

Title of Papers Presented at the 140th Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 Whole-genome resequencing of Japanese tomato cultivars provides insights into the history of modern breeding

○Yamamoto, E.¹, H. Matsunaga², A. Ohyama², T. Nunome², K. Shirasawa³, H. Hirakawa³, S. Isobe³ (1.Grad. Sch. of Agr. Meiji Univ., 2.NIVFS, NARO, 3.Kazusa DNA Res. Inst.)

102 Genome features of common vetch (*Vicia sativa*) in natural habitats provide an insight into new plant domestication

○Shirasawa, K.¹, S. Kosugi^{1,2}, K. Sasaki^{3,4}, A. Ghelfi^{1,5}, K. Okazaki¹, A. Toyoda⁶, H. Hirakawa¹, S. Isobe¹ (1.KDRI, 2.Present address: RIKEN, 3.U Tokyo, 4.Present address: JIRCAS, 5.Present address: NIG, 6.NIG)

103 *De novo* assembly of the rice variety “Yumepirika” using a nanopore sequencer

☆Nishiyama, N.¹, R. Sun¹, A. Nagalla¹, K. Naito², T. Izawa¹ (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Genetic Resources Center, NARO)

104 Chromosome-scale genome assembly of wheat cv. Fielder

○Sato, K.¹, F. Abe², K. Shirasawa³, S. Isobe³ (1.IPSR, Okayama Univ., 2.Inst. Crop Sci., NARO, 3.Kazusa DNA Res. Inst.)

105 Search for flower organ-determining genes in *Phalaenopsis*

☆Maekado, D., Y. Takahara (Department of Bioengineering, Nagaoka University of Technology)

106 A novel mitochondrial DNA molecule associated with the *Solanum stoloniferum* deriving tetrad sterility

☆Sanetomo, R.¹, K. Akai², A. Nashiki³ (1.Potato Germplasm Enhancement Laboratory, Obihiro Univ., 2.The Hokkaido Agricultural Research Center, NARO, 3.Graduate School of Science and Technology, Univ. Tsukuba)

107 Mapping of a gene locating in a low-recombination pericentromeric region in wheat

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

108 Detection of new sex determination loci in weedy melon (*Cucumis melo* ssp. *agrestis*)

☆Nashiki, A.¹, K. Takano¹, H. Matsuo², F. Fitriyah², S. Isobe³, K. Shirasawa³, Y. Yoshioka⁴ (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 3.Kazusa DNA Research Institute, 4.Fac. Life Env. Sci., Univ. Tsukuba)

109 New QTLs for a few days earlier in Koshihikari found in foreign cultivars

○Yonemaru, J.¹, K. Hori¹, M. Yano² (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agri. Info. Tech., NARO)

110 QTL analysis of fruit-related traits based on crosses among three varieties in melon

☆Takano, K.¹, H. Matuo², F. Fitriyah², S. Isobe³, K. Shirasawa³, Y. Yoshioka⁴ (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 3.Kazusa DNA Research Institute, 4.Fac. Life Env. Sci., Univ. Tsukuba)

111 Genome-wide association study to identify lodging resistance loci by using Canadian soybean varieties

○Kato, S.¹, S. Bahram^{2,3}, M. Morrison², W. Bekele², D. Torkamaneh⁴, I. Rajcan⁴, L. O'Donoghue⁵, F. Belzile⁶, E. Cober² (1.Inst. Crop Sci., NARO, 2.Ottawa Research and Development Centre, 3.Carleton University, 4.University of Guelph, 5.Centre de recherche sur les grains Inc., 6.Université Laval)

112 QTL-seq analysis of female flower frequency in bitter melon (*Momordica charantia*)

☆Karube, H.¹, M. Miyake¹, S. Suzuki¹, S. Moroi¹, N. Taniai², K. Tarora², N. Urasaki², H. Matsumura³ (1.Grad. Sch. Sci. Tech., Shinshu Univ., 2.Okinawa Pref. Agric. Res. Ctr., 3.Gene Res. Ctr., Shinshu Univ.)

113 Genetic analysis of inbreeding depression on abnormal leaf shape in common buckwheat

☆Takeshima, R.¹, Y. Yasui², H. Hirakawa³, K. Matsui¹ (1.Inst. Crop Sci., NARO, 2.Grad. Sch. Agr. Univ. Kyoto, 3.Kazusa DNA Res. Inst.)

114 QTL analysis for the grain numbers per ear of high-yield rice line 'Hokuriku 257' derived from 'Momiroman'

☆Ogura, M.¹, H. Sasahara², J. Tanaka¹ (1.Inst. Crop Sci., NARO, 2.WARC, NARO)

115 Genetic analysis of QTLs related with prostrate trait in barley

☆Fukushima, N., K. Shimoto, H. Nishida, K. Kato (Grad. Sch. Environ. Life Sci., Okayama U.)

116 Discovery of genetic regions controlling the southern root-knot nematode resistance in hexaploid sweetpotato and comparison of analytical results among races

☆Kurihara, M.¹, N. Obata², H. Tabuchi³, K. Shirasawa⁴, Y. Monden² (1.Fac. Agri., Okayama Univ., 2.Grad. Sch. Environ. Life Sci., Okayama Univ., 3.KARC/NARO, 4.Kazusa DNA Res. Inst.)

117 Identification of novel insertions found in the first intron and 5'-upstream region of *Raphanus FLC2* gene and their associations with late bolting of flower

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

118 Analysis of organellar genome copy number and gene expression under mitochondrial dysfunction in *Arabidopsis thaliana*

☆Ayabe, H.¹, A. Toyoda², N. Tsutsumi¹, S. Arimura¹ (1.Graduate School of Agricultural and Life Sciences, The University of Tokyo, 2.Genome Informatics Laboratory, National Institute of Genetics)

119 Targeted base editing in the plant organelle genome

☆Nakazato, I.¹, M. Okuno^{2,3}, C. Koizuka⁴, N. Tsunetomi⁴, Y. Tamura¹, T. Itoh², N. Koizuka⁴, H. Takanashi¹, N. Tsutsumi¹, S. Arimura¹ (1.Grad. Sch. Agr. and Life Sci., Univ. Tokyo, 2.Tokyo Tech. Life Sci. and Tech., 3.Kurume Univ. Med., 4.Tamagawa Univ. Agr.)

