki bean paste color using chromosomal segment substitution lines between cultivar Shumari and Bhutanese accession

○Horiuchi, Y.¹, S. Murayama², A. Takamitsu², K. Kato² (1.Tokachi Agr. Exp. Sta., HRO, 2.Obihiro Univ.Agr. & Vet. Med.)

111 Measurement and Genome-Wide Association Study of Embryo size in Wheat

☆OKADA, S.¹, F. KOBAYASHI², N. MIZUNO², K. HATTA², C. KIRIBUCHI-OTOBE², M. TOUGOU², Y. IKEDA¹, Z. NISIO¹ (1.Agr., Tokyo Univ. Agri, 2.Inst. Crop. Sci., NARO)

112 Gene mutations and origin of *Ppo-A1* null allele (*Ppo-A1i*) in common wheat

☆Nakamaru, A.¹, K. Kato², H. Ito¹, S. Ikenaga¹, T. Nakamura¹ (1.TARC/NARO, 2.WARC/NARO)

113 Genetic analysis of heat germination tolerance in bread wheat

☆Tsukada, M.¹, S. Matsunaga², S. Tadano², Y. Yamasaki³, Y. Gorafi³, M. Nitta⁴, S. Nasuda⁴, K. Akashi⁵, H. Tsujimoto^{1,3} (1.Grad. Sch. Sus. Sci., Tottori Univ., 2.United Grad. Sch. Agr. Sci., Tottori Univ., 3.Arid Land Research Center, Tottori Univ., 4.Grad. Sch. Agr., Kyoto Univ., 5.Fac. Agr., Tottori Univ.)

114 Elucidation of BaYMV sequences infected New Sachiho Golden in Takanezawa field

○Okiyama, T.¹, Y. Oono², K. Mishina², T. Komatsuda^{2,3}, T. Kato^{1,4} (1.Tochigi Pref. Agric. Exp. Stn., 2.NARO, 3.SAAS, 4.Shimotsuga Agriculture Promotion Office)

115 Identification of genetic loci controlling the SRKN resistance with GWAS using novel *Ipomoea trifida* genome sequence as a reference in sweetpotato

☆Kurihara, M.¹, H. Tabuchi², K. Shirasawa³, S. Isobe³, Y. Monden⁴ (1.Fac. Agri., Okayama Univ., 2.KARC/NARO, 3.Kazusa DNA Res. Inst., 4.Grad. Sch. Env. & Life Sci., Okayama Univ.)

116 Identification of genetic locus associated to vine growth habitat in hexaploid sweetpotato using BSA and GWAS

☆Suematsu, K. (Kyushu Okinawa Agricultural Research Center, NARO)

117 QTL analysis of resistance in potatoes to bacterial wilt caused by *Ralstonia solanacearum* phylotypes I and IV

○Habe, I.¹, K. Miyatake² (1.Nagasaki Agri. For. Dev. Ctr., 2.Inst. Veg. Tea Sci., NARO)

118 QTL analysis of fertility restoration for the tetrad pollen sterility caused by a wild potato *Solanum verrucosum*.

☆Okamoto, S., R. Sanetomo (Potato Germplasm Enhancement Lab., Obihiro Univ.)

119 Genome sequences of 11 *Vigna* species

○Naito, K.¹, T. Wakatake², K. Fukushima², K. Satou³, T. Hirano³, S. Shigenobu⁴, M. Hasebe⁵, H. Sakai⁶ (1.Res Cntr Genet Resource, NARO, 2.Botany Dpt, Univ Würzburg,

3.Okinawa Inst Adv Sci, 4.Lab Evol Genomics, NIBB, 5.Div Evol Biol, NIBB, 6.Adv Anal Cntr, NARO)

120 Estimating the origin of cultivation of Azuki bean by population genomic analysis of seed color and seed spot genes

☆Muto, C.¹, M. Kumagai², H. Sakai², K. Naito¹ (1.Genetic Resources Center, NARO, 2.Advanced Analysis Center, NARO)

121 Identification of QTL for seed quality traits in adzuki bean (*Vigna angularis*)

○Nagaoka, H.^{1,2}, M. Irikiin², M. Mori¹, K. Kato¹ (1.Obihiro Univ. Agr. & Vet. Med., 2.Biotech Co.,Ltd.)

122 Identification of QTLs associated with glume and grain size in sorghum

☆Makino, A.¹, M. Ishimori², K. Yamazaki², T. Fujiwara², H. Iwata², N. Tsutsumi², H. Takanashi² (1.Faculty of Agriculture, The University of Tokyo, 2.Graduate School of Agricultural and Life Sciences, The University of Tokyo)

123 Identification of chromosomal regions associated with genetic variations in γ -oryzanol content using rice chromosome segment substitution lines

○Araki, E.¹, J. Tanaka², K. Ebana³ (1.Inst. Food Res., NARO, 2.Inst. Crop. Sci., NARO, 3.Inst. Gen. Resources Cent., NARO)

124 The natural rice albino found in the breeder's seeds uncovered to be elicited by a frame-shift mutation on the *SWL1* gene

☆Balimponya, E.¹, M. Dwiyanthi¹, T. Ito¹, S. Sakaguchi¹, K. Yamamori¹, Y. Kanaoka¹, Y. Koide¹, Y. Nagayoshi², Y. Kishima¹ (1.Research Faculty of Agriculture, Hokkaido University, Sapporo 060-8589, Japan, 2.Miyazaki Agricultural Research Institute, Miyazaki 880-0212 Japan)

125 Genetic analysis of stomatal characteristics by using backcrossed populations between Takanari and Koshihikari

☆Sato, N.¹, K. Kondo^{2,4}, T. Tanabata³, T. Ueda⁴, K. Kojima⁴, K. Hori^{1,4} (1.Grad. Sch. Frontier Sci., Univ. Tokyo, 2.Res. Inst. Rice Prod. Technol., 3.Kazusa DNA Res. Inst., 4.NARO)

126 Genomics-based breeding of extremely early-maturing Koshihikari.

○Tomita, M. (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

127 GWAS and haplotype analysis using the expanded NARO rice core collection

○Shenton, M.¹, N. Tanaka¹, K. Ebana² (1.NARO Institute of Crop Science, 2.NARO Genetic Resources Centre)

201 Genetic diversity of Brassica juncea genetic resources in and around the southern Shan State of Myanmar.

☆Nohara, T.¹, S. Yoshida², K. Tanaka³, A. O. M⁴, H. Kikuno⁵, K. Irie⁵, K. Wakui⁶ (1.Grad Agri, Tokyo Univ of Agri, 2.Institute of Crop Science, NARO, 3.NODAI Genome Res Ctr, Tokyo Univ of Agri, 4.Dept of Agri Res, Min of Agri, Lifest and Irrig, Myanmar, 5.Fac of Intl Agri and Food Stud, Tokyo Univ of Agri, 6.Fac of Agri, Tokyo Univ of Agri)

202 Phylogenetic analysis of Zenteika (a group of Japanese *Hemerocallis*) speices in Tohoku and Hokkaido region

☆Tamagawa, K.¹, Y. Sato², 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 Geopark Promotion Council, 4.Fac. Life Design., Tohoku Inst. Tech.)

203 Phylogeographic study of wild wheat relative *Aegilops umbellulata* Zhuk.

☆Son, I.¹, N. Kasazumi¹, M. Okada¹, Y. Matsuoka¹, K. Yoshida^{1,2} (1.Grad. Sch. Agr. Sci., Univ. Kobe, 2.Grad. Sch. Agr., Univ. Kyoto)

204 Sensitivity evaluating for soybean cyst nematode in common bean

☆Nagasawa, H.¹, K. Nakagawa¹, Y. Saito², F. Kosaka³ (1.Hokkaido Research Organization Tokachi Agricultural Experiment Station, 2.HRO Kamikawa agri. Exp. stn., 3.HRO Central agri. Exp. stn.)

205 Genetic diversity of azuki bean (*Vigna angularis*) genetic resources and Hokkaido breeding lines using genome-wide SNP polymorphism

☆Doman, K.¹, H. Shimada^{1,2}, T. Maruta¹, M. Okuyama¹, H. Sato¹, C. Souma¹, T. Suzuki¹, K. Shirasawa³ (1.Central Agri. Exp. Stn., HRO, 2.Tokachi Agri. Exp. Stn., HRO, 3.Kazusa DNA Res. Inst.)

