

Title of Papers Presented at the 142nd Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 A *de novo* genome assembly of *Solanum verrucosum* Schlechtendal, a diploid A-genome species of potato relatives

☆Hosaka, A.^{1,2}, R. Sanetomo³, K. Hosaka³ (1.Nihon BioData Corporation, 2.KIBR., Univ. Yokohama-City, 3.Potato Germplasm Enhancement Laboratory, Obihiro University of Agriculture and Veterinary)

102 Isogenic varieties integrated with genes for robust, tiller and yield in Koshihikari.

○Tomita, M., Y. Taketani, H. Mori (Res. Inst. Green Sci. Technol., Shizuoka Univ.)

103 Molecular Phylogenetics of melon based on diversity analysis of chloroplast genome

☆Sogo, N.¹, M. Okuma¹, O. IMO¹, T. Nagai¹, T. Seiko², C. Muto², K. Naito², Y. Monden¹, M. Sugiyama³, G. Shigita⁴, K. Tanaka⁵, H. Nishida¹, Y. Kawazu³, N. Tomooka², K. Kato¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Genetic Resources Center, NARO, 3.Inst. Vegetable & Floriculture Sci., NARO, 4.TUM, 5.Fac. Agr. Life Sci., Hirosaki U.)

104 Evaluation of genetic diversity and population structure in the tetraploid wheat accessions ex situ conserved in NBRP-Wheat for development of a core collection

☆Su, Z.¹, S. Takenaka², M. Kakitani¹, M. Nitta¹, S. Nasuda¹ (1.Grad. Sch. Agr., Kyoto Univ., 2.Fac. Agr., Ryukoku Univ.)

105 Analysis of the origin of Japanese Moso bamboo

☆Nishiyama, N.¹, T. Matsumoto², A. Shinozawa^{2,3}, T. Izawa¹ (1.Grad.Sch.Agric.Life Sci., U.Tokyo, 2.Dept Bioscience, Tokyo Univ. Agric., 3.NODAI Genome Research Center, Tokyo Univ. Agric.)

106 Telomere-to-telomere assembly of the matsutake genome

○ Shirasawa, K.¹, H. Kurokochi², N. Tajima¹, M. Sato¹, K. Yoshitake², S. Asakawa², S. Isobe¹ (1.Kazusa DNA Res. Inst., 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

107 Genes underlying the unique salt tolerant mechanism of *Vigna luteola*

☆ Iki, Y.¹, K. Ito¹, F. Wang², T. Wakatake², K. Naito² (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO)

108 Targeted C to T base editing in ATP synthases-related genes in the mitochondria genome of *Arabidopsis thaliana*

☆ Zhou, C.¹, I. Nakazato¹, Y. Tamura¹, N. Tsutsumi¹, M. Takenaka², S. Arimura¹ (1.Grad. Agri., Univ. Tokyo, 2.Grad. Sci., Univ. Kyoto)

109 A machine-learning approach to validate mutations detected by whole-genome sequencing

☆ Ichida, H., N. Lei, R. Morita, T. Abe (RIKEN Nishina Center)

110 Identification of QTLs controlling glume-related traits in sorghum

☆ Makino, A., M. Ishimori, K. Yamazaki, T. Fujiwara, H. Iwata, N. Tsutsumi, H. Takanashi (Grad. Sch. Agric. Life Sci., Univ. Tokyo)

111 Genetic analysis of agronomic traits in progeny of fertile tetraploid hybrids between *O. sativa* and *O. glaberrima*

☆ Oka, T.¹, T. Furuta¹, K. Kashihara¹, Y. Kishima², T. Yamamoto¹ (1.Inst. Plant Sci. & Res., Okayama Univ., 2.Grad. Sch. Agr., Hokkaido Univ.)

112 Extremely early heading QTL of rice *indica* variety 'Kasalath' in sBBS environment

○ Tanaka, J., N. Tanaka, Y. Taniguchi, H. Itoh (NICS/NARO)

113 Identification of chromosome 1 region associated with variation in γ-oryzanol content using population derived from rice chromosome segment substitution line

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

114 Evaluation of novel loci involved in non-seed-shattering behaviour of *indica* rice cultivar, 'IR36'

☆Sakuta, M., S. Sugiyama, Y. Tsujimura, T. Htun, C. Inoue, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

115 Characterization of the QTL on chromosome 7AL improving both of two yield components grain number and grain weight in tetraploid wheat (*Triticum turgidum* L.)

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

116 Development of "degenerate oligonucleotide primer MIG-seq", an improved method of MIG-seq, and its application to crop genetic analysis

☆Nishimura, K.¹, H. Kokaji¹, K. Motoki¹, A. Yamazaki², K. Nagasaka¹, R. Takisawa³, Y. Yasui¹, T. Kawai⁴, K. Ushijima⁴, M. Yamasaki⁵, H. Saito⁶, R. Nakano¹, T. Nakazaki¹ (1.Grad. Sch. Agr., Kyoto Univ., 2.Fac. Agr., Kindai Univ., 3.Fac. Agr., Ryukoku Univ., 4.Grad. Sch. Environ. Life Sci., Okayama Univ., 5.Grad. Sch. Sci. and Tech., Niigata Univ., 6.JIRCAS)

117 Identification of QTLs controlling the resistance to multiple races of southern root-knot nematode and development of DNA markers for resistance selection

☆Kurihara, M.¹, H. Tabuchi², K. Shirasawa³, S. Isobe³, H. Nishida¹, K. Kato¹, Y. Monden¹ (1.Grad. Sch. Env. & Life Sci., Okayama Univ., 2.KARC/NARO, 3.Kazusa DNA Res. Inst.)

118 Sequence mutations in the *cis*-regulatory elements of a candidate gene controlling southern root knot nematode resistance in sweetpotato

☆Izumitani, M.¹, S. Ohata¹, H. Tabuchi², H. Nishida¹, K. Kato¹, Y. Monden¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.KARC/NARO)

119 Prediction of seed yield using historical data of soybean breeding in Japan

○Yamada, T.¹, A. Onogi², J. Yonemaru¹ (1.Institute of Crop Science, NARO, 2.Faculty of Agriculture, Ryukoku University)

120 Development of knowledge-graph-based trait prediction method

○Kajiya-Kanegae, H.¹, G. Kikui¹, K. Matsushita², M. Yano¹, T. Hayashi¹, J. Yonemaru^{1,2} (1.RCAIT, NARO, 2.Inst. Crop. Sci., NARO)

121 Improvement of Plant GARDEN, a portal site for plant genome information (2022, Q2 ver)

○Ichihara, H.¹, H. Hirakawa¹, M. Yamada¹, M. Kohara¹, S. Yamashita¹, S. Shirasawa¹, Y. Toda¹, Y. Nakamura^{1,2}, T. Tanabata¹, S. Tabata¹, S. Isobe¹ (1.Kazusa DNA Res. Inst., 2.Nat. Inst. Genet.)

122 Mi-GARDEN : A platform for comparison of user's genome sequence data and reference genomes in plants

○Isobe, S.¹, K. Horiguchi², M. Yamada¹, T. Misawa², Y. Nakamura³, H. Ichihara¹, M. Kohara¹, H. Hirakawa¹ (1.Kazusa DNA Res. Inst., 2.ANPLAT Co., Ltd., 3.Nat. Inst. Genet.)

123 Estimating genetic correlation between traits and environments based on the analysis of high-dimensional • multi-environmental multiomics data

☆Sakurai, K.¹, Y. Toda¹, Y. Fuji², Y. Ohmori¹, Y. Yamasaki³, H. Takahashi⁴, H. Takanashi¹, M. Tsuda⁵, M. Hirai², H. Tsujimoto³, M. Nakazono⁴, T. Fujiwara¹, A. Kaga⁶, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.RIKEN Ctr. for Sustainable Sci., 3.Arid Land Res. Ctr., Tottori Univ., 4.Grad. Sch. Bioagri. Sci., Nagoya Univ., 5.T-PIRC, Univ. Tsukuba, 6.Inst. Crop Sci., NARO)

124 A method for clustering high-dimensional microbiome data and selecting representative microbial species

☆Dang, T., H. Iwata (Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan)

125 Modeling of plant-microbe interactions using multi-omics data

☆Yoshioka, H.¹, Y. Toda¹, Y. Fuji², Y. Ohmori¹, Y. Ichihashi⁷, E. Usui⁷, K. Kumaishi⁷, T. Satou⁷, S. Kobori⁷, A. Kaga³, Y. Yamasaki⁴, H. Takahashi⁵, H. Takanashi¹, M. Tsuda⁶, M. Ishimori¹, H. Tsujimoto⁴, M. Nakazono⁵, M. Hirai², T. Fujiwara¹, H. Iwata¹ (1.Grad. Sch. Agr. Life. Sci., Univ. Tokyo, 2.RIKEN Ctr. for Sustainable Sci., 3.Inst. Crop Sci., NARO, 4.Arid Land Res. Ctr., Tottori Univ., 5.Grad. Sch. Bioagri. Sci., Nagoya Univ., 6.T-PIRC, Univ. Tsukuba, 7.RIKEN BioResource Res. Ctr.)