120 Evaluation of SNP Detection Accuracy among Tomato Cultivars Using Allegro Targeted Genotyping Method

○Isobe, S., K. Shirasawa (Kazusa DNA. Res Inst.)

121 Genome Analyses of more than 500 Japanese rice accessions

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

122 Genetic mapping of novel environment-sensitive restorer-of-fertility gene for Owen-type sterile cytoplasm in sugar beet

☆Kashikura, J.¹, Y. Honma¹, H. Matsuhira², Y. Kuroda², K. Kitazaki¹, T. Kubo¹ (1.Grad. Sch. Sci., Univ. Hokkaido, 2.NARO HARC)

123 Identification of a novel dwarfing gene introduced into the seed parent line of sorghum F₁ variety 'Tentakā': importance for stable production of F₁ seeds

☆Hashimoto, S.¹, H. Nakamura¹, S. Araki-Nakamura², K. Ohmae-Shinohara², T. Kikuchi³, K. Miura⁴, H. Kawaguchi⁵, S. Kasuga⁶, T. Sazuka² (1.Grad. Sch. Bioagri., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Sch. Agr., Nagoya Univ., 4.Dept. Biosci. Fukui Pref. Univ., 5.Grad. Sch. Sci. Tech. Innov., Kobe Univ., 6.AFC, Fac. of Agri. Shinshu Univ.)

124 Genetic dissection of the *qATL6.1* region into multiple QTLs governing anther length in African wild rice, *Oryza longistaminata*

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

125 Genome-wide association study for heading date using panel of African rice (*Oryza glaberrima* Steud.)

☆Hirao, A.¹, D. Fujita², R. Ishikawa³, Y. Koide⁴, H. Yasui¹, Y. Yamagata¹ (1.Fac. Agr., Grad. Sch., Kyushu Univ., 2.Fac. Agr., Saga Univ., 3.Agr. Sci., Kobe Univ., 4.Grad. Sch., Univ. Hokkaido)

126 Genetic analysis of F₁ pollen sterility using a backcrossed nested association mapping population derived from founder accessions of wild rice species

Umebara, A., H. Yasui, ○Y. Yamagata (Fac. Agr., Grad. Sch., Kyushu Univ.)

127 F₁ pollen sterility differentiated by *Oryza glumaepatula* donors in introgression lines at chromosome 11

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

201 Search for flower identity genes and morphological modifications in chamomile

☆Takeda, K., Y. Takahara (Nagaoka University of Technology Bioengineering)

202 Breeding of a new Adzuki bean cultivar "Toiku170" with resistance to several soil-borne diseases

☆Nagasawa, H.¹, Y. Horiuchi¹, S. Hagihara¹, K. Nakagawa¹, M. Okuyama², H. Satou², H. Kousaka², A. Tazawa³, H. Shimada¹, S. Aoyama⁴, R. Ogura³, A. Shinmura², A. Sawaguchi¹, O. Fujine⁵ (1.Hokkaido Research Organization Tokachi Agricultural Experiment Station, 2.HRO Central Agri. Exp. Stn., 3.HRO Kitami Agri. Exp. Stn., 4.HRO Donan Agri. Exp. Stn., 5.HRO Ornamental Plants and Vegetables Research Center)

203 Wheat and rice hybrid production via *in vitro* fertilization system

☆Maryenti, T.¹, T. Ishii², T. Okamoto¹ (1.Grad. Sch. Sci., Tokyo Met. Univ., 2.Arid Land Res. Center, Tottori Univ.)

204 Analysis of 120 Japanese rice cultivars using unfertilized fields in Nagoya University farm

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

205 Explore of the tomato mutants in trichome formation among the EMS-mutagenized seed pools developed by the National Bioresource Project-Tomato

○Sugimoto, K., Y. Fujimori, N. Ito, H. Ezura (Univ. Tsukuba, Tsukuba-Plant Innovation Research Center)

206 Exploitation of bread wheat lines capable of symbiosis with *Epichloë* endophytes from wheat-related species and their application to wheat improvement

☆Kato, S.¹, W. Simpson², R. Johnson², N. Ube³, M. Kodama⁴, T. Ishii⁵, H. Tsujimoto⁵ (1.Graduate School of Sustainability Science, Tottori U., 2.AgReserch, New Zealand,

3.Faculty of Engineering, Toyama Prefectural U., 4.United Graduate School of Agricultural Sciences, Tottori U., 5.Arid Land Research Center, Tottori U.)

207 Breeding of nutrient-enhanced rice lines using iron-hyperaccumulating mutants and search for the gene loci related to the high iron accumulation

○Saito, A., N. Kawano, T. Nakayama, Y. Koshika, K. Shimada, M. Kato, A. Higashimoto, H. Ichinokawa, K. Nakamura, J. Kumano, T. Ohyama, K. Higuchi (Dept. Agric. Chem., Tokyo Univ. Agric.)

208 Trend of the use of plant genetic resources in the Genebank Program, NARO

○Shibata, S., K. Ebana (Res. Cen. Gen. Res., NARO)

209 Present progress and future tasks of breeding of barley lines for whole crop silage with a hooded awn characteristic

○Taira, M.¹, M. Yanaka¹, M. Nakata¹, T. Tonooka^{1,2}, T. Sugita^{1,3}, I. Hattori^{1,4}, K. Hosoda¹, Y. Mori¹, H. Yatsu⁵, K. Fujii⁵, K. Osanai⁵, T. Honda⁵, K. Ishii⁵ (1.KARC/NARO, 2.NICS/NARO, 3.WARC/NARO, 4.Tokai Univ., 5.SNOW BRAND SEED CO., LTD.)