206 Nucleotide polymorphism and gene expression for candidate gene of lateral awn suppressions, *C2H2-ZF* gene in four species of the subsection Emarginata

☆Hosoi, S.¹, J. Tomita¹, M. Murakawa¹, M. Maeda¹, K. Yamane¹, A. Ohta² (1.Fac. Appl. Biol. Sch., Gifu U., 2.Grad. Sch. Agr. Kyoto U.)

207 Geographical distribution of *GNI-A1* genotypes controlling floret fertility in wheat

☆Takahashi, K.¹, K. Tanaka¹, M. Kasama², y. Murakami², Z. Nishio^{1,2} (1.Grad. Sch. Agr., Tokyo Univ. Agr, 2.2 Fac. Agr., Tokyo Univ. Agr)

208 Composition and Seasonal variation of glucosinolate in wasabi.

☆Hiraumi, M.¹, M. Morita¹, N. Haga¹, S. Takashima², K. Yamane¹ (1.Fac. Appl. Biol. Sch., Univ. Gifu, 2.Life Sci. Res. Ctr., Univ. Gifu)

209 Rizobacteria producing blue purple pigment and plant growth promoting effect detected in wheat germinating seeds.

○Ban, T.¹, M. Kodama², A. Ishihara², R. Kagei², K. Kido², N. Miyanishi³ (1.KIBR, Yokohama City Univ., 2.Fac. Agr., Tottori Univ., 3.Fac. Food & Nutri. Sci., Toyo Univ.)

210 Exploration and acquisition of low allergen characteristic lines for buckwheat anaphylaxis risk management.

○Hara, T.¹, R. Satoh², K. Okamoto³, K. Maruyama⁴, K. Matsui⁵, T. Suzuki⁶, K. Ishiguro¹, S. Otuka¹, R. Chen⁷, R. Teshima⁸, Y. Kondo³, Y. Yasui⁹ (1.HARC, NARO, 2.NFRI, NARO, 3.Fac. Medicine, Fujita Health Univ., 4.JIRCAS, 5.NICS, NARO, 6.KARC, NARO, 7.Fac. Life Env. Sci., Univ. Tsukuba, 8.Fac. Veterinary Medicine, Okayama Univ. Sci., 9.Grad. Sch. Agric., Univ. Kyoto)

211 Genetic analysis of data from performance tests for recommended rice varieties using pedigree and genomic information

○Iwata, H.¹, C. Sato², A. Abe³, C. Kim⁴, G. Morota⁵, H. Shimono⁶ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Ifuririn, Ltd., 3.Iwate Biotech. Res. Cntr., 4.Sky Ocean Technology Co., Ltd., 5.College of Agriculture and Life Sciences, Virginia Tech, 6.Fac. Agr., Iwate Univ.)

212 Improvement of a plant genome information portal site, Plant GARDEN (2021 · Q4 ver)

○Ichihara, H.¹, H. Hirakawa¹, A. Ghelfi¹, M. Kohara¹, M. Yamada¹, T. Tamura², A. Nakaya³, Y. Nakamura¹, S. Shirasawa¹, E. Sugihara², S. Tabata¹, S. Isobe¹ (1.KDRI, 2.PMC, Univ. Tsukuba, 3.GSFS, Univ. Tokyo)

213 Characteristics of brown rice metabolites depending on the appearance quality of rice suitable for sake brewing and consumption as food

○Adachi, N.^{1,2}, M. Wakayama¹, Y. Ishizuka³, T. Soga¹, M. Tomita¹ (1.Inst. Adv. Biosci., Keio Univ., 2.Yamagata Int. Agr. Res. Cent., 3.Rice Breed. Crop Sci. Res. Inst., Yamagata Int. Agr. Res. Cent.)

214 Genomic view of heavy-ion induced deletions associated with distribution of essential genes in *Arabidopsis thaliana*

☆Ishii, K.^{1,2}, Y. Kazama^{1,3}, T. Hirano^{1,4}, J. Fawcett⁵, F. Sakai⁶, Y. Shirakawa¹, S. Ohbu¹, T. Abe¹ (1.RIKEN Nishina Cent., 2.QST NIRS, 3.Fac. Biosci. Biotech., Fukui Pref. Univ., 4.Fac. Agr., Univ. Miyazaki, 5.RIKEN iTHEMS, 6.RIKEN CBS)

215 Dynamic morphological changes observed in the novel *Arabidopsis* mutant with chromosome rearrangements

☆Sugita, K.¹, A. Sanjaya¹, R. Nishijima¹, K. Murai¹, T. Abe², Y. Kazama^{1,2} (1.Fucul. Biosci. Biotech., Fukui Pref. U., 2.RIKEN Nishina Cent)

216 Cell size alteration observed in the petals of novel frill mutant in *Torenia Forunieri*

☆Mayuzumi, T.¹, A. Matsuta¹, M. Hatashita², K. Tagkagi², T. Abe³, K. Murai¹, Y. Kazama^{1,3} (1.Fucul. Biosci. Biotech., Fukui Pref. U., 2.Wakasa-wan Ener. Cent., 3.RIKEN Nishina Cent.)

217 Effects of heavy-ion beam irradiation on tuberous root formation in sweet potato

☆PARK, H.¹, Y. Narasako², T. Abe³, H. Kunitake^{1,4}, T. Hirano^{1,3,4} (1.Interdiscip. Grad. Sch. Agric. Eng., Univ. Miyazaki, 2.Kushima Aoi Farm Co., 3.RIKEN Nishina Center, 4.Fac. Agric., Univ. Miyazaki)

218 Genetic analysis of complex factors involving spikelet size of a particular wild rice species grown in Australia

☆Sasaki, R.¹, H. Kizaki¹, W. Sunaga¹, K. Katano^{2,3}, Y. Gatayama², Y. Maeda⁴, R. Takahashi⁴, K. Ichitani⁴, R. Henry⁵, R. Ishikawa¹ (1.Fac. Agr. And. Life. Sci., Hirosaki

Univ., 2.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 3.TAKII & Co., LTD., 4.Fac. Agr., Kagoshima Univ., 5.Univ. of Queensland)

219 Rapid development of CAPS markers using NGS to identify new seedless citrus cultivar 'Mizuki'

☆Nishimura, K., R. Nakano, T. Nakazaki (Grad. Sch. Agr., Kyoto Univ.)

220 Towards the construction of cross-crop information platform for effective and efficient breeding

Tanaka, J.¹, H. Kajiya-Kanegae², Y. Kawahara³, T. Wako¹, O.M. Ishimoto¹ (1.Inst. Crop. Sci., NARO, 2.RCAIT, NARO, 3.AAC, NARO)

221 Development of rice MNU-mutant library and database for in silico screening

○Kubo, T.¹, Y. Yamagata¹, H. Matsusaka¹, Y. Sato², T. Kumamaru¹ (1.Fac. of Agri., Kyushu Univ., 2.Nat. Inst. of Genet.)

222 Breeding and characterization of low-cadmium rice variety "Akitakomachi R"

○Takahashi, R.¹, K. Kato¹, S. Shibata¹, T. Abe², S. Ishikawa², T. Kawamoto¹ (1.Akita Pref. Agr. Exp. Sta., 2.Inst. Agro-Environ. Sci., NARO)

223 Combating vitamin A deficiency in Nigeria: The bio-fortified sweet potato development and deployment approach

Afuape, S.¹, E. Ebem², D. Igwe³, O.B. Ubi^{2,4} (1.Sweetpotato Programme, National Root Crops Research Institute (NRCRI), Umudike, Nigeria, 2.Department of Biotechnology, Ebonyi State University, Abakaliki, Nigeria, 3.School of Integrative Plant Science, Plant Pathology and Plant – Microbe Biology Section, Cornell University, Ithaca, NY, USA, 4.Arid Land Research Center, Tottori University, Japan)

224 A new potato cultivar "Yumeikoro"

○Shinada, H.¹, R. Fujita¹, H. Matsunaga¹, T. Wazaki¹, M. Oonami², S. Aoyama³, S. Ebe⁴, S. Iketani¹, S. Hagihara², H. Nakayama⁵, C. Suzuki², H. Tamura⁴, C. Souma⁴, S. Ikeda³, K. Onodera¹ (1.HRO Kitami Agricultural Experiment Station, 2.HRO Tokachi Agricultural Experiment Station, 3.HRO Donan Agricultural Experiment Station, 4.HRO Central Agricultural Experiment Station, 5.Niigata municipal government)

225 Southeast Asia is rich in melon landraces harboring resistant allele of MeVat gene for cotton aphid resistance

☆Imoh, O.¹, T. Dung¹, M. Pervin¹, K. Tanaka², G. Shigita³, H. Nishida¹, K. Kato¹
(1.Grad. Sch. Environ. Life Sci., Okayama Univ., 2.Fac. Agr. Life Sci., Hirosaki Univ., 3.TUM)

226 Characterization of melon accessions collected from the Maldives
Characterization of melon accessions collected from the Maldives

☆Sogo, N.¹, I. Odirichi², T. Nagai², G. Shigita³, K. Tanaka⁴, H. Nishida², K. Kato² (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.TUM, 4.Fac. Agr. Life Sci., Hirosaki U.)