201 Progress in recurrent selection of soybean in Hokkaido, northern Japan

○Yamaguchi, N.¹, H. Igarashi², C. Souma¹, A. Kaga³ (1.Central Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO, 3.Inst. Crop. Sci., NARO)

202 Cowpea speed breeding using regulated growth chamber conditions and seeds of oven-dried immature pods potentially accommodates eight generations per year

☆Edet, O., T. Ishii (Arid Land Research Center, Tottori University)

203 Genetic architecture of heat tolerance in *Solanum lycopersicum*: identifying QTL of reproductive traits under heat stress using a MAGIC population

☆Lin, Y.¹, Y. Hsu¹, L. Hsu^{2,3}, H. Khazaei¹, J. Yen¹, C. Lin¹, K. Hoshikawa^{1,4}, R. Schafleitner¹, P. Hanson¹ (1.World Vegetable Center, Headquarters, 2.Tainan District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan, Taiwan, 3.Taoyuan District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan, Taiwan, 4.Japan International Research Center for Agricultural Sciences, Biological Resources and Post-harvest Division)

204 Historical data reveals characterisitics in rice varieties bred at NARO

○Yonemaru, J.¹, K. Matsushita^{1,2}, H. Kajiya-Kanegae², A. Onogi^{2,3} (1.Inst. Crop. Sci., NARO, 2.RCAIT, NARO, 3.Faculty of Agr., Ryukoku Univ.)

205 Genome editing of *CAD* gene involved in lignin biosynthesis in bahiagrass (*Paspalum notatum*). – Production of genome edited plants and its evaluation –

○Gondo, T.¹, A. Watajima², R. Akashi² (1.FSRC, Univ. Miyazaki, 2.Agr., Univ. Miyazaki)

206 Establishment of transformation system and genome editing for the development of evergreen variety in *Zoysia matrella*

☆Ng, H.¹, M. Ushiyama², H. Taniguchi², M. Hirata², T. Gondo³, R. Akashi² (1.Grad. Sch. Agr. & Engr., Univ. Miyazaki, 2.Fac. of Agr., Univ. Miyazaki, 3.Frontier Science Research Center, Univ. Miyazaki)

207 Correlation between NDVI and leaf color information extracted from 3D model in zoysiagrass

☆Pongpiyapaiboon, S.¹, H. Tanaka², T. Hashiguchi³, M. Hashiguchi³, R. Akashi⁴ (1.Graduate School of Agriculture, University of Miyazaki, 2.Faculty of Agriculture, University of Miyazaki, 3.Faculty of Regional Innovation, University of Miyazaki, 4.University of Miyazaki)

208 Optimum Ethylmethane Sulfonate (EMS) treatment method for mutagenesis in groundnut (*Arachis hypogea* L.)

☆Hirose, W., B. Pachakil, K. Irie, H. Shiwachi (Tokyo university of agriculture)

209 Error prone elimination via comparative genomic information in next generation sequencing based genotyping

☆Furuta, T.¹, T. Toriba², Y. Kishima³, T. Yamamoto¹ (1.Inst. Plant Sci. & Res., Okayama Univ., 2.Grad. Sch. Food Agr. & Env. Sci., Miyagi Univ., 3.Res. Fac. Agr., Hokkaido Univ.)

210 Evaluation of genomic prediction methods for rice crossed progenies using simulated phenotypic values.

☆Taniguchi, S.¹, T. Hayashi¹, H. Kajiya-Kanegae¹, K. Matsushita², M. Yano¹, J. Yonemaru^{1,2}, A. Goto^{1,2} (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)

211 Development of individual tree-based phenotyping methods for larchs using LiDAR remote sensing

☆Sano, H.¹, Y. Unno², W. Guo¹, N. Miura¹, K. Kusunoki², H. Ito², H. Iwata¹ (1.Grad. Sch. Agri., Univ. Tokyo, 2.Sumitomo Forestry Co., Ltd.)

212 Proposal of a quantitative evaluation method for morphological variation of strawberry fruit tip and calyx

☆Nagamatsu, S.¹, T. Shimoda¹, A. Hayashi², T. Tanabata³, S. Isobe³ (1.Fukuoka Agriculture and Forestry Research Center, 2.Research Center for Agricultural Robotics, NARO, 3.Kazusa DNA Research Institute)

213 Predicting phenotypes using IBS/IBD-based genomic relationship and pedigree-based numerator relationship matrices.

☆Mochizuki, H.¹, M. Minamikawa^{1,2}, K. Hamazaki¹, M. Kunihisa³, S. Moriya³, K. Abe³, H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ., 2.IAAR, Chiba Univ., 3.NIFTS, NARO)

214 Prediction of phenotypic values of the world rice core collection based on genome and transcriptome

○Tanaka, R.¹, S. Yabe¹, T. Kawakatsu², N. Tanaka¹, M. Shenton¹, Y. Uga¹ (1.Institute of Crop Science, NARO, 2.The Institute of Agrobiological Sciences, NARO)

215 Using multi-omics data as an intermediate phenotype to improve the accuracy of genomic prediction

○Iwata, H.¹, 悠. 戸田¹, ユ. フジ², Y. Ohmori¹, Y. Yamasaki³, H. Takahashi⁴, H. Takanashi¹, M. Tsuda⁵, H. Kanegae¹, M. Hirai², Y. Ichihashi⁶, H. Tsujimoto³, A. Kaga⁷, M. Nakazono⁴, T. Fujiwara¹ (1.Graduate School of Agricultural and Life Sciences., Univ. Tokyo, 2.Center for Sustainable Resource Science, RIKEN, 3.Arid Land Research Center, Tottori Univ., 4.Graduate School of Bioagricultural Sciences, Nagoya Univ., 5.Faculty of Life Environmental Sciences, Univ. Tsukuba, 6.BioResource Research Center, RIKEN, 7.Institute of Crop Science, NARO)

216 Genomic prediction for quality-related metabolites in tea accessions

☆Ishiguro, Y.¹, H. Yamashita^{2,5}, T. Uchida¹, J. Kawaki³, H. Katai³, A. Nagano⁴, A. Morita^{2,5}, T. Ikka^{2,5,6} (1.Grad. Agr., Univ. Shizuoka, 2.Fac. Agr., Univ. Shizuoka, 3.Shizuoka Tea Res. Cent., 4.Fac. Agr., Univ. Ryukoku, 5.Shizuoka Univ. Res. Inst. Tea Sci., 6.Shizuoka Univ. Res. Inst. Green Sci. Tech.)

217 Future-oriented mating strategy via simulations optimizes breeding programs with selection indices

☆Hamazaki, K., H. Iwata (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

218 Genomic prediction using rice NAM population and its application to genomic breeding strategy

☆Sakai, T.¹, R. Terauchi^{1,2}, A. Abe² (1.Grad. Sch. Agri., Univ. Kyoto, 2.IBRC)

219 Development of technology for quantification of lotus (*Nelumbo nucifera*) growth

☆Kubota, C.¹, S. Shibata², T. Nakata², I. Takata², S. Nishiuchi² (1.Sch. Agr. Sci., Nagoya Univ., 2.Grad. Sch. Bioagri. Sci., Nagoya Univ.)

220 Acquisition of phenotypes related to cabbage uniformity using UAV

☆Takata, I., N. Kobayashi, T. Nakata, S. Shibata, S. Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)

221 Mapping of rice voluntaries using UAV imagery and object detection method

☆Shibata, S., K. Doi, S. Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)

222 Development of a UAV-based lodging evaluation method in soybean

○Kaga, A.¹, A. Fukuda¹, W. Guo² (1.NICS, NARO, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

223 Development of infiel soybean seed counting and localization method

Zhao, J.¹, A. Kaga², M. Hirafuji¹, S. Ninomiya¹, T. Yamada², K. Komatsu³, K. Hirata⁴, A. Kikuchi⁴, ○G. Wei¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NICS, NARO, 3.WARC, NARO, 4.TARC, NARO)

224 Development of a method for selecting superior strains of *Racomitrium japonicum*

☆Yakou, H.¹, Y. Takahara² (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering, Nagaoka University of Technology)

301 Development and characterization of pyramiding lines for brown planthopper resistance genes on the genetic background of *japonica* rice variety, Sagabiyori

☆Day Shar, S.¹, D. Nguyen², S. Zheng², D. Fujita² (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ.)