210 Variation of anthocyanin contents of black rice varieties and some case studies of colored rice in Japan

○Itani, T.¹, T. Seo², R. Yamamoto² (1.The Research Center for Satoyama Studied, Ryukoku University, 2.Faculty of Agriculture, Ryukoku University)

211 Multiple derivatives lines of durum wheat: a new resource for gene mining from wild emmer wheat

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

212 Development of a breeding method that dramatically improves the glucoraphanin content of intergeneric hybrids with functional deficiency of radish GRS1

○Endo, R.¹, H. Chikano¹, E. Itabashi², M. Kawasaki², T. Ohara², T. Kakizaki² (1.KAGOME CO., LTD., 2.Institute of Vegetable and Floriculture Science, NARO)

213 Trials of targeted base editing in the mitochondria genome of *Arabidopsis thaliana*

☆Zhou, C.¹, I. Nakazato¹, Y. Tamura¹, N. Tsutsumi¹, M. Takenaka², S. Arimura¹
(1.University of Tokyo, Graduate School of Agricultural and Life Science, Faculty of
Agriculture, 2.Kyoto University, Faculty of Science)

214 Development of a method for estimating the heading date of Japonica rice using UAV aerial images

☆Kato, Y., S. Inoue, N. Kobayashi, T. Nakata, T. Kondo, S. Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)

215 Design-oriented high-speed breeding on the genetic background of high-yield rice cultivar 'Hokuriku 193'

○Tanaka, J. (Inst. Crop Sci., NARO)

216 Assessment of the genetic relationship between vegetation index and drought tolerance in soybean using multi-trait model

☆Sakurai, K.¹, Y. Toda¹, Y. Omori¹, Y. Yamasaki², H. Takahashi³, H. Takanashi¹, M. Tsuda⁴, M. Ishimori¹, H. Tsujimoto², A. Kaga⁵, M. Nakazono³, T. Fujiwara¹, H. Iwata¹
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217 Estimation of the bias of founder haplotypes in the breeding process based on genealogical and marker information: Application to apple varieties

☆Mochizuki, H.¹, M. Minamikawa¹, M. Kuniyama², K. Noshita^{3,4}, S. Moriya², K. Abe², T. Hayashi⁵, Y. Katayose⁶, T. Yamamoto², H. Iwata¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NIFTS, NARO, 3.Faculty of Sci., Kyushu Univ., 4.Plant Fron. Res. Cent., Kyushu Univ., 5.RCAIT, NARO, 6.NICS, NARO)

218 A Bayesian model for genomic prediction utilizing metabolite networks

○Onogi, A. (Faculty of Agr., Ryukoku Univ.)

219 Development of a nested association mapping (NAM) population representing genetic diversity of Asian common wheat

○Nitta, M.¹, S. Takenaka², Z. Su¹, K. Kuroki^{1,3}, K. Onishi⁴, H. Matsunaka⁵, S. Nasuda¹
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220 Investigation of ear emergence in high-density wheat fields using UAV

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221 Short-range remote sensing of wheat NAM population to analyze heading and flowering periods through deep learning

☆Kuroki, K.^{1,2}, K. Yan³, S. Yoshioka¹, M. Nitta¹, J. Nie⁴, M. Ishii⁴, H. Wang⁴, S. Takenaka⁵, H. Iwata⁴, K. Shimizu^{6,7}, S. Nasuda¹, W. Guo⁴ (1.Grad. Sch. Agri., Kyoto Univ., 2.Grad. Sch. Sci., Univ. Tokyo, 3.LabRomance Inc., 4.Grad. Sch. Agri and Life Sci., Univ. Tokyo, 5.Fac. Agr., Ryukoku Univ., 6.Kihara Inst. of Biol., Yokohama City Univ., 7.Dept. of Evo. Biol. and Env. Studies, Univ. Zurich)

222 Exploration of wheat blast resistance resources in the NBRP hexaploid wheat core collection: Geographic distribution, genetic diversity and GWAS

☆Su, Z.¹, S. Asuke², M. Yoshioka², S. Takenaka³, M. Nitta¹, Y. Tosa², S. Nasuda¹ (1.Grad. Sch. Agr., Kyoto Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ., 3.Fac. Agr., Ryukoku Univ.)

223 Study of stable color correction for time-series images of wheat in the field

○Goto, T.¹, T. Tameshige^{2,3}, A. Tonouchi¹, R. Akiyama⁴, R. Shimizu-Inatsugi⁴, K. Shimizu⁴, N. Kutsuna¹, Y. Shimahara¹ (1.LPIXEL Inc., 2.Kihara Institute for Biological Research, Yokohama City University, 3.Faculty of Science, Niigata University, 4.Department of Evolutionary Biology and Environmental Studies)

224 Verification of environmental factors for the speed and uniformity of germination using the phenotyping system

☆Amagai, Y.^{1,2}, E. Hayashi^{1,3}, T. Kozai¹ (1.Japan Plant Factory Association, 2.Center for Env. Health & Field Sci., Chiba Univ., 3.Grad. Sch. Hort., Chiba Univ.)

225 Exploration of commercial radish cultivars for genetic transformation

☆Ogata, K., K. Tonosaki, K. Hatakeyama (Fac. Agr., Iwate. Univ.)