301 Haplotype Analysis Using Multi-Parental Advanced Generation Inter-Cross Lines Reveals Phenology QTLs for Canopy Height in Rice

○Ogawa, D.¹, T. Sakamoto², H. Tsunematsu¹, Y. Nonoue¹, N. Kanno¹, J. Yonemaru¹
(1.Inst. Crop. Sci., NARO, 2.Inst. Agro-Env. Sci., NARO)

302 UAV-based phenological characteristics of 30 rice varieties including recently bred ones in Japan

☆Taniguchi, S.¹, T. Sakamoto², R. Imase³, Y. Nonoue³, H. Tsunematsu³, A. Goto³, K. Matsushita³, S. Ohmori³, H. Maeda³, Y. Takeuchi³, T. Ishii³, H. Kajiya-Kanegae¹, J. Yonemaru³, D. Ogawa³ (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Agro-Env. Sci., NARO, 3.Inst. Crop Sci., NARO)

303 Development of the detection methods for rice contaminants by UAV remote sensing

☆Shibata, S.¹, S. Nishiuchi² (1.Sch. Agr. Sci., Nagoya Univ., 2.Grad. Sch. Bioagr. Sci., Nagoya Univ.)

304 Prediction of wheat NDVI change at jointing stage using satellite remote sensing

☆Takata, I., T. Nakata, S. Nishiuchi (Grad. Sch. Bioagri., Nagoya Univ.)

305 Development of Biomass Estimation method for High Yielding Sorghum by UAV Remote Sensing

☆Nakata, T.¹, S. Inoue¹, T. Sazuka², S. Nishiuchi¹ (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ.)

306 Prediction of potential yield using canopy temperature measured by UAV and thermography at a wheat breeding program

○Ohnishi, S.¹, H. Kiuchi¹, T. Iijima², T. Uraike², Y. Sato¹, T. Sonoda¹, K. Araki¹ (1.HRO Kitami AES, 2.HRO Industrial RI)

307 Evaluation of a digital shape measurement using 3D model based on multi-view images in zoysiagrass

☆Pongpiyapaiboon, S.¹, H. Tanaka², T. Hashiguchi³, M. Hashiguchi⁴, A. Hayashi⁵, T. Tanabata⁶, K. Kodama⁶, S. Isobe⁶, R. Akashi⁷ (1.Graduate School of Agriculture, University of Miyazaki, 2.Center for the Promotion of Institutional Research, University of Miyazaki, 3.Faculty of Agriculture, University of Miyazaki, 4.Faculty of Regional Innovation, University of Miyazaki, 5.Research Center for Agricultural Robotics, National Agriculture and Food Research Organization, 6.Department of Frontier Research and Development, Kazusa DNA Research Institute, 7.University of Miyazaki)

308 Time-course analysis of morphological changes in leaf lettuce with 3D measurement

☆Wada, K.¹, H. Itoh¹, A. Hayashi¹, T. Tanabata², S. Isobe², N. Kochi¹ (1.Inst. Crop. Sci., NARO, 2.Kazusa DNA Res. Inst.)

309 Quantitative evaluation and genetic analysis of soybean drought tolerance using deep learning models for classification of wilting

☆Imachi, Y.¹, Y. Toda¹, Y. Omori¹, Y. Yamasaki², H. Takahashi³, H. Takanashi¹, M. Tsuda⁴, H. Kajiya-Kanegae⁶, H. Tsujimoto², A. Kaga⁷, M. Hirai⁵, M. Nakazono³, T. Fujiwara¹, W. Guo¹, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Arid Land Res. Ctr., Tottori Univ., 3.Grad. Sch. Bioagri. Sci., Nagoya Univ., 4.T-PIRC, Univ. Tsukuba, 5.Ctr. for Sustainable Resource Sci., RIKEN, 6.Res. Ctr. for Agr. Info. Tech., NARO, 7.Inst. Crop Sci., NARO)

310 Modeling of header loss in reel-header combine harvester in adzuki bean

☆Hosokawa, Y., N. Yamaguchi, K. Sekiguchi, H. Nagasawa, Y. Horiuchi, K. Yoshida (Tokachi Agr. Exp. Stn., HRO)

311 Genome-wide association study and genomic prediction for eating quality of cooked rice grains.

○Hori, K.¹, K. Mochizuki^{2,3}, Y. Tsujii², K. Iijima¹, K. Shu¹, K. Suzuki¹, S. Yabe¹, M. Shenton¹ (1.NICS, NARO, 2.Tokyo Agr. Univ., 3.KARC, NARO)

312 Crossing simulator for the range of trait values in progeny from the parental genome data based on historical data and its validation.

○Goto, A.^{1,2}, T. Hayashi², S. Taniguchi², H. Kajiya-Kanegae², K. Matsushita¹, G. Kikui², M. Yano², J. Yonemaru^{1,2} (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)

313 Development of a population ATHN derived from 4-way cross among high-yield and good-eating quality rice with four important genes and wide diversity using sBBS

○Tanaka, J.¹, H. Maeda^{1,2}, D. Ogawa¹, K. Matsushita¹, A. Goto¹, I. Nagaoka³, Y. Taniguchi¹, H. Sasahara⁴ (1.NICS/NARO, 2.MAFF, 3.CARC/NARO, 4.WARC/NARO)

314 In preparation to increase the content of γ -oryzanol in rice by the combination system of sBBS and Smart Outcross Facilitator (SOF)

○Taniguchi, Y.¹, E. Araki², K. Ebana³, J. Tanaka¹ (1.Inst. Crop. Sci., NARO, 2.Inst. Food. Res., NARO, 3.Genetic Resources Center, NARO)

315 Introduction of targeted base substitution into miR172 targeting site on TaAP2 by a transient expression of a plasmid DNA vector in wheat.

○Ogawa, T.¹, K. Negishi¹, F. Abe², S. Toki^{1,3,4} (1.NIAS, 2.NICS, 3.Fac. Agr., Ryukoku Univ., 4.Grad.Sch.Nonobio., Yokohama City Univ.)

316 Effects of promoters for gRNA expression and cultivation temperatures on genome editing efficiency in wheat.

☆Kishi-Kaboshi, M.¹, F. Abe¹, Y. Kamiya², K. Kawaura², H. Hisano³, K. Sato³ (1.Inst. Crop Sci., NARO, 2.KIBR, Yokohama City Univ., 3.IPSR, Okayama Univ.)

317 Development of the error correction tool "GBScleanR" for genotype data of multiparental populations.

☆Furuta, T.¹, M. Ashikari², T. Yamamoto¹ (1.Inst. Plant Sci. and Res., Okayama University, 2.Biosci. and Biotech. Center, Nagoya University)

318 Prediction of flowering and maturity time of soybean using genes and meteorological factors

○Onogi, A.¹, K. Fujii², A. Kikuchi³, K. Komatsu⁴, Y. Kono⁵, N. Oki⁶, S. Watanabe⁷, A. Kaga² (1.Faculty of Agr., Ryukoku Univ., 2.NICS, NARO, 3.TARC, NARO, 4.WARC, NARO, 5.CARC, NARO, 6.KARC, NARO, 7.Univ. Saga)

319 Tadukan-type cytoplasmic male sterile rice forms normal pollen in indehiscent anther and exhibits sporophytic recovery of fertility

☆Takatsuka, A.¹, T. Kazama², K. Toriyama¹ (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Grad. Sch. Agri., Kyushu Univ.)

320 Identification of a novel fertility restorer gene, *Rfs*, to the Ogura cytoplasmic male sterility of radish. 1. Back ground and the position of *Rfs*.

○Yamagishi, H.¹, A. Hashimoto², A. Fukunaga³, M. Takenaka⁴, T. Terachi³ (1.Inst. Comprehensive Acad. Res., Kyoto Sangyo Univ., 2.Res. Center Botany, Kyoto Sangyo Univ., 3.Fac. Life Sci., Kyoto Sangyo Univ., 4.Grad. Sch. Sci., Kyoto Univ.)

321 Identification of a novel fertility restorer gene, *Rfs*, to the Ogura cytoplasmic male sterility of radish. 2. Structure and function of RFS protein.