302 Estimation and characterization of brown planthopper resistance gene from *Oryza glaberrima*

☆Baba, K.¹, Y. Yamagata², H. Yasui², S. Zheng³, D. Fujita³ (1.Grad. Sch. Fac. Agr., Saga Univ., 2.Grad. Sch. Fac. Agr., Kyusyu Univ., 3.Fac. Agr., Saga Univ.)

303 Characterization of near-isogenic lines and pyramided lines for brown planthopper resistance genes on the genetic background of *indica* rice variety 'IR64'

☆Kamal, M.^{1,3}, D. Nguyen², S. Zheng², D. Fujita² (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ., 3.Agrotech. Disc., Khulna Univ.)

304 RNA-seq analysis associated with Cd low accumulation in wheat.

☆Seto, S.¹, Y. Ban², N. Mizuno³, K. Kato², F. Kobayashi³, y. Hyuga¹, H. Handa⁴ (1.Fac. Life Envi. Sci., Kyoto Pref. Univ., 2.WARC, NARO, 3.NICS, NARO, 4.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ.)

305 Evaluation of Japanese wheat accessions for resistance to wheat blast in the field

○Handa, H.¹, S. Asuke², K. Roy³, M. Kishii⁴, M. Kabir³, Y. Tosa², P. Singh⁴ (1.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ., 2.Grad. Sch. Agri. Sci., Kobe Univ., 3.BWMRI, Bangladesh, 4.CIMMYT)

306 Exploring the novel gene for defensive trichome formation in tomato

○Sugimoto, K., Y. Fujimori, H. Ezura (Univ. Tsukuba, T-PIRC)

307 Isolation of rice blast resistance gene *Pias* and blast fungus gene *AVR-Pias* recognized by *Pias*.

○Shimizu, M.¹, Y. Sugihara², N. Miyaji¹, A. Abe¹, R. Terauchi^{1,2} (1.Iwate Biotech. Res. Center, 2.Grad. Sch. Agr., Univ. Kyoto)

308 Understanding coexistence strategy with *Plasmodiophora brassicae* in a radish cultivar 'Shogoin'

☆Ogura, T., T. Ohnishi, S. Bang (Sch. Agric., Utsunomiya. Univ.)

309 Identification of Quantitative Trait Loci responsible for *Fusarium oxysporum* disease resistance in *Raphanus sativus*

☆Ezeah, C.^{1,4}, J. Shimazu², S. Kawashima², M. Kaji³, T. Kawanabe⁵, E. Fukai⁴, K. Okazaki⁴ (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Nanto Seed Co. Ltd., 3.Watanabe Seed Co. Ltd., 4.Nigeria Federal Ministry of Agriculture and Rural Development, 5.Fac. Agric. Tokai Uni.)

310 Evaluation of salt tolerance in heterosis of *Arabidopsis thaliana*

☆Kamiya, Y., H. Mehraj, T. Yasuda, R. Fujimoto (Grad. Sch. Agric. Sci., Kobe Univ.)

311 Searching for reduced-soil stress tolerance genes using *Oryza glumaepatula* introgression lines

○Shiono, K.¹, M. Ejiri¹, T. Miyashita¹, Y. Uga² (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.Inst. Crop Sci., NARO)

312 Analysis of waterlogging tolerance in the field using five wheat varieties

☆Yamada, T.¹, S. Atumi¹, M. Arakawa², S. Ota², A. Itou², H. Takahashi¹, M. Nakazono¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Aichi Agric. Res. Cent.)

313 Control of heading dates by low-temperature and its relationship with photosensitive genes.

☆Takatori, M.¹, S. Sakaguchi¹, Y. Koide², K. Fujino³, Y. Kishima² (1.Graduate School of Agriculture, Hokkaido University, 2.Research Faculty of Agriculture, Hokkaido University, 3.National Agriculture and Food Research Organization, NARO)

314 Identification of a QTL, *qSG11* causing pollen and spikelet sterility in an interspecific cross between *Oryza sativa* L. and *O. glumaepatula* Steud.

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

315 Construction of foundation seeds producing system in Toyama Prefectural Agricultural Research Institute

○Kojima, Y.¹, K. Murata¹, G. Mimuro¹, Y. Muraoka² (1.Toyama Agr. Fores. Fish. Res. Cent., 2.Toyama Agr. Fores. Prom. Cent., Tonami)

316 Mapping of a novel fertility restorer gene from an indica cultivar Samba Mahsuri for CW-type cytoplasmic male sterility in rice

☆Inada, Y.¹, A. Takatuka¹, H. Ichida², K. Toriyama¹ (1.Grad. Sch. Agri., Univ. Tohoku, 2.RIKEN Nishina center)

317 Examining the reproductive organ induction conditions of *Racomitrium japonicum*

○Ozaki, y.¹, Y. Takahara² (1.Grad. Sch. Department of Bioengineering, Nagoya University of Technology, 2.Department of Materials Science and Engineering)

318 Detection of meiotic abnormality in interspecific hybrids between Asian and African rice species by immunostaining method

☆Ishihara, M.¹, D. Kuniyoshi², Y. Koide³, K. Nagaki⁴, Y. Kishima³ (1.Graduate School of Agriculture, Hokkaido University, 2.Tropical Agriculture Research Front, JIRCAS, 3.Research Faculty of Agriculture, Hokkaido University, 4.Institute of Plant Science and Resources, Okayama University)

319 Ca²⁺ imaging inside pollen of cytoplasmic male sterile tomato

☆Kuwabara, K.¹, T. Ariizumi² (1.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 2.Fac. Life Env. Sci., Univ. Tsukuba)

320 Internal structure analysis of anthers of G-type cytoplasmic male sterility in sugar beet.

☆Katsura, N.¹, K. Itoh¹, H. Matsuhira², Y. Kuroda², K. Kitazaki¹, T. Kubo¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)

321 Search for the genes responsible for fertility restoration of cytoplasmic male sterility derived from *Oryza sativa* cv. Tadukan

☆Takatsuka, A.¹, T. Kazama², H. Ichida³, T. Abe³, K. Toriyama¹ (1.Grad. Sch. Agri. Sci., Univ. Tohoku, 2.Grad. Sch. Agri., Univ. Kyushu, 3.RIKEN Nishina center)

322 Complementation tests and transcriptome analysis of *REDUCED POLLEN NUMBER1* in *Arabidopsis thaliana*

○Kakui, H.^{1,2}, T. Tsuchimatsu³, M. Yamazaki², K. Shimizu^{2,4} (1.Grad. Sch. Agr., Kyoto Univ., 2.Dept. Evo. Biol. Env. Studies, U. Zurich, 3.Grad. Sch. Sci., Univ. Tokyo, 4.Kihara Inst. Biol. Res., Yokohama City Univ.)

323 Phenotyping of pollen-related traits and genome-wide association study in the tetraploid wheat core collection.

☆Kojima, H.¹, H. Kakui², T. Yoshikawa², Z. Su², S. Nasuda² (1.Fac. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Kyoto Univ.)

401 CRISPR/Cas9-Mediated Genome Editing of *RsGL1a* and *RsGL1b* in Radish (*Raphanus sativus* L.)

☆Muto, N., T. Matsumoto (Tokyo University of Agriculture, Graduate School of Agriculture)

402 Development of the k-mer based analytical method for foreign DNA detection in genome-edited organisms

○Sakai, H.¹, T. Itoh², R. Onuki³, M. Endo⁴, M. Tsuda⁵, S. Yasumoto⁶, Y. Tabei⁷ (1.NAAC, NARO, 2.National Taiwan Univ., 3.Saitama Pref. Canc. Cent., 4.NIAS, NARO, 5.T-PIRC, Univ. Tsukuba, 6.Grad. Sch. Eng., Osaka Univ., 7.Fac. Food Nutr. Sci., Toyo Univ.)

403 Creation of genome-edited potato mutants with novel starch properties

○Shimada, H.¹, A. Takeuchi¹, K. Asano², T. Noda², H. Kusano¹, M. Ohnuma¹, H. Teramura¹, T. Asahi¹, Y. Okubo¹, Y. Akatsu¹, K. Ito¹, K. Hamada¹, A. Hokura³ (1.Dept.