226 Development of the procedure for comprehensive mutation detection by whole-exome sequencing in tobacco EMS mutants

☆Ichida, H.¹, H. Udagawa², T. Takeuchi², T. Abe¹, Y. Takakura² (1.RIKEN Nishina Center, 2.Leaf Tob. Res. Ctr., JT)

301 Field resistance to bacterial blight (*Xanthomonas oryzae* pv. *oryzae*.) in rice variety Koshihikari

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302 Bacterial blight resistance conferred by *xa42* gene in rice is enhanced after the initiation of reproductive growth phase

☆Gatayama, Y.¹, T. Anai², K. Shimizu³, S. Taura⁴, K. Ichitani³ (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ., 3.Fac. Agr., Kagoshima Univ., 4.Inst. Gene Res., Kagoshima Univ.)

303 Identification of a causal rice gene for resistance to bacterial seedling rot and development of the Hitomebore near-isogenic lines harboring its genomic region

☆Ishikawa, K.¹, K. Ito¹, H. Utsushi¹, Y. Ogasawara¹, E. Kanzaki¹, H. Kikuchi¹, T. Takeda¹, R. Terauchi^{1,2}, A. Abe¹ (1.Iwate Biotechnology Research Center, 2.Graduate School of Agriculture, Kyoto University)

304 Attempts to breeding for BLYV resistance in sugar beet: evaluation method and genetic effect of the resistance

○Kuroda, Y., H. Matsuhira, T. Narihiro, M. Sano (Hokkaido Agr. Res. Cent., NARO)

305 Identification of a novel candidate gene and its causal mutation associated with resistance to the southern root-knot nematode in sweetpotato

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

306 Comparison of morphological and anatomical traits of seminal root between wild rice *Oryza glumaepatula* and cultivated rice Taichung 65

☆Ejiri, M., K. Shiono (Grad. Sch. Biosci. & Biotech., Fukui Pref. Univ.)

307 Varietal differences detected in the accumulation levels of protein aggregates involved in high temperature-induced lethality of rice seedlings

☆Sato, T., Y. Shinozaki, T. Yamada (Grad. Sch. Agr., Tokyo U. Agr. Tech.)

308 Effect of triterpenoid deficiency on the morphology and physiological function of soybean secondary aerenchyma

☆Abo, C.¹, H. Suzuki², T. Oi¹, A. Yanagawa¹, T. Gorai¹, Y. Tomisaki², H. Seki², T. Muranaka², A. Kaga³, M. Nakazono¹, H. Takahashi¹ (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Grad. Sch. Engineering, Osaka Univ., 3.Inst. Crop Sci., NARO)

309 Population structure of rice varieties collected in Bangladesh to explore salt tolerance alleles

☆Inada, N., Y. Yamagata, H. Yasui (Fac. Agr., Grad. Sch., Kyushu Univ.)

310 Searching for QTLs that controls Na⁺ concentration in young leaf blades of rice under salinity stress

☆Toda, F.¹, R. Ishikawa², Y. Amarasinghe³, T. Ishii², T. Horie¹ (1.Grad. Sch., Div. Appl Biol., Shinshu Univ., 2.Grad. Sch., Agric Sci., Kobe Univ., 3.GLORDC, Sri Lanka)

311 Ectopic expression of PHZ induces anther pigmentation via upregulation of genes involved in the late steps of anthocyanin biosynthesis in petunia

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

312 Regulation of germination by targeted mutagenesis of grain dormancy genes in barley

○Hisano, H.¹, R. Hoffie², F. Abe³, H. Munemori¹, T. Matsuura¹, M. Endo⁴, M. Mikami⁴, S. Nakamura³, J. Kumlehn², K. Sato¹ (1.IPSR, Okayama U., 2.Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany, 3.Inst. Crop Sci., NARO, 4.Inst. Agrobiol. Sci., NARO)

313 PRIMA: a rapid and cost-effective genotyping method to detect single-nucleotide differences of DNA using probe-induced heteroduplexes

☆Kakui, H.^{1,2}, M. Yamazaki¹, K. Shimizu^{1,2} (1.Dept. Evo. Biol. Env. Studies, Univ. Zurich, 2.Kihara Inst. Biol. Res., Yokohama City Univ.)

314 Site-directed Mutagenesis of allergenic gene coding Gly m 4 in soybean using CRISPR/Cas9 system

☆Hibara, M.¹, N. Maruyama², J. Abe¹, T. Yamada¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.Grad. Sch. Agr., Univ. Kyoto)

315 Improving the efficiency of genome editing using proxy-CRISPR strategy in rice

☆Negishi, K.¹, S. Toki^{1,2,3} (1.Inst. Agrobio. Sci., NARO, 2.Fac. Agr., Ryukoku Univ., 3.Grad. Sch. Nanobio., Yokohama City Univ.)

316 Genetic analysis of a chasmogamous mutant allele *cly1.b4* in barley

○Kakeda, K., N. Kushibe, A. Nanape (Fac. Bioresour., Mie Univ.)

317 Determination of mutations induced by ion-beam irradiation of different LETs in rice

○Morita, R.¹, H. Ichida¹, Y. Hayashi¹, K. Ishii², Y. Shirakawa¹, S. Usuda¹, K. Ichinose¹, M. Hatashita³, K. Takagi³, K. Miura⁴, M. Kusajima⁴, H. Nakashita⁴, T. Endo⁵, Y. Okumoto⁶, T. Sato^{1,7}, K. Toriyama⁷, T. Abe¹ (1.RIKEN Nishina Center, 2.National Institutes for Quantum and Radiological Science and Technology, 3.The Wakasa Wan Energy Research Center, 4.Grad. Sch. Bioshi. Fukui Pref., 5.Miyagi Pref. Eastern Regional Promotion Office, 6.Faculty of Agri., Setsunan Univ., 7.Grad. Sch. Agri. Sci., Tohoku Univ.)