○Terachi, T.¹, A. Hashimoto², A. Fukunaga¹, M. Takenaka³, H. Yamagishi⁴ (1.Fac. Life Sci., Kyoto Sangyo Univ., 2.Res. Center Botany, Kyoto Sangyo Univ., 3.Grad. Sch. Sci., Kyoto Univ., 4.Inst. Comprehensive Acad. Res., Kyoto Sangyo Univ.)

322 Identification of *MALE STERILITY 4* gene in Japanese cedar

☆Kakui, H.¹, T. Ujino-Ihara², Y. Hasegawa², E. Tsurisaki¹, N. Futamura², J. Iwai³, Y. Higuchi³, T. Fujino⁴, Y. Suzuki⁴, M. Kasahara⁴, K. Yamaguchi⁵, S. Shigenobu⁵, M. Otani⁶, M. Nakano⁶, S. Ueno², Y. Moriguchi¹ (1.Grad. Sch. Sci. Tec., Niigata Univ., 2.FFPRI, 3.Niigata Pref. Forest Res. Inst., 4.Grad. Sch. Front. Sci., Univ. Tokyo, 5.NIBB, 6.Fac. Agr., Niigata Univ.)

323 A novel mitochondrial gene, *orf137*, triggers cytoplasmic male sterility in tomato

☆Kuwabara, K.¹, S. Arimura², K. Shirasawa³, T. Ariizumi⁴ (1.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 2.Grad. Sch. Agri. and Life. Sci., Univ. Tokyo, 3.Kazusa DNA Res. Inst., 4.Fac. Life Env. Sci., Univ. Tsukuba)

324 Random inactivation of sex chromosome cause post-zygotic sex ratio distortion in persimmon

○Akagi, T.^{1,2}, S. Sugano³, D. Charlesworth⁴, L. Comai⁵, I. Henry⁵ (1.Grad. Sch. Environ. Life Sci., Okayama Univ., 2.JST-PRESTO, 3.Bioprod. Res. Inst., AIST, 4.Inst. Evol. Biol., Univ. Edinburgh, 5.Genome Cent., UC Davis)

325 Genetic analysis to identify female and male factors controlling unilateral incompatibility between inbred lines in Japanese Oguni population of *Brassica rapa*

☆Kon, A.^{1,2}, Y. Takada¹, M. Shimizu³, S. Takayama⁴, G. Suzuki⁵, Y. Kobayashi², M. Watanabe¹ (1.Grad. Sch. Life Sci., Tohoku Univ., 2.Dept. Nat. Sci., Miyagi Univ. Educ., 3.Iwate Biotech. Res. Ctr., 4.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 5.Div. Natl. Sci., Osaka Kyoiku Univ.)

326 Dominance relationships among class-II S haplotypes on pollen side in *Raphanus sativus* self-incompatibility

☆Ishii, T., M. Yamamoto, H. Kitashiba (Grad. Sch. Agri. Sci., Tohoku Univ.)

327 Analysis of the characteristics of amino acid residues located in the receptor domain of AISRKb essential for self-incompatibility response.

○Yamamoto, M.¹, S. Ohtake¹, A. Sinosawa², M. Shiota³, Y. Mitsui⁴, H. Kitashiba¹ (1.Grad. Sch. of Agri., Tohoku Univ., 2.NODAI Genome Research Center, Tokyo Univ. of Agri., 3.Grad. Sch. of Med., Tohoku Univ., 4.Grad. Sch. of Agri., Tokyo Univ. of Agri.)

401 Analysis of florigen intercellular transport and concentration gradient formation in the shoot apical meristem of rice

☆Nakamura, J., M. Tanaka, H. Tsuji (Kihara Institute for Biological Research, Yokohama City Univ.)

402 Spatial integration of florigen and cytokinin signalling regulates reproductive development in rice

☆Sato, M.¹, Y. Sakamoto², M. Tanaka¹, J. Ito¹, K. Taoka¹, M. Mikami³, M. Endo³, H. Kitano⁴, S. Matsunaga⁵, H. Tsuji¹ (1.KIBR, Yokohama City Univ., 2.Dept. Biol. Sci., Grad. Sch. Sci., 3.Inst. Agrobiol. Sci., NARO, 4.Biosci. and Biotech. Cen., Nagoya Univ., 5.Grad. Sch. Front. Sci., Univ. Tokyo)

403 Regulation of chromatin accessibility by florigen activation complex

☆Funayama, E.¹, A. Hosaka^{1,2}, H. Akashi¹, K. Yamaguchi¹, A. Yoshida¹, H. Kida¹, H. Yoshida³, J. Ito¹, T. Kawakatsu⁴, H. Tsuji¹ (1.Kihara Institute for Biological Research, Yokohama City Univ., 2.Rhelixa Inc., 3.Institute of Fermentation Sciences, Fukushima Univ., 4.Institute of Agrobiological Sciences, National Agriculture and Food Research Organization)

404 Genetic analysis of a globosum seed mutant of barley

○Taketa, S.¹, M. Shiraga¹, M. Oozeki², T. Sotome² (1.IPSR, Okayama University, 2.Tochigi Prefecture)

405 Plant physiological analysis of an Arabidopsis Cngc2-deficient mutant that shows an early transition from flower bud to silique.

☆Katano, K.^{1,2}, H. Kiyono¹, A. Nagao¹, N. Suzuki¹ (1.Sophia University, 2.JSPS Research Fellowship for Young Scientist)

406 Evaluation of vernalization characteristics of extremely late bolting lines in *Brassica rapa*

Akter, A., ○R. Fujimoto (Grad. Sch. Agric. Sci., Kobe Univ.)

407 A novel role for lipid-transfer protein in the control of wheat seed dormancy

○Himi, E.¹, S. Kurihara², F. Abe³, H. Takahashi⁴, K. Tanaka⁵, T. Matsuura⁶, M. Maekawa⁶, K. Rikiishi⁶ (1.Sch. Agri., Kibi International Univ., 2.HARC, NARO, 3.NICS, NARO, 4.Cluster of Agricultural Sci., Fukushima Univ., 5.NGRC, Tokyo Univ. Agri., 6.IPSR, Okayama Univ.)

408 The ectopic expression of *Btr2* in *Aegilops tauschii* switches the disarticulation layer from above to below the rachis node

☆Zeng, X.^{1,2,3}, A. Tagiri¹, S. Kikuchi², H. Sassa², T. Komatsuda^{1,2,3} (1.Institute of Crop Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Japan, 2.Graduate School of Horticulture, Chiba University, Matsudo, Chiba, Japan, 3.Shandong Academy of Agricultural Sciences (SAAS) Crop Research Institute, Jinan, Shandong, China)

409 *PCL1* is causal gene for early and extra early mutations in the pedigree of wheat cultivar "Blackhull".

☆Fujioka, A.¹, N. Sogo¹, T. Nishina², K. Murata³, K. Shimizu^{4,5}, H. Nishida², S. Nasuda³, K. Kato² (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.Grad. Sch. Agri., Kyoto U., 4.Dept. Evo. Biol. Env. Studies, U. Zurich, 5.Kihara Inst. Biol. Res., Yokohama City U.)

410 Genetic analysis of novel QTLs for heading time on chromosomes 4H and 5H in barley

☆Okuma, M.¹, Y. Atsuji¹, K. Kato², H. Nishida² (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U.)

411 Analysis of unknown inflorescence structure "double ridge" in by 3D imaging and laser microdissection-RNA-seq

☆sato, n.¹, J. Ito¹, Y. Nomura¹, M. Sugimura¹, N. Takeda-Kamiya², K. Toyooka², H. Tsuji¹ (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN)

412 *Dominant Awn Inhibitor* in sorghum

○Takanashi, H.¹, H. Kanegae², A. Nishimura¹, J. Yamada¹, M. Ishimori¹, M. Kobayashi², K. Yano³, H. Iwata¹, N. Tsutsumi¹, W. Sakamoto⁴ (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.RCAIT, NARO, 3.Dept. Life Sci., Fac. Agric., Meiji Univ., 4.Inst. Plant Sci. Res., Okayama Univ)

413 Analysis of axis formation and auxin response in rice early embryo

☆Tezuka, T.¹, K. Ta², S. Shimizu-Sato², M. Nosaka-T^{1,2}, Y. Sato^{1,2} (1.Sch. Life Sci., SOKENDAI, 2.Plant genet., NIG)

414 Pleiotropic function of *QHB/OsWOX5* gene in root system development of rice

☆Kawai, T.¹, K. Shibata¹, M. Sato², H. Tsuji², H. Takahashi¹, M. Nakazono¹, M. Takahashi-Nosaka³, Y. Sato³, Y. Inukai⁴ (1.Grad. Sch. Bioagri., Nagoya Univ., 2.KIBR, Yokohama City Univ., 3.Natl. Inst. Genet., 4.ICREA, Nagoya Univ.)