404 Trials of modifying and developing the method for target base editing of chloroplast genomes using TALECD

☆Nakazato, I., N. Tsutsumi, S. Arimura (Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo)

405 Genome-wide association analysis for the eggplant fruit shape

Shimada, K.^{1,2}, ○H. Takahashi³, K. Miyatake⁴, K. Sakurai¹ (1.Fac. Biores. Sci., Akita Pref. Univ., 2.Grad. Sch. Arts Sci., Iwate Univ., 3.Fac. Food Agri. Sci., Fukushima Univ., 4.Inst. Vege. Floricult. Sci., NARO)

406 Searching for pearl millet genes associating agricultural traits by analyzing genetic variations

☆Kambara, K., D. Tsugama, T. Takano (Grad.Sch.Agr., Univ. Tokyo)

407 GWAS on rice seed storage protein content using wild and cultivated species

☆Kurokawa, Y.¹, R. Funakoshi², E. Kimoto¹, K. Matsumiya¹, Y. Sato³, T. Yoshikawa¹ (1.Grad. Sch. Agri., Kyoto Univ., 2.Fac. Agri., Kyoto Univ., 3.National Institute of Genetics)

408 Dissection of the genetic architecture for soybean seed weight by GWAS and validation using RIL populations

○Li, F.¹, R. Takeshima¹, S. Kato¹, R. Yano², S. Matthew¹, S. Hiraga¹, A. Kaga¹, M. Hajika¹, M. Ishimoto¹ (1.Institute of Crop Sciences, NARO, 2.The Research Center for Advanced Analysis, NARO)

409 Validation of effectiveness using genomic selection and genome-wide association study in selection of strawberry breeding

○Kashiwaya, Y.¹, A. Toyoda¹, T. Abe¹, Y. Nakazawa¹, S. Yasuno¹, Y. Matsushima¹, T. Shigeno¹, S. Isobe², K. Shirasawa², M. Sato², E. Yamamoto³, K. Iimura^{1,4}, K. Tasaki^{1,5} (1.Tochigi Pref. Agric. Exp. Stn., 2.Kazusa DNA Res. Inst., 3.Grad. Agri. Sci. Meiji Univ., 4.Shimotsuga Agricultural Promotion Office, 5.Agricultural Management Division)

410 Development of KASP marker that efficiently discriminate male sterility of cultivated strawberry

☆MONDEN, H. (Fukuoka Agric. Forest. Res. Cent.)

411 Mutagenesis in rice by neutron irradiation on seed using J-PARC facility

☆Kojima, K.¹, K. Ishibasi², K. Oikawa⁵, H. Katsuyama¹, N. Kikuchi², T. Kohzuma³, M. Harada⁵, A. Hoshikawa⁴, T. Kuboyama¹ (1.Col. Agr., Ibaraki U., 2.QFF, 3.Col. Sci., Ibaraki U., 4.iFRC,Ibaraki U., 5.JAEA)

412 Origins and convergent evolutions in molecular pathways of climacteric fruit ripening.

☆Kuwada, E.¹, T. Akagi^{1,2} (1.Grad. Sch. Environ. & Life Sci., Okayama Univ., 2.JST-PRESTO)

413 Variety differentiation in hexaploid persimmon, with a wide fruit shape diversity

☆Horiuchi, A.¹, K. Masuda^{1,2}, N. Onoue³, R. Matsuzaki³, K. Shirasawa⁴, Y. Kubo¹, K. Ushijima¹, T. Akagi¹ (1.Grad. Sch. Environ. LifeSci., Okayama Univ., 2.Grad. Sch. Agri. LifeSci., Univ. Tokyo, 3.Inst. Fruit Tree and Tea Sci., NARO, 4.Kazusa DNA Res. Inst.)

414 Analysis of *Phalaenopsis* blue flower color gene

☆Igarashi, T.¹, Y. Takahara² (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering)

415 Chromosome structural changes during fruit set in tomato

☆Suzuki, H.¹, K. Ezura², Y. Okabe², R. Yano^{2,3}, K. Shirasawa⁴, H. Ezura², T. Ariizumi² (1.Graduate School of Life and Environmental Sciences, University of Tsukuba, 2.Faculty of Life and Environmental Sciences, University of Tsukuba, 3.NARO, 4.Kazusa DNA Research Institute)

416 Molecular Mechanisms of Inducible Aerenchyma Formation by ROS and Ca²⁺ Signaling in rice

☆Li, J.¹, T. Ishii¹, M. Yoshioka¹, H. Yoshioka¹, H. Takahashi¹, T. Yamauchi², M. Nakazono¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Biosci. Biotech. Ctr., Nagoya Univ.)

417 Genes involved in anthocyanin biosynthesis pathway and transcriptional regulatory networks underlying anther pigmentation in petunia

☆Yuhazu, M., R. Hara, A. Kanazawa (Res. Fac., Hokkaido Univ.)

418 Expression analysis of the genes altered by targeted mutations of grain dormancy genes in barley

○Hisano, H., H. Munemori, K. Sato (IPSR, Okayama Univ.)

419 Mutagenesis of Potato Polyphenol Oxidase and Vacuolar Invertase Genes by CRISPR-Cas9 System

☆Tanaka, H.¹, A. Endo¹, S. Yasumoto², H. Sasaki³, T. Igarashi³, N. Umemoto⁴, T. Muranaka², M. Mori³, T. Yamada¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.Grad. Sch. Eng., Univ. Osaka, 3.Calbee Potato,Inc., 4.CSRS, RIKEN)

420 Targeted base editing in *Arabidopsis* nuclear genes via DNA recognition by TALE domain

☆Hosoda, A.¹, I. Nakazato¹, M. Okuno², T. Ito³, H. Takanashi¹, N. Tsutsumi¹, S. Arimura¹ (1.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 2.Sch. of Med., Kurume Univ., 3.Sch. of Life Sci. and Tech., Tokyo Institute of Tech.)

421 Genome editing for nuclear and organelle genes in *Brassicaceae*

○Koizuka, N.¹, I. Nakazato², A. Okuzaki¹, S. Arimura² (1.Col. Agr., Tamagawa Univ., 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

422 Widespread LTR retrotransposon activation in inter- and intra-species recombinant inbred populations of *Lotus japonicus*

○Fukai, E.^{1,2,3,4,5}, M. Yoshikawa², N. Shah³, N. Sandal³, A. Miyao², S. Ono⁴, H. Hirakawa⁵, T. Akyol³, Y. Umehara², K. Nonomura⁴, J. Stougaard³, H. Hirochika², M. Hayashi^{2,6}, S. Sato^{5,7}, S. Andersen³, K. Okazaki¹ (1.Niigata Univ, 2.National Agriculture and Food Research Organization, 3.Aarhus University, 4.National Institute of Genetics, 5.Kazusa DNA Research Institute, 6.RIKEN, 7.Tohoku University)

423 Substitution mapping and characterization of stable QTLs for vascular bundle number at panicle neck in rice (*Oryza sativa* L.)

☆Nguyen, T.^{1,2}, S. Zheng², D. Fujita² (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ.)

424 Developmemt of gluten-forming barley I. Gluten formation using a mutant fund in genetic resources.

○Ikeda, T.¹, M. Seki², T. Nagamine², Y. Nakano², D. Tezuka³, R. Imai³ (1.Western Reg. Agr. Res. Ctr., NARO, 2.Central Reg. Agr. Res. Ctr., NARO, 3.Inst. Agrobiol. Sci., NARO)

425 Development of gluten-forming barley II . Creation of hordein with glutenin-like structure by genome editing

☆Tezuka, D.¹, T. Ikeda², M. Seki³, T. Nagamine³, Y. Nakano³, R. Imai¹ (1.Institute of Agrobiological Sciences, NARO, 2.Western Region Agricultural Research Center, NARO, 3.Central Region Agricultural Research Center, NARO)

501 Genome-wide association study on irregulare inflorescence in Barley

☆Morita, M., K. Sato (IPSR, Okayama Univ.)

502 Interspecific variation and genome wild association analysis for heat stress tolerance adaptation in wild emmer wheat

☆Balla, M.¹, Y. Gorafi^{1,2}, N. Kamal^{1,2}, M. Abdalla³, I. Tahir³, H. Tsujimoto² (1.United Grad. Sch., Tottori Univ., 2.Arid Land Research Center, Tottori Univ., 3.Agricultural Research Corporation, Sudan)

503 Variation of prolamin and prolamin gene family among green foxtail (*Setaria viridis*) accessions in Japan

Nagata, T.¹, M. Numamoto², T. Masumura¹, A. Nagano^{3,4}, Y. Yasui⁵, ○T. Ohsako¹ (1.Grad. Sch. Life Env. Sci., Kyoto Pref. Univ., 2.Fac. Agr., Setsunan Univ., 3.Fac. Agr., Ryokoku Univ., 4.Inst. Adv. Biosci., Keio Univ., 5.Grad. Sch. Agr., Kyoto Univ.)