318 A *CHS* inverted repeat is missing in a novel soybean seed coat pigmented mutant

☆Yuhazu, M.¹, S. Mikuriya², A. Mori², M. Senda³, A. Kanazawa² (1.Sch. Agr., Hokkaido Univ., 2.Res. Fac. Agr., Hokkaido Univ., 3.Fac. Agric. Life Sci., Univ. Hirosaki)

319 Comparative analysis of histone H3K9 methylation patterns in rice leaf and anther genomes

☆Yamamori, K.¹, Y. Kanaoka¹, S. Hoshi¹, Y. Koide¹, J. Kim², Y. Kishima¹ (1.Grad. Sch. Agr. Sci., Hokkaido U., 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

320 Is the mitochondrial gen *orf181* responsible for the male sterility of a common wheat with *Aegilops mutica* cytoplasm?

☆Shoji, Y.¹, M. Tsujimura², S. Takenaka², 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.)

321 Development of the autonomously-replicating chloroplast transformation vectors

☆Baba, H.¹, T. Mita², K. Nakamoto³, K. Uemura³, T. Terachi³ (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Fac. Life Sci., Kyoto Sangyo U., 3.Fac. Life Sci., Kyoto Sangyo U.)

322 Plant Organelle Genome Editing

○Arimura, S. (Graduate School of Agricultural Sciences, The University of Tokyo)

323 Multi-omics analysis of F₁ hybrid rice showing heterosis

☆Hosaka, A.^{1,2}, H. Kida¹, Y. Koide³, H. Tsuji¹ (1.KIBR., Yokohama City Univ., 2.Rhelixa, Inc., 3.Res. Fac. Agr., Hokkaido Univ.)

324 Phenome analysis on root traits of world-wide rice varieties in the upland field

☆Teramoto, S.¹, S. Takayasu¹, N. Maruyama¹, Y. Kitomi¹, R. Nishijima², T. Kawakatsu², Y. Uga¹ (1.NICS, 2.NIAS)

325 The transcriptomic landscapes of rice cultivars with diverse root system architectures grown in upland field conditions

○Kawakatsu, T.¹, S. Teramoto², R. Nishijima¹, S. Takayasu², N. Maruyama², Y. Kitomi², Y. Uga² (1.NIAS, 2.NICS)

401 Tissue-specific gene expression analysis of barley shoot apex using laser microdissection

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

402 Identification of the causal gene for soybean dwarf mutant *mini*

☆Takama, K., S. Nasuda, T. Yoshikawa (Grad. Sch. Agr. Kyoto U.)

403 Genetic Analysis of four Spikelet Mutants with the elongation of Sterile Lemmas and Rudimentary Glumes in Rice

☆Nagai, M.¹, J. Garcon¹, K. Koyasaki², E. Inada², Y. Koide², I. Takamure^{1,2} (1.Grad. Sch. Global Food Resources., Hokkaido Univ., 2.Grad. Sch. Agri., Hokkaido Univ.)

404 Genetic analysis of split palea mutants of barley

○Taketa, S.¹, T. Sotome², T. Yoshikawa³ (1.IPSR, Okayama University, 2.Tochigi Prefecture, 3.Graduate School of Agriculture, Kyoto University)

405 Developmental trajectory analysis of the shoot apex in barley by single meristem transcriptome

☆Ito, J.¹, Y. Nomura¹, N. Sato¹, S. Okada², K. Takahagi³, M. Sugimura¹, M. Seki¹, D. Saisho², K. Mochida³, T. Hirayama², H. Tsuji¹ (1.KIBR, Yokohama City Univ., 2.IPSR, Okayama Univ., 3.CSRS, RIKEN)

406 Earliness effect of novel sequence variants of *Ppd-B1* in wheat

○Kato, K., H. Nishida (Grad. Sch. Environ. Life Sci., Okayama U.)

407 Spatiotemporal analysis of phase transition and gibberellin biosynthesis in rice (1)

☆Niimi, Y.¹, K. Nagai¹, T. Hobo¹, Y. Mizuta², Y. Takebayashi³, M. Kojima³, H. Sakakibara⁴, Z. Shimatani⁵, R. Terada⁶, H. Tsuji⁷, M. Ashikari¹ (1.Bioscience and Biotechnology Center, Nagoya University, 2.Institute of Transformative Bio-Molecules, Nagoya University, 3.RIKEN Center for Sustainable Resource Science, 4.Graduate School of Bioagricultural Sciences, Nagoya University, 5.Kobe University Graduate School of Science, Technology and Innovation, 6.Agriculture, Meijo University, 7.Kihara Institute for Biological Research, Yokohama City University)

408 Regulation mechanisms of lateral root primordium size in response to auxin distribution patterns in rice

Kawai, T.¹, R. Akahoshi¹, T. Kojima¹, M. Takahashi-Nosaka², Y. Sato², H. Takahashi¹, M. Nakazono¹, M. Sato³, H. Tsuji³, A. Yamauchi¹, ○Y. Inukai⁴ (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.Natl. Inst. Genet., 3.KIBR, Yokohama City Univ., 4.ICREA, Nagoya Univ.)

409 Study on morphological development in moss

☆Furutsuji, N., Y. Takahara (Department of Bioengineering, Nagaoka University of Technology)

410 Pyramiding effects of three genes regulating panicle morphology on final panicle architecture and traits associated with yield in rice

☆Agata, A.^{1,2}, S. Ota¹, Y. Sato², H. Sakakibara^{1,3}, M. Ashikari⁴, H. Kitano⁴, T. Hobo⁴
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411 Gene identification and SNP effects in floury rice mutant FloTR1

☆Muroyama, R.¹, H. Ito², D. Kang¹, S. Hamada¹ (1.Fac. Agric. Life Sci., Hirosaki U.,
2.Dept. Chem. Biol. Eng., NIT. Akita College)

412 Genetic region responsible for the differences of starch properties in two glutinous rice cultivars in Hokkaido

☆Ikegaya, T.¹, K. Ashida² (1.HARC., NARO, 2.Inst. Food. Res., NARO)