415 Factors involved in antibiotic-induced seedlessness

○Nishimura, A., C. Honda, N. Tsutsumi (The University of Tokyo)

416 First report of *Colletotrichum orbiculare* race 2 overcomes the resistance gene *Ar-1* of watermelon in Japan

☆Matsuo, H.¹, K. Mine², T. Sano³, H. Yoneda², Y. Ishiga⁴, Y. Kubo⁵, Y. Yoshioka⁴ (1.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 2.Nara Agr. Res. Cen., 3.Workforce and Farmland Mgmt. Div., Nara Pref., 4.Fac. Life Env. Sci., Univ. Tsukuba, 5.Fac. Agr., Setsunan Univ.)

417 Development and validation of a DNA marker associated with resistance to Phytophthora stem rot of adzuki bean derived from "Toiku 170"

☆Sato, K.¹, K. Horikawa², M. Nagahama², H. Nagasawa³, Y. Horiuchi³, C. Souma¹, T. Suzuki¹ (1.Central Agr. Exp. Stn., HRO, 2.Kamikawa Agri. Exp. Stn., HRO, 3.Tokachi Agr. Exp. Stn., HRO)

418 Comprehensive gene expression analysis in response to two SRKN races (SP1, SP2) with different resistance responses in one sweetpotato variety

☆Izumitani, M.¹, S. Ohata¹, H. Tabuchi², Y. Monden¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.KARC/NARO)

419 Identification of novel causative mutations in the *SSII* gene of sweetpotato

☆Shimo, K.¹, K. Tada², M. Tanaka³, A. Kobayashi³, Y. Monden² (1.Fac. Agri., Okayama Univ., 2.Grad. Sch. Env. & Life Sci., Okayama U., 3.KARC/NARO)

420 Reaction to Soybean leaf rugose mosaic virus in soybean Germplasm.

○Saruta, M.¹, Y. Takada² (1.Inst. Crop. Sci., NARO, 2.WARC, NARO)

421 Yielding ability and chilling tolerance of a soybean line "Toiku 273" derived from the cross between Hokkaido and Polish cultivars.

☆Takahashi, H.¹, N. Yamaguchi¹, S. Hagihara¹, M. Kurushima¹, C. Suzuki¹, F. Kousaka², S. Kobayashi¹ (1.Tokachi Agr. Exp. Sta., HRO, 2.Central Agr. Exp. Sta., HRO)

422 Functional analysis of a gene for the formation of radial oxygen loss barrier in genus *Zea*

☆Ito, T.¹, H. Takahashi¹, H. Mori¹, M. Nomoto², Y. Tada², Y. Inukai³, H. Takahashi⁴, F. Omori⁵, Y. Mano⁵, M. Nakazono¹ (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.Center Gene Res., Nagoya Univ., 3.ICREA, Nagoya Univ., 4.Fac. Food & Agri. Sci., Fukushima Univ., 5.Inst. Livest. Grassl. Sci., NARO)

423 Molecular analysis of abscisic acid receptor-mediated powdery mildew resistant mechanism in wheat

☆Shimazaki, T.¹, J. Kim², R. Mega³, F. Abe⁴, K. Miyamoto⁵, H. Yamane⁵, K. Nihei⁶, K. Yoshida⁷, M. Okamoto¹ (1.Ctr. for Biosci. Res. & Educ., Univ. Utsunomiya, 2.CSRS., RIKEN, 3.Grad. Sci. & Tech. Innov., Univ. Yamaguchi, 4.Inst. Crop. Sci., NARO, 5.Sci. & Eng., Univ. Teikyo, 6.Grad. Agri. chem., Univ. Utsunomiya, 7.Grad. Sch. Agric., Univ. Kyoto)

424 Genetic analysis for improving cold tolerance of Basmati 370

☆Kuroki, R., V. Reyes, A. Mabreja, S. Nishiuchi, K. Doi (Grad. Sch. Bioagri. Sci., Nagoya U.)

425 The effect of starch breakdown on coleoptile elongation in rice under submergence.

☆Hirano, H., M. Fukuda, T. Fukao (Bioscience and Biotechnology, Fukui Prefectural Univ.)

426 The expression of mitochondrial genes may be positively regulated by an increase in genome copy number under respiratory failure in *Arabidopsis thaliana*.

☆Ayabe, H.¹, A. Toyoda², A. Iwamoto³, N. Tsutsumi¹, S. Arimura¹ (1.GGrad. Sch. of Agri. and Life Sci., Univ. Tokyo, 2.Department of Genomics and Evolutionary Biology, National Institute of Genetics, 3.Fac. of Sci., Univ. Kanagawa)

427 Fine mapping and candidate gene analysis of pre-harvest sprouting resistance QTLs, *qSdr6a* and *qSdr6b*, in rice

☆Sano, S.¹, J. Haung², N. Iijima¹, K. Sugimoto³, T. Hoshino^{1,2} (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ., 3.Inst. Crop. Sci., NARO)

501 A novel mutant allele at the *Cleistogamy 1* locus for closed flowering in barley

○Komatsuda, T.^{1,2}, N. Wang^{1,3}, M. Tomokazu⁴, C. Liu^{1,2}, M. Yoshida^{5,6}, N. Kawada⁷, K. Kakeda³ (1.Inst. Crop. Sci., NARO, 2.Shandong Academy of Agricultural Sciences (SAAS), Crop Research Institute, 3.Graduate School of Life and Environmental Sciences, University of Tsukuba, 4.Graduate School of Bioresources, Mie University, 5.Institute for Plant Protection, NARO, 6.Research Center for Agricultural Information Technology, NARO, 7.Kyushu Okinawa Agricultural Research Center, NARO)

502 Pleiotropic effects of mutation at the miR172 target site in the wheat orthologs of *Cly1*

☆Nanape, A., K. Kakeda (Grad. Sch. Biores., Mie Univ.)

503 *SNORKEL* genes relating to flood tolerance were pseudogenized in normal cultivated rice

○Nagai, K., M. Ashikari (Biosci. Biotech. Ctr., Nagoya Univ.)

504 Effects of different promoters to express phosphate transporter TaPT2 on Pi uptake and transport in transgenic Arabidopsis

○TADA, Y., Y. NOIKE (Sch. Biosci. Biosci., Tokyo Univ. Technol.)

505 Expression analysis of orf181 in cytoplasmically substituted wheat with *Aegilops mutica* cytoplasm

☆Shoji, Y.¹, M. Tujimura², T. Terachi³ (1.Grad. Sch. Life Sci., Kyoto Sangyo Univ, 2.Fac. Agr. Dept. Plant Life Sci., Ryukoku Univ., 3.Fac. Life Sci., Kyoto Sangyo Univ.)

506 Plant genome editing using engineered BICas9

○Endo, M.^{1,2}, K. Negishi¹, H. Nishimasu³, O. Nureki⁴, S. Toki^{1,2,5} (1.Inst. Agrobiol. Sci., NARO, 2.Grad. Sch. Nanobiol., Yokohama City Univ., 3.RCAST, Univ. Tokyo, 4.Grad. Sch. Sci., Univ. Tokyo, 5.Facal. Agri., Ryukoku Univ)

507 Classification of cytoplasmic male sterility genes in alloplasmic lines of common wheat and efforts to create knockout lines using mitochondrial genome editing

○Tsujiimura, M.¹, Y. Shoji², M. Nakata¹, S. Arimura³, S. Takenaka¹, T. Terachi⁴ (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 3.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 4.Fac. Life Sci., Kyoto Sangyo Univ.)

508 Characterization of the novel retrotransposon SbdRT identified in *Chrysanthemum seticuspe*

○Nakano, M.¹, E. Fukai², I. Shiraiwa³, T. Kozuka³, K. Taniguchi³, M. Kusaba³ (1.Fac. Agr. and Marine Sci., Kochi Univ., 2.Fac. of Agr., Niigata Univ., 3.Grad. Sch. Int. Sci. Life, Hiroshima Univ.)