504 Amadokoro, As a New Crop (Vegetable)

○Takada, H. (NARO Fellow)

505 3D analysis of wild rice architecture using photogrammetry

☆Tokuyama, Y.¹, S. Kushida², K. Hikichi¹, Y. Kishima³, Y. Koide³ (1.Graduate School of Agriculture, Hokkaido University, 2.School of Agriculture, Hokkaido University, 3.Research

506 Time-series 3D analysis of tiller rotation around the apical-basal axis in wild rice

☆Kushida, S.¹, Y. Tokuyama², Y. Kishima³, Y. Koide³ (1.School of Agriculture, Hokkaido University, 2.Graduate School of Agriculture, Hokkaido University, 3.Research Faculty of Agriculture, Hokkaido University)

507 Variation of seed-shattering degree in African cultivated rice, *Oryza glaberrima*

☆Yamazaki, M.¹, A. Maeda¹, S. Lim¹, T. Ishii¹, Y. Yamagata², Y. Koide³, D. Fujita⁴, R. Ishikawa¹ (1.Grad. Sch., Agr. Sci., Kobe Univ., 2.Fac. Agr. Grad. Sch., Kyushu Univ., 3.Grad. Sch. Agr., Hokkaido Univ., 4.Fac. Agr., Saga Univ.)

508 On the possibility of introgression involved in garden beet domestication.

☆Hayakawa, R.¹, Y. Kanomata¹, E. Taniguchi¹, H. Matsuhira², Y. Kuroda², K. Kitazaki¹, T. Kubo¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)

509 Establishment of a non-destructive evaluation method for root zone elongation of cowpea (*Vigna unguiculata* L. Walp.) in Tottori sandy field

○Ubi, B.^{1,2}, T. Ishii¹ (1.Molecular Breeding Laboratory, Arid Land Research Center, Tottori University, 1390 Hamasaki, Tottori 680 – 0001, Japan, 2.Department of Biotechnology, Ebonyi State University, PMB 053 Abakaliki, Nigeria)

510 Development of a workflow for efficient DNA mutation detection in a radish (*Raphanus sativus* L.) mutant population

Hoshikawa, Y., A. Tian, S. Miyashita, J. Ji, M. Yamamoto, ○H. Kitashiba (Grad. Sch. Agric. Sci., Tohoku Univ.)

511 A new new high-yield, good-tasting rice cultivar for export "Etsunan 305".

☆Nakaoka, F., A. Kobayashi, K. Tomita, Y. Machida, T. Hayashi, M. Tanoi, T. Shimizu, Y. Morozumi, S. Watanabe, K. Sakai, K. Watanabe, Y. Sato, N. Sato (Fukui Agri. Exp. Stn.)

512 A new rice variety, 'Shinfuku 1', which contains about three times as much dietary fiber in white rice as 'Koshihikari'.

○Kobayashi, A.¹, M. Nishimura^{2,3}, F. Nakaoka¹, K. Tomita¹, Y. Machida¹, Y. Morozumi¹, R. Morita², S. Watanabe¹, T. Hayashi¹, T. Shimizu¹, Y. Sato¹, N. Sato¹, K. Hori² (1.Fukui

513 Breeding of a new sweetpotato variety "Amahazuki" with sweet even immediately after harvest.

○Nishinaka, M.¹, K. Taguchi¹, K. Katayama², T. Kuranouchi³ (1.Central Reg. Agri. Res. Cent., NARO, 2.Hokkaido Reg. Agri. Res. Cent., NARO, 3.Inst. Crop. Sci., NARO)

514 High-yielding and high-quality cultivar "Yukikomachi", approaching northern limit of Sweet potato

○Taguchi, K.¹, M. Nishinaka¹, K. Katayama², K. Ishiguro², T. Kuranouchi³ (1.Central Reg. Agri. Res. Cent., NARO, 2.Hokkaido Reg. Agri. Res. Cent., NARO, 3.Inst. Crop. Sci., NARO)

515 Analysis of the diversity of rice - wheat hybrid plants

☆Tarutani, H.¹, T. Maryenti², T. Okamoto², M. Takasawa⁴, H. Tsujimoto^{1,3}, T. Ishii^{1,3} (1.Grad. Sch. Sus., Univ. Tottori, 2.Grad. Sch. Sci., Univ. Tokyo Metro, 3.Arid Land Research Center., Univ. Tottori, 4.Facul. Sci., Univ. Tokyo Metro)

516 Analysis of genetic diversity and traits of a native soybean variety 'Hayama Tanokuro'

○Tada, Y., S. Amakawa (Tokyo Univ. of Technol., Sch. of Biosci. Biotechnol.)

517 Genetic diversity analysis for *Amaranthus tricolor* germplasm based on genome-wide single-nucleotide polymorphisms

☆Hoshikawa, K.^{1,2}, Y. Lin², R. Schafleitner², K. Shirasawa³, S. Isobe³, D. Nguyen^{4,5}, Y. Yoshioka⁶ (1.JIRCAS, 2.World Veg, 3.Kazusa DNA Res. Inst., 4.VAAS, 5.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 6.Fac. Life & Environ. Sci., Univ. Tsukuba)

518 Evaluation of genetic variation in Shiikuwasha and finding non-seasonal flowering landraces

☆Sasaki, R., T. Masu, R. Ishikawa (Fac. Agri. And Life Sci., Hirosaki Univ.)

519 Research and development of sustainable raw materials for brewing II : An inherited characteristic of novel traits in "N68-411".

○Kihara, M., T. Hoki, N. Hirota, W. Saito, Y. Tokizono, R. Kanatani, R. Makimoto, T. Zhou, N. Suda (Crop Research Laboratories, SAPPORO BREWERIES LTD.)

520 Evaluation of the amount of total soluble protein in etiolated rice seedlings

Watanabe, A.¹, Y. Takeshima^{2,3}, A. Kanouchi^{2,4}, S. Takahashi^{2,5}, K. Sasaki^{2,6}, N. Takahashi^{2,7}, ○Y. Ito^{1,2} (1.Grad Sch Agri Sci, Tohoku Univ, 2.EGGS, Tohoku Univ, 3.Akita High School, 4.Yamagata Higashi High School, 5.Hanamaki Kita High School, 6.Renaissance High School, 7.Sakata Higashi High School)

521 Analysis of molecular effects in developing seeds by drought stress

☆Mega, R.¹, J. Kim², T. Ishii³, H. Tanaka⁴, F. Abe⁵, M. Okamoto⁶ (1.Grad. Sch. Sci. Tech. Innov., Yamaguchi Univ., 2.RIKEN · CSRS, 3.ALRC, Torrori Univ., 4.Faculty of Agriculture, Tottori Univ., 5.Food Res. Inst., NARO, 6.C-Bio, Utsunomiya Univ.)

522 Analysis of the mechanism of heterosis for shoot growth during early stages by non-destructive measurement in sugar beet.

☆Iwahori, R.¹, K. Hiroki¹, H. Ogawa¹, M. Ohkubo¹, H. Matsuhira², K. Kitazaki¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)

523 Identification of the genetic region related to heterosis in *Arabidopsis thaliana*

☆Fujiwara, K.¹, N. Miyaji², T. Yasuda¹, R. Fujimoto¹ (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Iwate Biotechnol. Res. Ctr.)

524 Evaluation of the process of seed-shattering loss during rice domestication

○Ishikawa, R.¹, C. Castillo^{1,2}, T. Htun¹, K. Numaguchi¹, K. Inoue¹, Y. Oka¹, M. Ogasawara¹, S. Sugiyama¹, N. Takama¹, C. Orn¹, C. Inoue¹, K. Nonomura³, R. Allaby⁴, D. Fuller², T. Ishii¹ (1.Grad. Sch., Agr. Sci., Kobe Univ., 2.University College London, 3.National Institute of Genetics, 4.University of Warwick)

525 Development of OsSh1 genome editing lines using Indica rice varieties and their shattering characteristics.

○Komatsu, A.¹, M. Otake¹, A. Shimizu², H. Kato³, F. Li² (1.Institute of Agrobiological Sciences, NARO, 2.Institute of Crop Science, NARO, 3.Research Center of Genetic Resources, NARO)

601 Effects of strigolactones on varietal differences of leaf incrementation in rice

○Umehara, M.^{1,2}, K. Sakai¹, S. Yamamoto¹, M. Shindo², K. Shimomura² (1.Dept. Appl. Biosci., Fac. Life Sci., Toyo Univ., 2.Grad. Sch. Life Sci., Toyo Univ.)