413 Identification of a novel locus that regulates glutamate accumulation in tomato fruit

☆Tomioka, M.¹, H. Ezura², M. Kanekatsu¹, T. Yamada¹, Y. Shinozaki¹ (1.Grad. Sch. Agr.,
Tokyo U. Agr. Tec., 2.Fac. Life Environ. Sci., Univ. Tsukuba)

414 Effect of damaged starch and arabinoxylan on water absorption of hard wheat in Hokkaido

○Ashikaga, N.¹, K. Hayashi¹, S. Ohnishi¹, Y. Ishida², K. Kizawa², K. Hayakawa²
(1.Kitami Agri. Exp. Stn., HRO., 2.Cereal Sci. Res. Cent. of Tsukuba, Nisshin Flour Mil.
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415 The amount of protein produced in rice seedlings grown in darkness and a search for conditions that increase protein production

☆Watanabe, A.¹, Y. Hatanaka^{2,3}, Y. Takeshima^{2,4,7}, K. Sasaki^{2,5}, N. Takahashi^{2,6}, Y.
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Sch., 4.Akita High Sch., 5.Renaissance High Sch., 6.Sakata Higashi High Sch., 7.current:
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416 Mapping of a gene for higher saccharification yields from rice straws and expression analysis of genes in the candidate region

☆Ono, A., K. Ito, T. Abe, Y. Ito (Grad. Sch. Agri. Sci., Tohoku Univ.)

417 Development of sorghum biomass estimation methods using UAV images

☆Inoue, S.¹, T. Nakata¹, T. Sazuka², S. Nishiuchi¹ (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ.)

418 Establishment of an efficient culture system in Yacon (*Smallanthus sonchifolius*) cultivars

☆Ito, C., Y. Masuda, Y. Matsuda (Grad. Sch. Agri., Tokai U.)

419 Analysis of CMS-related genes in *Oryza glaberrima* with Taichung 65 cytoplasm

☆Takeda, S.¹, H. Ichida², T. Abe², S. Arimura³, T. Kazama⁴, S. Chen⁵, Y. Kanaoka⁵, Y. Kishima⁵, K. Toriyama¹ (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Riken, Nishina Center, 3.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 4.Grad. Sch. Agri., Kyushu Univ., 5.Grad. Sch. Agri., Hokkaido Univ.)

420 mitoTALEN promotes homologous recombination repair inducing reconstruction of the mitochondrial genome in TA-CMS rice

☆Takatsuka, A.¹, T. Kazama², S. Arimura³, K. Toriyama¹ (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Grad. Sch. Agri., Kyushu Univ., 3.Grad. Sch. Agri. Life Sci., Univ. Tokyo)

421 Molecular genetic analysis on cytoplasmic male sterile rice originated from *Oryza nivara*

Asanuma, S.¹, K. Toriyama^{1,2}, N. Hamaoka³, Y. Yamagata³, H. Yasui³, ○T. Kazama³ (1.Fac. Agr., Tohoku Univ., 2.Grad. Sch. Agr. Sci., Tohoku Univ., 3.Grad. Sch. Agr., Kyushu Univ.)

422 Molecular mechanisms of temperature sensitive hybrid breakdown in *japonica* rice cultivars

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

423 Hyper callose accumulation to premeiotic anther lobes is essential for timely initiation of meiosis

Somashekar, H.^{1,2}, M. Mimura¹, K. Tsuda^{1,2}, ○K. Nonomura^{1,2} (1.Plant Cytogenetics, Natl. Inst. Genet., 2.Fac. Life Sci., SOKENDAI)

424 Study on the organelle genome from the progeny of a somatic hybrid between *Brassica oleracea* and *Arabidopsis thaliana*

☆Niihara, Y.¹, H. Yamagishi², M. Tsujimura³, T. Terachi⁴ (1.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 2.Inst. Comprehensive Ac. Res., Kyoto Sangyo Univ., 3.Fac. Agr. Dept. Plant Life Sci. Ryukoku Univ., 4.Fac. Life Sci. Kyoto Sangyo Univ.)

Poster presentations

P01-A Pyramiding *Ba* (blue aleurone) genes to develop darker blue grain wheat: The effect of visual selection

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

P02-B Regional comparison of alleles frequency related to barley heading time on early generations in breeding

○Sekii, M.¹, E. Aoki^{2,6}, H. Aoki¹, Y. Nakano¹, H. Maejima³, S. Ikenaga⁴, A. Takahashi², M. Nakata⁵ (1.CARC, NARO, 2.Inst. Crop Sci., NARO, 3.Nagano Prefecture Agricultural Experiment Station, 4.TARC, NARO, 5.KARC, NARO, 6.Agriculture, Forestry and Fisheries Research Council)

P03-C Trends in Regulation of Genome Editing in Japan and Overseas

☆Moriyama, R.¹, M. Tachikawa², M. Matsuo³, H. Ochiai¹, M. Takahara¹, Y. Tabei¹ (1.New Technology Promotion Section, Strategic Planning Headquarters, NARO, 2.Graduate School of Environmental Studies, Univ. Nagoya, 3.Graduate School of Public Policy, Univ. Tokyo)

P04-A Large-grain new variety "Koshihikari Suruga Gg" and late-maturing new variety "Koshihikari Suruga Hd16" developed via whole-genome sequencing

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

P05-B Breeding of new line [Line 10] in Miyazaki original vegetable [Hyuga squash] using interspecific hybridization method

○Chen, L.^{1,2}, K. Goto², Y. Iwamoto², T. Fukuta¹ (1.Fac. Environ. Hirt., Minami Kyusyu U., 2.Grad. Sch. Hort. Food Sci., Minami Kyusyu U.)