509 Heterotrimeric G protein $\gamma 5$ subunit regulates plant height by functionally overlapping with *DEP1* in rice

☆Chaya, G.¹, S. Segami², M. Fujita¹, Y. Morinaka¹, K. Miura¹, Y. Iwasaki¹ (1.Dep.Biosci., Fukui Pref.Univ., 2.Res. Inst. Env. Agr. Fish. Osaka)

510 Fertilization controls tiller numbers via transcriptional regulation of a MAX1-like gene in rice cultivation

☆CUI, J.¹, N. Nishide¹, K. Kuroha², K. Sugimoto^{2,3}, T. Izawa¹ (1.Fac. Agric.Univ. Tokyo, 2.Natl. Inst. Crop. Sci. NARO, 3.Inst. Crop. Sci. NARO)

511 Identification of a novel NRL2-interacting protein involved in leaf morphology in rice

☆Ishikawa, K.¹, Y. Sugihara², K. Ito¹, H. Utsushi¹, Y. Ogasawara¹, E. Kanzaki¹, T. Sakai², R. Terauchi², A. Abe¹ (1.Iwate Biotechnology Research Center, 2.Graduate School of Agriculture, Kyoto University)

512 Comparative analysis on somaclonal mutants for fruit shape determination in persimmon

☆Horiuchi, A.¹, K. Masuda², R. Matsuzaki³, N. Onoue³, Y. Kubo², K. Ushijima², T. Akagi² (1.Grad. Sch. Agri., Okayama Univ., 2.Grad. Sch. Environ. LifeSci., Okayama Univ., 3.Inst. Fruit Tree and Tea Sci., NARO)

513 Explainable deep learning uncovers novel *cis-trans* regulatory networks in kiwifruit ripening responses.

☆Kuwada, E.¹, K. Takeshita², N. Fujita¹, K. Ushijima¹, Y. Kubo¹, S. Uchida³, T. Akagi^{1,4} (1.Grad. Sch. Environ. & Life Sci., Okayama Univ., 2.Dept. Adv. Info. Tech., Kyushu Univ., 3.Fac. of Agric., Kagawa University, 4.JST-PRESTO)

514 Analyses of RNA editing with the targeted base editing method for mitochondrial genomes of *Arabidopsis thaliana*

☆Nakazato, I.¹, C. Zhou¹, Y. Tamura¹, R. Masuda¹, N. Tsutsumi¹, M. Takenaka², S. Arimura¹ (1.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 2.Grad. Sch. Sci., Kyoto Univ.)

515 QTL analysis of mineral content in soybean seeds using RILs between Japanese and modern US varieties.

☆Ikegami, M.¹, K. Toda^{1,7}, K. Fujii¹, A. Kikuchi², K. Komatsu³, Y. Kono⁴, N. Oki⁵, S. Watanabe⁶, K. Hirata², T. Yamada¹, A. Kaga¹ (1.NICS, NARO, 2.TARC, NARO, 3.WARC,

NARO, 4.CARC, NARO, 5.KARC, NARO, 6.Univ. Saga, 7.Res. Cent. Genet. Resources, NARO)

516 Quantitative trait loci associated with seed yield in a high yield cultivar.

○Oki, N.¹, A. Kaga², F. Taguchi-Shiobara², T. Shimizu², U. Ohashi³ (1.NARO, KARC, 2.NARO, NICS, 3.Sch. Med., Univ. Hokkaido)

517 Identification of the corresponding gene in a sugary endosperm mutant in sorghum and its potential for breeding use

☆Hashimoto, S.¹, S. Araki-Nakamura², K. Ohmae-Shinohara², H. Nakamura¹, K. Miura³, S. Kasuga⁴, T. Sazuka² (1.Grad. Sch. Bioagri. Sci, Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Dept. Biosci. Fukui Pref. Univ., 4.Academic Assembly, Shinshu Univ.)

518 Selection of high-yielding soybean lines by marker-assisted pyramiding for seed yield and lodging tolerance

○Yamaguchi, N.¹, Y. Sato^{2,3}, F. Taguchi-Shiobara⁴, F. Kousaka⁵, M. Ishimoto⁴, M. Senda² (1.Tokachi Agr. Exp. Sta., HRO, 2.Fac. Agric. Life Sci., Hirosaki Univ., 3.Kitami Agr. Exp. Sta., HRO, 4.Inst. Crop. Sci., NARO, 5.Central Agr. Exp. Sta., HRO)

520 Research and development of sustainable raw materials for brewing. I. Characteristics of a barley mutant line with higher malt modification.

○Kihara, M., N. Hirota, R. Kanatani, T. Hoki, N. Suda (Crop Res. Lab., SAPPORO BREWERIES LTD.)

521 Effects of a Slow-Staling wheat genotype on starch properties, bread and noodle qualities in different genetic backgrounds

○Inokuma, T.¹, P. Vrinten¹, T. Shimbata¹, A. Sunohara¹, M. Fujita², K. Nakamura², N. Ishikawa³, K. Takata⁴, C. Otobe⁵, T. Nakamura⁶ (1.Central Lab., NIPPON Corp., 2.HQ, NARO, 3.Western Region Agri. Res. Cent., NARO, 4.Dept. Life and Food Sci., Obihiro Univ. Agri. Vet. Med., 5.Inst. Crop. Sci., NARO, 6.Tohoku Agri. Res. Cent., NARO)

522 Wheat quality related ideotypes to classify Japanese wheat varieties.

○Ikeda, T. (Western Reg. Agr. Res. Ctr., NARO)

523 Isolation of a novel lodging resistance gene *qGF1* involved in strong culm in rice

☆Agata, A.^{1,2}, R. Ishihara², T. Kuroha³, K. Nishitani⁴, Y. Sato¹, H. Sakakibar^{2,5}, M. Ashikari⁶, H. Kitano⁶, T. Hobo⁶ (1.National Institute of Genetics, 2.Grad. Sch. Bioagr. Sci., Nagoya U, 3.Inst. Agrobiological Sci., NARO, 4.Kanagawa U, 5.RIKEN, 6.Biosci. Biotec. Ctr., Nagoya U)

524 Causal relationship among the levels of heterosis at different growing periods and conditions in sugar beet.

Iwahori, R.¹, H. Matsuhira², M. Ohkubo¹, T. Kubo¹, ○K. Kitazaki¹ (1.Hokkaido University Research Faculty of Agriculture, 2.NARO · Hokkaido Agricultural Research Center)

525 Identification of the responsible gene for soybean seed isoflavone QTL, *qMgly-11*.

○Watanabe, S.¹, R. Yamada¹, A. Maeda¹, M. Horitani¹, T. Anai² (1.Fac. Agri., Univ. Saga, 2.Fac. Agri., Univ. Kyushu)

526 Comprehensive genome-wide association study of multi-omics data for soybean drought tolerance

☆Toda, Y.¹, K. Hamazaki¹, M. Okada¹, K. Sakurai¹, Y. Fuji², Y. Omori¹, Y. Yamasaki³, H. Takahashi⁴, H. Takanashi¹, M. Tsuda⁵, H. Kajiya-Kanegae⁶, M. Hirai², H. Tsujimoto³, A. Kaga⁷, M. Nakazono⁴, T. Fujiwara¹, Y. Ichihashi⁸, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Ctr. for Sustainable Resource Sci., RIKEN, 3.Arid Land Res. Ctr., Tottori Univ., 4.Grad. Sch. Bioagri. Sci., Nagoya Univ., 5.T-PIRC, Univ. Tsukuba, 6.Res. Ctr. for Agr. Info. Tech., NARO, 7.Inst. Crop Sci., NARO, 8.BioResource Res. Ctr., RIKEN)

527 Predict genetic variation in drought tolerance of soybean based on a vegetation index and genomic information

☆Sakurai, K.¹, Y. Toda¹, Y. Ohmori¹, Y. Yamasaki², H. Takahashi³, H. Takanashi¹, M. Tsuda⁴, M. Ishimori¹, H. Tsujimoto², A. Kaga⁵, M. Nakazono³, T. Fujiwara¹, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Arid Land Res. Ctr., Tottori Univ., 3.Grad. Sch. Bioagri. Sci., Nagoya Univ., 4.T-PIRC, Univ. Tsukuba, 5.Inst. Crop Sci., NARO)

Poster presentations

P001-A Effects of yield potential evaluation at line selection in rice breeding program.

○Nakaoka, F., A. Kobayashi, S. Watanabe, Y. Machida (Fukui Agr. Exp. Stn.)

P002-B Practical validation of genomic selection for brewing traits in hop breeding

○Shibamura, M.¹, M. Uemoto¹, T. Hoki¹, K. Koie¹, N. Suda¹, H. Iwata² (1.Crop Research Laboratories, SAPPORO BREWERIES LTD., 2.Grad.Sch.Agric.Life.Sci., U.Tokyo)

P003-C Detection of quantitative trait loci for appearance of cooked rice by image analysis

☆Akita, K., H. Ishikawa, M. Hirayama, K. Okano (Plant Biotech. Inst., Ibaraki Agri. Cent.)