602 Impacts of growing environment on barley cultivation under double cropping system

○Saisho, D., K. Kishiro, N. Yamaji, A. Tani (IPSR, Okayama Univ.)

603 Development of a heatshock-inducible clonal analysis system and its application to observe internode initiation in rice.

○Tsuda, K. (National Institute of Genetics)

604 Mechanisms controlling differences in the degree of development of pedicellate spikelets in sorghum germplasm

○Takanashi, H., M. Shichijo, J. Yamada, M. Ishimori, H. Iwata, N. Tsutsumi (Grad. Sch. Agric. Life Sci., Univ. Tokyo)

605 Modulation mechanism of lateral root primordium in rice

☆Akahoshi, R.¹, T. Kawai², M. Inari (Ikeda)³, M. Sato⁴, H. Tsuji^{4,5}, M. Takahashi (Nosaka)⁶, H. Takahashi¹, Y. Sato⁶, M. Nakazono¹, Y. Inukai⁷ (1.Grad. Sch. Bioagr., Nagoya U., 2.Inst. Crop. Sci., NARO, 3.Sch. Hel. Nut., Univ. Tokai Gakuen, 4.KIBR, Yokohama City U., 5.BBC., Nagoya U, 6.NIG, 7.ICREA, Nagoya U.)

606 Analysis of new genes involved in rice leaf development

☆Miya, M., H. Takanashi, J. Itoh (Grad. Sch. Agr. & Life Sci., Univ. Tokyo)

607 Evaluation of diversity in the panicle morphology using the wild *Oryza* genetic resources

☆Agata, A., Y. Sato (National Institute of Genetics)

608 Evaluates inbreeding effects on reproductive organs and compare the methylome and transcriptome profiles in common buckwheat

☆Takeshima, R.¹, Y. Yasui², K. Matsui¹ (1.Inst. Crop. Sci., NARO, 2.Grad. Sch. Agr. Univ. Kyoto)

609 Analysis of Gene Expression Using RNA-Seq for Secondly Growth in Potato Microtuber

☆Zhang, X., K. Fujino, H. Shimura (Grad. Sch. Agri., Hokkaido Univ.)

610 Analysis of the effect of *qJA1* controlling juvenile-adult phase transition on transcriptome alteration in rice seedling

Watanabe, T.¹, M. Mimura², J. Ito², ○T. Yoshikawa¹ (1.Grad. Sch. Agri. Kyoto Univ., 2.Grad. Sch. Agric. Life Sci., U. Tokyo)

611 Changes in gene expression of carrot somatic embryogenesis by stress treatment

☆Nakazawa, A.¹, Y. Takahara² (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering, Nagaoka University of Technology)

612 Polarity establishment of rice embryo by auxin localization

☆Tezuka, T.¹, K. Ta², S. Shimizu-Sato², M. Nosaka-T^{1,2}, T. Hattori³, Y. Sato^{1,2} (1.Sch. Life Sci., Grad. Univ. Adv. Study/SOKENDAI, 2.Plant Genet., Natl. Inst. Genet., 3.Grad. Sch. Bioagr. Sci., Nagoya U.)

613 Characterization of low-temperature germinability of the Japanese native red rice cultivar "Awa-akamai"

☆Kuronuma, S.¹, T. Yamaguchi², K. Murata³, M. Yamamoto¹, T. Yamada¹, M. Kanekatsu¹ (1.Grd. Sch. Agr., Tokyo U. Agr. Tec., 2.Tonami Agr. For. Prom. Cent., 3.Toyama Pref. Agr. Forest. Fish. Res. Cent.)

614 Genetic analysis of breaking seed dormancy by machine-threshing in barley

○Kai, H.¹, T. Tanaka², Y. Haraguchi¹, T. Todoroki¹, T. Abiko³, D. Saisho⁴ (1.Fukuoka Agric. Forest. Res. Cent., 2.NAAC, NARO, 3.Kyushu Univ., 4.IPSR, Okayama Univ.)

615 Imaging of microtubules in the shoot apical meristem of rice

☆Takata, R., J. Ito, H. Tsuji (KIBR., Yokohama City Univ.)

616 Identification of a novel QTL that has contributed to the early heading of Japanese wheat varieties

☆Mizuno, N.¹, H. Matsunaka², M. Yanaka³, G. Ishikawa¹, F. Kobayashi¹, K. Nakamura³
(1.NICS, NARO, 2.HARC, NARO, 3.KARC, NARO)

617 Surgical manipulations of inflorescence development in barley

Tanaka, M.¹, H. Akashi¹, ○H. Tsuji^{1,2} (1.KIBR, Yokohama City Univ., 2.Bioscience and Biotechnology Center, Nagoya Univ.)

618 Genetic analysis for heading date in weak photoperiod sensitivity and early heading rice variety, TNAU6484

☆Yoshida, M.¹, S. Hirano¹, S. Zheng², D. Fujita² (1.Grad. Sch. Fac. Agr., Saga Univ., 2.Fac. Agr., Saga Univ.)

619 *late-heading1*, an einkorn wheat mutant which suppresses the early-heading phenotype of early-heading mutant with a deletion of clock gene *WPCL1*

Ueda, J.², Y. Kazama², T. Abe³, ○K. Murai¹ (1.Dep. Sust. Agri-Culture, Fukui Pref. Univ., 2.Dep. Biothech., Fukui Pref. Univ., 3.Nishina Cent., RIKEN)

620 Genetic study on earliness QTLs which interact with *PCL1* in durum wheat

☆Fujioka, A., Y. Monden, H. Nishida, K. Kato (Grad. Sch. Environ. Life Sci., Okayama U.)

621 Prostrate trait of barley is a complex trait regulated by several QTLs with different functions

☆Fukushima, N.¹, T. Matsuura², Y. Monndenn¹, H. Nisida¹, T. Hirayama², K. Katou¹
(1.Grad. Sch. Environ. Life Sci., Univ. Okayama, 2.IPSR, Okayama Univ.)

622 Analysis of the mechanism in the regulation of tomato fruit set by jasmonic acid

☆Nomura, Y.¹, Y. Lu², H. Enomoto³, K. Harada¹, R. Yano⁴, M. Kojima⁵, Y. Takebayashi⁵, H. Sakakibara⁶, H. Ezura^{2,7}, T. Ariizumi^{2,7} (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Dept. Biosci., Univ. Teikyo, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)

623 Molecular mechanism of increased aliphatic glucosinolate content by polyploidization in Brassicaceae

☆Oyama, K.¹, T. Suzuki², S. Bang¹, T. Ohnishi¹ (1.Sch. Agric., Utsunomiya. Univ,
2.Center for Bioscience Research and Education, Utsunomiya. University)

Poster presentations

P001 A simple set of plasmids for multiple genome editing and a method for high-density crop hydroponics in a plant incubator

○Kuroda, M. (Inst. Agrobiol. Sci., NARO)

P002 Efficient method of breaking dormancy of strawberry seeds without using concentrated sulfuric acid

Tanaka, J.¹, ○R. Otsuka^{1,2}, R. Yamaguchi³, Y. Taniguchi¹, S. Kataoka⁴ (1.NICS/NARO,
2.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 3.Nagaoka Univ. of Tech., 4.NIVFS/NARO)

P003 Breeding by crossings between egg plant varieties and 「Sadowara」 of Miyazaki original vegetable - A new line obtained in F₅ of 'Kurowashi' x 「Sadowara」 -

○Chen, L.^{1,2}, T. Hiejima^{1,2}, N. Emoto¹, K. Yoshimura^{1,2}, S. Yoshizaki¹ (1.Fac. Environ. Hirt., Minami Kyusyu U., 2.Grad. Sch. Hort. Food Sci., Minami Kyusyu U.)

P004 Synthetic octaploid wheat production with wide hybridization between bread wheat and *Aegilops tauschii*

☆Gao, Y.¹, Y. Matsuoka², H. Tsujimoto^{1,3}, M. Kishii⁴, S. Sakuma⁵, T. Ishii^{1,3} (1.Grad. Sch. Sus., Univ. Tottori, 2.Grad. Sch. Agri., Univ. Kobe, 3.Arid Land Research Center., Univ. Tottori, 4.JIRCAS, 5.Facul. Agri., Univ. Tottori)

P005 Evaluation of *Brassica rapa* accessions with resistance to three TuMV isolate groups

☆Tian, A., H. TAKAHASHI, M. YAMAMOTO, H. KITASHIBA (Grad. Sch. Aric. Sci., Univ. Tohoku)

P006 Conformation of already detected grain-size alleles from a large grain rice cultivar, BG 1, through next generation sequencing using near-isogenic lines

☆Suzuki, H.¹, A. Horibata^{1,2} (1.Grad. Sch. of Biol.-Oriented Sci. and Tech., Kindai Univ,
2.Fac. of Biol.-Oriented Sci. and Tech., Kindai Univ.)