P06-C Development of heavy-ion induced mutant line of *Torenia fournieri*

☆Mayuzumi, T.¹, A. Matsuta¹, M. Hatashita², K. Takagi², T. Abe³, K. Murai¹, Y. Kazama^{1,3} (1.Fucul. Biosci. Biotech., Fukui Pref., 2.Wakasa-wan Ener. Cent, 3.RIKEN)

P07-A Genetic diversity and population structure of wild *Camellia* species in Vietnam revealed by SSR analysis

☆Nguyen, T.¹, V. Luong², N. Le³, H. Katayama⁴, K. Fukuyama¹, C. Uematsu¹ (1.Grad. Sch. Sci., Osaka City Univ., 2.Faculty of Biology, Dalat Univ., 3.Faculty of Agriculture and Forestry, Hoa Lu Univ., 4.Grad. Sch. Agr, Kobe Univ.)

P08-B Is introgression involved in the domestication of garden beet?

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

P09-C A high-through-put phenotyping of vegetation cover by a UAV in high-density plots of a hexaploidy wheat NAM population

☆Yoshioka, S.¹, K. Kuroki^{1,3}, M. Nitta¹, J. Nie¹, M. Ishii², S. Takenaka⁴, K. Shimizu^{5,6}, H. Iwata², W. Guo², S. Nasuda¹ (1.Grad. Sch. Agri., Kyoto Univ., 2.Grad. Sch. Agri and Life Sci, Univ. Tokyo, 3.Grad. Sch. Sci., Univ. Tokyo, 4.Fac. Agr., Ryukoku Univ., 5.Kihara Inst. of Biol., Yokohama City Univ., 6.Dept. of Evo. Biol. and Env. Studies, Univ. Zurich)

P10-A Development of SNP markers associated with flowering time in gentian by RNA-Seq analysis

☆Takahashi, S.¹, T. Takase¹, M. Shimizu¹, K. Nemoto¹, A. Abe¹, F. Goto¹, C. Yoshida¹, M. Odajima², M. Nishihara¹ (1.Iwate Biotechnol. Res. Cent., 2.Iwate Agr. Res. Cent.)

P11-B Comparative analysis of sex chromosomes in *Spinacia* species

○Onodera, Y.¹, H. Fujita², S. Sugiyama³, A. Toyoda⁴, H. Hirakawa⁵ (1.Res. Fac. Agr., Hokkaido Univ., 2.Grad. Sch. Agr., Hokkaido Univ., 3.Sch. Agr., Hokkaido Univ., 4.Nat. Inst. Genet., 5.Kazusa DNA Res. Inst.)

P12-C Application of MIG-seq to crop genomics: High-throughput genotyping of wheat is realized by MIG-seq

☆Nishimura, K.¹, K. Motoki¹, A. Yamazaki¹, Y. Yasui¹, R. Takisawa², T. Kawai³, K. Ushijima³, R. Nakano¹, T. Nakazaki¹ (1.Grad. Sch. Agr., Kyoto Univ., 2.Fac. Agr., Ryukoku Univ., 3.Grad. Sch. Environ. Life Sci., Okayama Univ.)

P13-A Polyploid QTL-seq towards rapid development of tightly linked DNA markers for potato and sweetpotato breeding through whole-genome resequencing

○Yamakawa, H.¹, E. Haque², M. Tanaka², H. Takagi³, K. Asano⁴, E. Shimosaka⁴, K. Akai⁴, S. Okamoto⁴, K. Katayama⁴, S. Tamiya⁴ (1.NICS, NARO, 2.KARC, NARO, 3.Ishikawa Pref. Univ., 4.HARC, NARO)

P14-B Identification of the genomic region controlling light independent anthocyanin accumulation in the tuber of the turnip variety "Akamaru"

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

P15-C Validation of QTL for yield components using DH lines derived from wheat varieties "Kitahonami" and "Yumechikara"

☆Takahashi, K.¹, K. Kawaguchi², Y. Terasawa², S. Sekine³, Y. Takayama³, K. Tanaka¹, Z. Nishio^{1,3} (1.Grad. Sch. Agr., Tokyo Univ. Agr., 2.NARO/HARC, 3.Fac. Agr., Tokyo Univ. Agr.)

P16-A Genome-wide association analysis for the thorns in eggplant

Shimada, K.¹, K. Sakurai¹, ○H. Takahashi² (1.Fac. Biores. Sci., Akita Pref. U., 2.Fac. Food Agri. Sci., Fukushima Univ.)

P17-B Development of a Haplotype Visualization Tool for Modern Rice Cultivars

☆Kwon, Y.¹, H. Kajiya-Kanegae¹, T. Hayashi¹, K. Matsushita^{1,2}, A. Goto^{1,2}, G. Kiui¹, M. Yano¹, J. Yonemaru^{1,2} (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)

P18-C Development of a plant regeneration system and attempts of establishing genetic transformation in radish

○Takahara, M.^{1,2}, A. Okuzaki³, K. Komatsu⁴, Y. Mitsui⁴, T. Matsumoto⁵, N. Koizuka³, Y. Tabei² (1.NIAS, NARO, 2.Strategic Planning HQ, NARO, 3.Col. of Agri., Univ. Tamagawa, 4.Facul. of Agri., Tokyo Univ. of Agri., 5.Grad. Sch. of Agri., Tokyo Univ. of Agri.)

P19-A MitoTALEN aiming to knockout the candidate gene of cytoplasmic male sterility in eggplant

☆Tsujiyama, M.¹, A. Susami², S. Arimura³, H. Yamagishi⁴, T. Terachi⁵ (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 3.Grad. Sch. Agr. Life Sci.,

Univ. Tokyo, 4.Inst. Comprehensive Acad. Res. Kyoto Sangyo Univ., 5.Fac. Life Sci., Kyoto Sangyo Univ.)

P20-B Genome editing-mediated development of cleistogamous rice

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

P21-C Functional analysis of *GAMYB* gene in *Trifolium repens* L.

☆Waizumi, H., T. Tamura, Y. Saito (Fac. Agri., Univ. Iwate)

P22-A The effect of transgenic expression of *Oryza*;KRP3 mutants on seed size

☆Itou, T., M. Takahashi, Y. Saitoh (Fac. Agri., Iwate Univ.)