P004-A Development of transformation system for tartary buckwheat 2

○Miyahara, K. (Inst. Agrobiological. Sci., NARO)

P005-B Breeding of new variety of [NANKYU WHITE No.2GO] in Miyazaki original vegetable [Itomaki Daikon] using mass selection method

○Chen, L.¹, K. Kumamoto¹, Y. Tanaka², Y. Nakahata², J. Haze² (1.Fac. Environ. Hirt., Minami Kyusyu U., 2.Grad. Sch. Hort. Food Sci., Minami Kyusyu U.)

P006-C Pyramiding *Ba* (blue aleurone) genes to develop darker blue grain wheat: Prospect of nine-dose of *Ba* gene

○Watanabe, N.¹, P. Martinek² (1.The Little Nursery, 2.Agrotest Fyto, Ltd.)

P007-A Phylogenetic analysis of *Cucumis* species inferred from their genome size

☆Nagai, T.¹, G. Shigita², N. Sogo³, O. IMOH¹, K. Tanaka⁴, H. Nishida¹, K. Kato¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.TUM, 3.Fac. Agr., Okayama U., 4.Fac. Agr. Life Sci., Hirosaki U.)

P008-B Toward the establishment of a method for the identification of soybean rhizobium species using the Next Generation Sequencer

☆Sakaguchi, K., T. Tsuchimoto, T. Yoshikawa, M. Teraishi (Grad. Sch. Agri., Kyoto Univ.)

P009-C Improvement of preharvest sprouting resistance with combination of *MOTHER OF FT AND TFL 1* and mutated *ABA 8'-hydroxylase* in white-seeded durum wheat

○Ban, Y.¹, K. Kato¹, M. Ito¹, M. Yanaka^{1,2}, K. Takata^{1,3} (1.Western Region Agr. Res. Cent., NARO, 2.Kyushu Okinawa Agr. Res. Cent., NARO, 3.Obihiro Univ. Agric. Vet. Med.)

P010-A A 75-year history of rice breeding in Fukui, interpreted by traits and whole genome sequences.

○Kobayashi, A.¹, H. Yoshida², Y. Morinaka³, K. Miura³, S. Watanabe¹, Y. Machida¹, F. Nakaoka¹, M. Matsuoka² (1.Fukui Agri. Exp. Stn., 2.Fukushima Univ., 3.Fukui Pref. Univ.)

P011-B Development of DNA marker to distinguish the large deletion of Ccs gene causing non-red fruit color in pepper and its utilization for genotyping

○Sasanuma, T.^{1,2}, S. Ohmori¹, K. Tsurumaki² (1.Fac. Agr., Yamagata Univ., 2.United Grad. Sch. Agr. Sci., Iwate Univ.)

P012-C Development and application of genetic variant catalogs of agronomically important soybean genes based on target resequencing

○Kaga, A.¹, H. Kanamori¹, K. Machita¹, K. Kurita¹, M. Kobayashi¹, K. Fujii¹, A. Kikuchi², K. Komatsu³, Y. Kono⁴, N. Oki⁵, S. Watanabe⁶, M. Ikegami¹, T. Yamada¹, M. Hajika¹ (1.NICS, NARO, 2.TARC, NARO, 3.WARC, NARO, 4.CARC, NARO, 5.KARC, NARO, 6.Univ. Saga)

P013-A Development of novel markers closely linked to Barley yellow mosaic disease-resistance gene *rym3*

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P014-B Development of a marker near the *rym3* gene for resistance to the strain III of the barley yellow mosaic virus.

☆Aoki, H.¹, Y. Nakano¹, M. Seki¹, M. Nakata², G. Ishikawa³, T. Nagamine¹ (1.Central Region Agricultural Research Center, NARO, 2.Kyushu Okinawa Agricultural Research Center, NARO, 3.Institute of Crop Science, NARO)

P015-C How to extract DNA from tissue of crops which contain polyphenol.

Ando, T., ○F. Taguchi-Shiobara (Inst. Crop. Sci., NARO)

P016-A Identification of QTLs associated with pod maturity of adzuki bean (*Vigna angularis*)

☆Kachapila, M.¹, Y. Horiuchi², T. Kodama¹, T. Yoshida¹, K. Kato¹, M. Mori¹ (1.Obihiro Univ. Agr. and Vet. Med., 2.Tokachi Agr. Exp. Sta., HRO)

P017-B QTL analysis for plant architecture traits in adzuki bean (*Vigna angularis*)

○MORI, M.¹, M. Kachapila¹, Y. Horiuchi², H. Nagasawa², N. Michihata¹, T. Yoshida¹, K. Kato¹ (1.Obihiro Univ. Agr. and Vet. Med., 2.Tokachi Agr. Exp. Sta., HRO)

P018-C Identification of *qATL9*, a QTL governing anther length derived from an African wild rice *Oryza longistaminata* A. Chev. & Roehrich

☆Tamakoshi, Y., T. Ogami, H. Yasui, Y. Yamagata (Fac. Agr., Grad. Sch., Kyushu Univ.)

P019-A Genomic regions associated with days to heading under temperate area estimated in hybrid populations of *Oryza glaberrima* Steud.

☆Hirao, A., H. Yasui, Y. Yamagata (Fac. Agr., Grad. Sch., Kyushu Univ.)

P020-B Functional analysis of *FCL* gene in *Trifolium repens* L.

☆Waizumi, H., T. Tamura, Y. Saitoh (Fac.agri.,Univ.Iwate)

P021-C Home-made magnetic beads suspension and magnetic separator for effective, rapid and low-cost purification of dideoxy-sequencing reactions

☆Ikebe, K., H. Sassa (Graduate School of Horticulture, Chiba Univ)

P022-A Genetic analysis of rice early growth using chromosome segment substitution lines.

○Fukui, K., K. Ebana (Genetic Resources Center, NARO)

P023-B Method of chromosome preparation focusing on cell cycle synchronization in the root tips of *Silene latifolia*

☆Kobayashi, T.¹, M. Takahashi², R. Sugiyama³, K. Ishii^{4,5}, S. Kawano^{2,6}, Y. Kazama^{1,5} (1.Fucul. Biosci. Biotech., Fukui Pref. U, 2.Dep. Integ. Biol. Sci., Grad. Sch., Front. Sci., U. Tokyo, 3.Facul. Agri., Tokyo Univ. Agr., 4.NIRS, QST, 5.RIKEN Nishina Cent., 6.Future Center Initiative, U. Tokyo)

P024-C Transcriptome analysis of *Dianthus hybrida* 'Telstar Scarlet' flower buds upon touch stimulation

☆Nishijima, R., S. Alvin, H. Shinoyama, Y. Kazama (Facul. Biosci. Biotech., Fukui Pref. Univ.)

P025-A Trait prediction for the optimal artificial light environment based on the omics approaches

☆Yamashita, H.¹, K. Wada¹, Y. Nakai², N. Inagaki³, Z. Fujimoto³, J. Yonemaru^{1,4}, H. Itoh¹ (1.Inst. Crop. Sci., NARO, 2.Kyushu Okinawa Agr. Res. Cent., NARO, 3.Res. Cent. Adv. Anal. , NARO, 4.Res. Cent. Agr. Info. Tech., NARO)

P026-B Analysis of temporal changes in metabolite accumulation and phytohormone content in wheat during infection process of powdery mildew

☆Sato, Y.^{1,2}, T. Shimazaki², Y. Weng², J. Kim³, K. Nihei¹, M. Okamoto² (1.Sch. Agri., Utsunomiya Univ., 2.Ctr. for Biosci. Res. & Educ., Utsunomiya Univ., 3.RIKEN, CSRS)

P027-C Pyramiding effects of brown planthopper(BPH) resistance genes in rice variety, "Nikomaru".

○Hirabayashi, H.¹, H. Yasui² (1.Inst. of Crop Sci., NARO, 2.Grad. Sch. Agric., Kyushu Univ.)

P028-A Screening of water-saving wheat genotypes from natural mutation populations

☆Mega, R.¹, Y. Yamasaki², H. Tsujimoto² (1.Grad. Sch. Sci. & Tech. for Innovation, Yamaguchi Univ., 2.Arid Land Res. Center, Tottori Univ.)