P007 Search for variations on the occurrence rate and on the size of white core in rice (*Oryza sativa* L.) grains by using *mPing* taglines

☆Hibi, T.¹, H. Tanaka², A. Horibata^{1,2} (1.Gra. Sch. of Biol.-Oriented Sci. and Tech., Kindai Univ., 2.Fac. of Biol.-Oriented Sci. and Tech., Kindai Univ.)

P008 Genetic evaluation of sex expression in Japanese weedy melon

☆Nashiki, A.^{1,2}, Y. Yoshioka³ (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.JSPS Research Fellowship for Young Scientists, 3.Fac. Life Env. Sci., Univ. Tsukuba)

P009 A Novel Combination of Genes Causing Temperature-Sensitive Hybrid Weakness in Rice

☆Kutay Soe, T.¹, M. Kunieda¹, H. Sunohara^{1,2}, Y. Inukai³, V. Reyes¹, S. Nishiuchi¹, K. Doi¹ (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.Environmental Control Center Co., Ltd., 3.ICREA, Nagoya Univ.)

P010 Identification of a novel QTL controlling seed dormancy in wheat originated from *Aegilops tauschii*.

☆AHMED, M.^{1,2}, Y. Gorafi^{2,3}, N. Kamal^{2,4}, I. Tahir², H. Tsujimoto⁴ (1.United Graduate School of Agricultural Sciences, Tottori University, Tottori Japan, 2.Agricultural Research Corporation (ARC), P. O. Box 126, Wad-Medani, Sudan, 3.International Platform for Dryland Research and Education, Tottori University, Tottori, Japan, 4.Arid Land Research Center, Tottori University, Tottori, Japan)

P011 A role of the *qSH3* mutation involved in a loss of seed shattering and its variation in wild and cultivated rice

☆Numaguchi, K., T. Htun, Y. Oka, M. Ogasawara, S. Sugiyama, N. Takama, C. Orn, C. Inoue, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

P012 Evaluation of *qCSS3*, a locus involved in non-seed-shattering behaviour of *japonica* rice cultivar, 'Nipponbare'

☆Nagayanagi, H., Y. Tsujimura, T. Matsuda, K. Otsuka, T. Htun, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

P013 Effect of selection of Peony (*Paeonia lactiflora* Pall.) based on medicinal ingredient paeoniflorin content

○Kawashimo, M., T. Tsusaka, M. Sakurai (Tsumura Co., Ltd.)

P014 Diversity analysis between cultivars and homoeologs in wheat using pan genome information

○Tanaka, T. (NAAC, NARO)

P015 Explore of sex determination region in mulberry (*Morus spp.*) using genome resequencing data

○Matsumura, H.¹, R. Shimizu², M. Suzuki², S. Yoshinobu², A. Mizoguchi², R. Atsumi²
(1.Gene Res., Shinshu Univ., 2.Grad. Sch. Sci. Tech., Shinshu Univ)

P016 Linkage map development of mulberry using F2 population from "Sekizaiso" x "Kokuso21"

☆Suzuki, M.¹, A. Koyama², M. Uemoto¹, S. Kajita², H. Matsumura¹ (1.Grad. Sch. Sci. Tech., Shinshu Univ, 2.Tokyo U Agr. Tech)

P017 The ratio of introgression of C genome in BC1F1 individuals developed by backcrossing *Brassica rapa* to *B. napus*

☆Segawa, T., R. Kumazawa, T. Hanano, M. Nishikawa, S. Saiga, H. Takagi (Ishikawa Prefectural University)

P018 Developing co-dominant type DNA marker for *PFRU* controlling flowering habit in cultivated strawberry.

☆Saiga, S.¹, M. Tada¹, T. Segawa¹, M. Nishikawa¹, N. Makita¹, M. Sakamoto², K. Tanaka², T. Wada², H. Takagi¹ (1.Ishikawa Prefectural University, 2.Takii Seed)

P019 Development of SNP-molecular markers from RNA sequencing in Japanese cultivated gentian

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P020 QTL analysis of femaleness in monoecious spinach

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P021 Comparative study on structures and expression of spinach FT homologs between early- and late- bolting lines.

☆Ishikawa, R., K. HAMADA, K. YAMANO, Y. ONODERA (Res. Fac. Agr., Hokkaido Univ.)

P022 QTL analysis of rosette size in head lettuce using UAV

☆Takamori, H.¹, K. Seki², Y. Kobayashi³, M. Okada⁴, K. Komatsu⁵, K. Tanaka⁶, Y. Uno⁷, O. Watanabe⁸, S. Nishiuchi⁹, H. Matsumura¹⁰, N. Hayashida³ (1.Grad. sch. Textile, Shinshu Univ., 2.Nagano Vegetable and Ornamental Crops Experiment Station, 3.Division of Applied Biology, Fac. Textile, Shinshu Univ., 4.Grad. Sch. Agric. and Life Sci., Tokyo Univ., 5.Fac. Agric., Tokyo Univ. Agric., 6.NODAI Genome Research Center, Tokyo Univ. Agric., 7.Fac. Agric., Kobe Univ., 8.Fac. Agric., Shinshu Univ., 9.Fac. Agric., Nagoya Univ., 10.Gene Research Center, Shinshu Univ.)

P023 Evaluation of the novel seed-shattering locus estimated on chromosome 12 using rice cultivar 'Kasalath'

☆Yamaguchi, Y., N. Shionari, N. Takama, Y. Oka, Y. Takenaka, T. Htun, C. Inoue, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

P024 Predicting Chromosomal Contributions to Genetic Gain in Medicinal Components of Red Perilla Cross-breeding Populations

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P025 Validation and genetic characterization of a seed weight quantitative trait locus, *qSW17.1*, in progenies of cultivated and wild soybeans

○Xu, D.¹, D. Liu^{1,2}, C. Park¹, Q. Wang² (1.Japan International Research Center for Agricultural Science, 2.College of Plant Science, Jilin University, China)

P026 GWAS analysis of parameters related to growth rate calculated from multiple environment cultivation of rice MAGIC population

○Yamamoto, T.¹, T. Furuta¹, K. Kashihara¹, Q. Zhang¹, Y. Nonoue², D. Ogawa², J. Yonemaru² (1.IPSR, Okayama Univ., 2.NICS, NARO Institute of Crop Science)

P027 GWAS analysis of elemental contents in straw and grain by using rice MAGIC population

☆ZHANG, Q.¹, T. Furuta¹, K. Kashihara¹, D. Ogawa², J. Yonemaru², J. MA¹, T. Yamamoto¹ (1.IPSR, Okayama Univ, 2.NICS, NARO Institute of Crop Science)

P028 Genome-wide association studies for root-system breeding of sorghum.

☆Okada, S.¹, Z. Hu², Y. Inukai³, S. Nishiuchi², T. Yamauchi¹, S. Araki-Nakamura¹, K. Ohmae-Shinohara¹, H. Nakamura², K. Miura⁴, S. Kasuga⁵, T. Sazuka¹ (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Grad. Sch. Bioagri., Nagoya Univ., 3.ICREA, Nagoya Univ., 4.Dept. Biosci. Fukui Pref. Univ., 5.AFC, Fac. of Agri. Shinshu Univ.)

P029 Large scale resequencing of commercial melon cultivars and its application to marker-assisted breeding

○Yano, R.¹, K. Shimomura², M. Sugiyama², Y. Kawazu² (1.Research Center for Advanced Analysis, NARO, 2.Inst. Vegetable and Floriculture Sci., NARO)

P030 Analyzing the effect of the insertion in *BrFT2* promoter region controlling non-vernalization flowering habit in *Brassica rapa* cv. 'CHOY SUM EX CHINA 3'

☆Nishikawa, M., T. Segawa, S. Saiga, N. Makita, T. Imamura, H. Takagi (Ishikawa Prefectural University)

P031 Genomic prediction using combined genotypic data obtained by different genotyping tools

☆Minamikawa, M.^{1,2}, M. Kunihisa³, S. Moriya³, K. Abe³, M. Inamori², H. Iwata² (1.IAAR, Chiba Univ., 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.NIFTS, NARO)

P032 Toward establishment of a novel breeding technology using molecular genetic screening and genome-editing-mediated amino acid substitutions

☆Nozaka, A., T. Kuroha, M. Kimizu, S. Chechetka, H. Yoshida (National Agriculture and Food Research Organization, NARO)

P033 CRISPR/Cas9 genome editing of *TaGAD* in common wheat

☆Murayama, H., Y. Kamiya, K. Kawaura (Kihara Institute for Biological Research, Yokohama City University)

P034 Identification of the gene responsible for the male sterility in eggplant by mitochondrial genome editing

☆SUSAMI, A.¹, M. Tsujimura², S. Arimura³, T. Terachi⁴ (1.Grad.Sch.Life Sci., Kyoto Sangyo Univ, 2.Fac.Agr.Dept.Plant Life Sci., Ryukoku Univ, 3.Agr Life Sci., Tokyo Univ, 4.Fac. Life Sci., Kyoto Sangyo Univ)

P035 Genome editing to generate Ppd-H1-deficient barley and evaluation of growth characteristics in a net greenhouse.