P23-B Brown rice metabolites of various cooking and sake rice under high temperature conditions during ripening period

☆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.)

P24-C Transcriptome profiling of the photoperiodic flowering induction in gentian

○Takase, T., S. Takahashi, M. Shimizu, K. Nemoto, A. Abe, M. Nishihara (Iwate Biotechnol. Res. Cent.)

P25-A A knowledge-based information resource for identifying a genome-scale functional network of tomato genes

○Kanno, M.¹, K. Hirata¹, S. Tsuboko-Ishii¹, B. Kong¹, K. Sugimoto², T. Ariizumi², K. Aoki³, Y. Kubo⁴, H. Ezura², E. Yamamoto¹, K. Yano¹ (1.Sch. Agri., Meiji Univ., 2.Fac. of Life Environ. Sci., Univ. of Tsukuba, 3.Grad. Sch. Life Environ. Sci., Osaka Pref. Univ., 4.Grad. Sch. of Env. and Life Sci., Okayama Univ.)

P26-B Genetic factor of seed hilum pigmentation induced by low temperature in soybean cultivar 'Akimiyabi' and its relationship to soybean root rot

○Hishinuma, A.¹, K. Toda², S. Kato³, A. Kikuchi¹ (1.Tohoku Agri. Res. Center, NARO, 2.Res. Cent. Genet. Resources, NARO, 3.Inst. Crop Sci., NARO)

P27-C Evaluation of inducible surface roots in a wild rice (*Oryza glumaepatula*) under waterlogging

☆Miyashita, T.¹, Y. Uga², K. Shiono¹ (1.Graduate School of Bioscience, Fukui Prefectural University, 2.Institute of Crop Science, National Agriculture and Food Research Organization)

P28-A Morphological variation in progenies derived from a cross between green and red leaf cultivars in *Amaranthus tricolor*

☆Okubo, H.¹, K. Hoshikawa², Y. Yoshioka³ (1.Col. Agr. Bio. Res. Sci., Univ. Tsukuba, 2.JIRCAS, 3.Fac. Life Env. Sci., Univ. Tsukuba)

P29-B Genomic predictions and genome-wide association studies for regulating aluminum levels in tea leaves

☆Fukuda, Y.¹, H. Yamashita⁵, A. Ohno², T. Uchida¹, Y. Tanaka^{2,3}, H. Katai⁷, J. Kawaki⁷, A. J. Nagano⁶, A. Morita^{2,4}, T. Ikka^{2,4} (1.Grad. Agr., Shizuoka Univ., 2.Fac. Agr., Shizuoka Univ., 3.Uni. Grad. Agr., Gifu Univ., 4.Inst. Tea Sci., Shizuoka Univ., 5.Inst. Crop Sci., NARO, 6.Fac. Agr., Ryukoku Univ., 7.Shizuoka Tea Res. Cent.)

P30-C Study on the mechanism of heterosis in different parents combinations of sugar beet during early growth

☆Iwahori, R.¹, M. Ohkubo¹, K. Satoh¹, H. Matsuhira², T. Kubo¹, K. Kitazaki¹ (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)

P31-A Alteration of DNA methylation patterns of *Wheat CONSTANS 1 (WCO1)* during hexaploidization

☆Hayamizu, S.¹, Y. Kazama¹, S. Takumi², K. Murai¹ (1.Grad. Sch. Biosci. Biotech., Fukui Pref. U., 2.Grad. Sch. Agr., Kobe U.)

P32-B Shifting of diurnal expression pattern of *CO*-like gene is cause of earliness in *extra early-flowering 4 (exe4)*

☆Hashimoto, K.¹, Y. Kazama¹, T. Abe², K. Murai¹ (1.Grad. Sch. Biosci. Biotech., Fukui Pref. U., 2.RIKEN Nishina Center)

P33-C Purification of florigen activation complex

☆Funayama, E.¹, K. Taoka¹, Y. Fukao², H. Tsuji¹ (1.Kihara Institute for Biological Research, Yokohama City Univ., 2.Col. of Life Sci., Ritsumeikan Univ.)

P34-A Analysis of cellular dynamics in the barley inflorescence meristem during its abortion at the single-cell resolution

☆Matsumoto, H.¹, J. Ito¹, S. Arai¹, Y. Nomura¹, M. Sugimura¹, N. Sato¹, M. Seki¹, K. Uno^{2,3}, Y. Sato^{4,5}, D. Saisho⁶, H. Tsuji¹ (1.KIBR, Yokohama City Univ., 2.Grad. Sch. of Sci., Nagoya Univ., 3.Department of NanoBiophotonics, Max Planck Institute for Biophysical Chemistry, 4.Grad. Sch. of Sci., Nagoya Univ., 5.Grad. Sch. of Sci., Nagoya Univ., 6.IPSR, Okayama Univ.)

P35-B A Computational Model of Rice Plant Shape Formation: The Effects of Genes Controlling Tiller Dynamics

☆Tokuyama, Y.¹, K. Ohnishi², T. Ishii³, I. Takamura⁴, Y. Kishima⁴, Y. Koide⁴ (1.Graduate School of Agriculture, Hokkaido University, 2.Obihiro University of Agriculture and Veterinary Medicine, 3.Kobe University, 4.Research Faculty of Agriculture, Hokkaido University)

P36-C Estimation of inheritance of nectar guide in *Brassica napus* based on UV image analysis

Matsuo, H.¹, R. Chen², S. Isobe³, K. Shirasawa³, ○Y. Yoshioka² (1.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 2.Fac. Life Env. Sci., Univ. Tsukuba, 3.Kazusa DNA Res. Inst.)

P37-A Analysis of novel pollen-pistil unilateral incompatibility occurred between inbred lines of *B. 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.)