P029-B Combined heat and drought resilience breeding in bread wheat: alleles, metabolites, and water conservation mechanisms

☆Itam, M., T. Hisashi (Arid Land Research Center, Tottori University)

P030-C Valuation of a QTL for *SOIL SURFACE ROOTING 1* (*qSOR1*) using salinity monitoring in saline paddy fields

○Hanzawa, E.¹, H. Kanno², Y. Oba³, Y. Kitomi⁴, T. Sato², S. Sato¹, Y. Uga⁴ (1.Grad. Sch. LifeSci., Univ. Tohoku, 2.Grad. Sch. Agri. Sci., Univ. Tohoku, 3.Murata. Manufacturing Co., Ltd., 4.Inst. Crop. Sci., NARO)

P031-A Selection of salt tolerant mutants in Tomato

☆Sakamoto, K.¹, T. Yaguchi¹, C. Matsukura² (1.Grad. Sch. Lif., Univ. Tsukuba, 2.T-PIRC, Univ. Tsukuba)

P032-B Evaluation of waterlogging tolerance during germination and the establishment of evaluation method in self-pollinating common buckwheat.

☆Kaminaga, Y.¹, M. Oshima² (1.Grad. Sch. Sci. Tec., Univ. Tsukuba, 2.Fac. Life. Env. Sci., Univ. Tsukuba)

P033-C Comprehensive analysis of metabolites in response to drought stress in wheat

☆Weng, Y.¹, J. Kim², R. Mega³, H. Tsujimoto⁴, M. Okamoto¹ (1.Utsunomiya Univ., 2.RIKEN · CSRS, 3.Yamaguchi Univ., 4.Tottori Univ.)

P034-A Lost robustness in a regulatory mechanism determining epidermal cell identity of leaves from an *Arabidopsis argonaute1* mutant

○Watanabe, A., H. Ando, M. Ohnishi, K. Ueda, K. Sakurai, H. Akagi (Fac. Bioresource Sci., Akita Prefectural Univ.)

P035-B Metabolite profiling for towards the development of heat-tolerant bread wheat

☆Matsunaga, S.¹, Y. Yamasaki², Y. Gorafi³, Y. Toda⁴, H. Tsujimoto^{1,2} (1.United Grad. Sch. Agr. Sci., Tottori Univ., 2.Arid Land Res. Ctr., Tottori Univ., 3.Int. Platform for Dryland Res. and Edu., Tottori Univ., 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P036-C Physiological analysis for selective breeding of heat tolerant on bread wheat

☆Yamasaki, Y.¹, S. Matsunaga², Y. Toda⁴, Y. Gorafi³, H. Tsujimoto¹ (1.Arid Land Research Center, Tottori University, 2.The United Graduated School of Agricultural Sciences, Tottori University, 3.International Platform for Dryland Research and Education, Tottori University, 4.Graduate School of Agricultural and Life Sciences, The University of Tokyo)

P037-A Significance of Transcriptional Co-Activator, MBF1c in Responses to Heat stress during the Reproductive Stages of *Arabidopsis thaliana*

☆Putrawisesa, N., N. Suzuki (Sophia University Graduate School of Science and Technology)

P038-B Yield-related traits of near isogenic lines of rice carrying genes for large or small grains.

☆Aoshima, C.¹, J. Tanaka² (1.NIT, Numazu College, 2.NICS)

P039-C Elucidation of genetic basis of starch content in the storage root of sweetpotato (*Ipomoea batatas*)

☆Haque, E.¹, K. Shirasawa², K. Suematsu¹, H. Tabuchi¹, S. Isobe², M. Tanaka¹
(1.Kyushu Okinawa Agricultural Research Center, NARO, 2.Kazusa DNA Res. Inst., Japan)

P040-A A new phenomenon in dough properties discovered in a bread wheat cultivar "Natsukogane"

○Ikenaga, S.¹, T. Nakamura¹, s. Aono², K. Hayakawa², H. Ito¹, A. Nakamaru¹, T. Takayama¹ (1.Tohoku Agric. res. cent.,NARO, 2.Nisshin Flour Milling Inc.)

P041-B Development of barley mutant with reduced starch and high sugar accumulation

○Matsushima, R.¹, H. Hisano¹, G. Ivan¹, Y. Takenaka², N. Oitome³, T. Ishimizu², N. Fujita³, K. Sato¹ (1.Okayama University, Institute of Plant Science and Resources, 2.Ritsumeikan University, College of Life Sciences, 3.Akita Prefectural University, Faculty of Bioresource Sciences)

P042-C Identification of a gene causing floury endosperm in rice

☆Lin, T., N. Tetsuhiro, K. Toshihiro, K. Takahiko (Grad. Sch.Biores. and Bioenv.Sci., Kyushu University)

P043-A Comparison of first-year and second-year soybean in drained paddy field with heavy clay soil in Hokuriku region.

○Kono, Y. (Cent.Reg.Agr.Res.Ctr.,NARO)

P044-B Exploring the loci derived from wild *Oryza* affecting panicle traits in the genetic background of cultivated rice

☆Hirata, S.¹, A. Agata², T. Hobo³, S. Shimizu-Sato², Y. Sato² (1.Advance course, National Institute of Technology (KOSEN), Numazu College, 2.National Institute of Genetics, 3.Biosci. Biotec. Ctr., Nagoya U)

P045-C Hampered swelling ability of lodicules in the rice cleistogamous mutant, *cls3*

Kimizu, M., T. Kuroha, ○H. Yoshida (Inst. Agrobiological Sci., NARO)

P046-A Analysis of a novel seed-shattering mutant in rice

☆Sakuta, M.¹, R. Ishikawa¹, H. Yasui², Y. Yamagata² (1.Grad. Sch., Agr. Sci., Kobe Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ.)

P047-B Causal gene identification in a short anther mutant of rice

☆Kuroha, T., F. Lombardo, A. Nozaka, S. Chechetka, H. Yoshida (Inst. Agrobiological Sci., NARO)

P048-C *Ppd-1* and *Vrn-1* haplotypes show different effects on heading time depending on the environment in wheat

☆Mizuno, N.¹, H. Matsunaka², M. Yanaka³, M. Nakata³, K. Nakamura³, A. Nakamaru⁴, H. Kiuchi⁵, S. Ohnishi⁵, K. Kawaguchi², G. Ishikawa¹, K. Hatta¹, M. Chono¹, C. Otobe¹, M. Fujita¹, F. Kobayashi¹ (1.NICS, NARO, 2.HARC, NARO, 3.KARC, NARO, 4.TARC, NARO, 5.Kitami Agri. Exp. Stn. HRO)

P049-A CRISPR/Cas9-mediated mutagenesis of *EPHEMERAL1* homolog delays corolla senescence in Japanese gentian

○Takahashi, S.¹, C. Yoshida¹, H. Takahashi², M. Nishihara¹ (1.Iwate Biotechnology Research Center, 2.Liberal Arts Education Center. Tokai Univ.)

P050-B Somatic embryo culture on MS medium containing aluminium in tea plant (*Camellia sinensis*)

☆Ochiai, S.¹, S. Hirata², S. Yonezawa³, T. Ikka⁴, K. Furukawa¹ (1.National Institute of Technology (KOSEN), Numazu College, 2.Advance Course, National Institute of Technology (KOSEN), Numazu College, 3.Grad. Sch. Agr., Univ. Shizuoka, 4.Fac. Agri., Univ. Shizuoka)

P051-C Haplotype analysis of the region surrounding *HLA1*, a gene causing hybrid lethality in interspecific hybrids of *Nicotiana*.

☆Nagai, S.¹, S. Yokoi^{1,2}, T. Tezuka^{1,2} (1.Grad. Sch. Life Envi. Sci., Osaka Pref. Univ., 2.Educ. Res. Field, Col. Life Envi. Adv. Sci., Osaka Pref. Univ.)

P052-A Rare allele of *THB1* causes hybrid breakdown in intra-subspecies *japonica-japonica* hybrids of rice

☆Wakabayashi, T., K. Kato (Obihiro University of Agriculture and Veterinary Medicine)

P053-B Differences in the rates of overcoming hybrid lethality detected in interspecific hybrids of genus *Nicotiana* using *N. tabacum* as pollen parent

☆Inaba, N.¹, K. Nakata¹, W. Marubashi², Y. Shinozaki¹, M. Kanekatsu¹, T. Yamada¹
(1.Grad. Sch. Agr., Tokyo U. Agr. Tech., 2.Fac. Agr., Meiji U.)

P054-C Where did you select the maintainer line? A possible interaction between *Rf1* allele and environmental factor

Matsui, K.¹, H. Matsuhira², Y. Kuroda², K. Kitazaki¹, O.T. Kubo¹ (1.Res. Fac. Agr., Hokkaido Univ., 2.Hokkaido Agr. Res. Ctr., NARO)