Tezuka, D.¹, H. Cho¹, H. Onodera¹, Q. Linghu¹, T. Chijimatsu², ○R. Imai¹ (1.NIAS, NARO, 2.Sasaki Food Co.Ltd.)

P036 Morphological abnormalities observed in the floral organs of a tobacco BC3 line produced by the backcrosses between mutable and wild-type lines.

☆hanamoto, s.¹, t. terachi² (1.Grad. Sch Life Sci., Univ. Kyoto Sangyo, 2.Fac. Life Sci., Univ. Kyoto Sangyo)

P037 Analysis of rice short grain and cleistogamous mutant

○Ohmori, S., T. Mizubayashi, A. Shomura, U. Yamanouchi, S. Yamamura (Inst. Crop. Sci., NARO)

P038 Silencing mechanism by canonical and non-canonical RdDM pathway in egg cell

☆Yashiro, M., C. Kamada, A. Hasegawa, R. Kaneko, D. Susaki, N. Sugi, K. Tonosaki, D. Maruyama, T. Kinoshita (Kihara Inst. Biol. Res., Yokohama City Univ.,)

P039 Investigation of the male sterility observed in alloplasmic lines of wheat (cv. Chinese Spring) with *Triticum-Aegilops* cytoplasm. 1. Plasmon Type: U,M,T²,C,G

○Tsujimura, M.¹, S. Takenaka¹, M. Nakata¹, N. Mori², T. Terachi³ (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Agr. Sci., Kobe U., 3.Fac. Life Sci., Kyoto Sangyo Univ.)

P040 Characterization of the mitochondrial gene *orf181* specific to alloplasmic male-sterile wheats

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P041 Transcriptome analysis of root plasticity under high soil temperature in rice

☆Yoshida, S.¹, Y. Numajiri², K. Yoshino³, S. Teramoto², T. Kawakatsu³, Y. Uga² (1.Fac. of Agri., Tokyo Univ. of Agri., 2.Inst. Crop Sci., NARO, 3.Inst. Agrobiological sci., NARO)

P042 Non-destructive 3D image analysis of root system architecture in rice under drought.

☆Numajiri, Y.¹, S. Yoshida², T. Hayashi³, Y. Uga¹ (1.Crop Sci., NARO, 2.Bioresource, Tokyo Nodai, 3.Agric. Info. Tech., NARO)

P043 Functional characterization of a *NLR* gene in the clubroot resistant locus *Crr3* in *Brassica rapa*

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P044 Nanopore sequencing of clubroot resistance (CR) cabbage genome and DNA marker development of CR-QTL region

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P045 Effect of above-ground and underground parts on the occurrence of green stem disorder in soybean.

○Ogata, D.^{1,2}, A. Ishitsuka³, R. Matsumoto³, O. Uchikawa³, M. Miyazaki⁴, Y. Ishibashi¹ (1.Grad. Sch. of Bior. and Bioe. Sci., Kyushu Univ., 2.Yame Agric. Ext. Cent., 3.Fukuoka Agric. Forest. Res. Cent., 4.Fukuoka Pref. Office)

P046 Evaluation of heterosis in seedlings derived from crosses between Taichung 65 and cultivars in the world rice core collection

☆Nakamura, Y.¹, K. Ichitani², S. Matthew³, N. Tanaka³, T. Kuboyama¹ (1.Col. Agr., Ibaraki U, 2.Fac. Agr., Kagoshima U, 3.Inst.Crop.Sci, NARO)

P047 Molecular biological analysis of abscission layer formation using rice non-seed shattering mutants.

☆Tanimoto, R., S. Sugita (Konishi) (Grad. Sch. Agri., Univ. Kagawa)

P048 Molecular genetic analysis for the isolation of a novel seed shattering gene in rice.

○Sugita-Konishi, S., T. Inamo, R. Tanimoto, K. Nishikawa (Grad. Sch. Agri., Univ. Kagawa)

P049 Characteristics of cracking seed tolerant soybean lines in Hokuriku region

○Kono, Y.¹, M. Ikegami², K. Toda^{2,7}, K. Fujii², A. Kikuchi³, K. Komatsu⁴, N. Oki⁵, S. Watanabe⁶, K. Hirata³, Y. Tetsuya², A. Kaga² (1.CARC,NARO, 2.NICS,NARO, 3.TARC,NARO, 4.WARC, NARO, 5.KARC, NARO, 6.Univ. Saga, 7.Res. Cent. Genet. Resources, NARO)

P050 Genome-wide association study and genomic prediction for essential oil components in *Ataractyloides lancea*

☆Tsusaka, T.¹, K. Shirasawa², S. Isobe² (1.Tsumura & Co., 2.Kazusa DNA Res. Inst.)

P051 Evaluation of traits in a medicinal plant, *Bupleurum falcatum* Linne

○Hiyama, H., Y. Aoki, M. Sakurai (Tsumura & Co.)

P052 A novel white-flower mutant of Japanese morning glory induced by gamma irradiation

☆Yamamura, R.¹, R. Okano¹, H. Katsuyama¹, Y. Takahashi¹, T. Mizuno², A. Hoshino⁴, E. Nitashaka³, T. Kuboyama¹ (1.Col. Agr., Ibaraki U., 2.Dept. Botany, NMNS, 3.Grad. Sch. Sci., Kyushu U., 4.Natl. Inst., Basic Biol.)

P053 Identification of a gene altering tocopherol synthesize pathway in soybean

☆Park, C.¹, D. Liu^{1,2}, Q. Wang², D. Xu¹ (1.Japan International Research Center for Agricultural Science, 2.College of Plant Science, Jilin University, China)

P054 Genetic analysis of lines showing reiterative branching phenotype resulted from the cross between *lax2-5* and cv. Kasalath.

○Oyori, T., N. Satoh-Nagasawa, M. Tsuchida, N. Nagasawa (Biores Sci., Akita Pref. Univ.)

P055 Changes in cellular structures in the barley inflorescence meristem during abortion

☆Matsumoto, H.¹, J. Ito¹, S. Arai¹, Y. Nomura¹, M. Sugimura¹, N. Sato¹, M. Seki¹, M. Wakazaki², M. Sato², N. Takeda-Kamiya², K. Uno^{4,5}, Y. Sato^{4,6}, D. Saisho⁷, K. Toyooka², H. Tsuji^{1,3} (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.Nagoya Univ., 4.Grad. Sch.

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P056 Genetic analysis of interactions between *ADAXIAL-ABAXIAL BIPOLEAR LEAF* genes in rice

☆Shimizu, H., N. Nagasawa, N. Satoh-Nagasawa (Grad. Sch. Biores. Sci., Univ. Akita Pref.)

P057 Gene expression analysis of the unique inflorescence structure in barley

☆Ito, J.¹, N. Sato¹, Y. Nomura¹, S. Arai¹, K. Takahagi², S. Okada^{3,4}, N. Takeda-Kamiya², K. Toyooka², D. Saisho³, T. Hirayama³, K. Mochida², H. Tsuji^{1,4} (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Bioscience and Biotechnology Center, Nagoya Univ.)

P058 Demonstration of environment-dependent genetic interactions in the control of rice flowering time

○Saito, H.¹, Y. Fukuta¹, A. Tomita², E. Fushimi³, Y. Okumoto⁴ (1.JIRCAS, 2.Fac. Agr., Okayama Univ., 3.NARO, 4.Fac. Agr., Setsunan Univ.)

P059 Analysis of light regulation in stunting seedling growth of albino-like rice mutant

○Rikiishi, K., A. Ono, M. Maekawa, M. Sugimoto (Inst. Plant Sci. Res., Okayama U.)

P060 Analysis of level of self-incompatibility in *S*-tester lines of *Brassica rapa*

○Yamamoto, M., M. Ogura, H. Kitashiba (Graduate School of Agricultural Science, Tohoku University)
