

Title of Papers Presented at the 126th Meeting of The JAPANESE SOCIETY Oral presentations

Oral Presentations

101 QTL mapping for leaf rust and powdery mildew resistance in a doubled-haploid population between wheat cultivars Shunyo and Nebarigoshi

☆Takenaka, S. ¹, M. Nitta ¹, H. Ito ², G. Ishikawa ², T. Nakamura ², M. Saito ², K. Nakamura ³, S. Nasuda ¹ (1.Grad. Sch. Agri., Kyoto Univ., 2.NARO Tohoku Agricultural Research Center, 3.NARO Kyushu Okinawa Agricultural Research Center)

102 Fine mapping and characterization of rice pre-harvest sprouting resistance QTLs, *Sdr12* and *Sdr13*, on chromosome 9 of upland rice, Owarihatamochi

☆Mizuno, Y. ^{1,2}, U. Yamanouchi ², T. Hoshino ⁴, Y. Nonoue ³, K. Nagata ², S. Fukuoka ², T. Ando ², M. Yano ⁵, K. Sugimoto ² (1.Grad. Sch. Life Environ. Sci., Univ. Tsukuba, 2.National Institute of Agrobiological Science (Natl. Inst. Agrobiol. Sci), 3.Iwate Agricultural Research Center (Iwate Agric. Res. Ctr.), 4.Faculty of Agriculture, Yamagata University (Yamagata univ.), 5.NARO Institute of Crop Science (NARO Inst. Crop Sci.))

103 Verification of QTL for the occurrence of white-back rice kernel under high temperature stress during ripening

○Miyahara, K. ¹, T. Wada ¹, M. Miyazaki ¹, J. Sonoda ², T. Tsukaguchi ³, M. Kondo ⁴ (1.Fukuoka Agric. Forest Res. Cent., 2.Kagoshima Pref. Inst. Agric. Dev., 3.Ishikawa Pref. Univ., 4.NARO, Inst. Crop Sci.)

104 *DRO3*, a QTL for root growth angle on rice chromosome 7 identified in the genetic pathway of *DEEPER ROOTING 1*

☆Kitomi, Y., E. Yamamoto, N. Kanno, S. Kawai, T. Mizubayashi, S. Fukuoka, Y. Uga (NIAS)

105 Improving of the sequence qualities for the MTP BAC clones of wheat chromosome 6B

☆Kanamori, H. ¹, K. Kurita ¹, S. Katagiri ¹, H. Fujisawa ¹, W. Karasawa ¹, M. Hamada ¹, F. Kobayashi ¹, T. Tanaka ¹, M. Shimomura ², N. Namiki ², H. Ikawa ², T. Matsumoto ¹, Y. Katayose ¹, J. Wu ¹, H. Handa ¹ (1.National Institute of Agrobiological Sciences, 2.MITSUBISHI SPACE SOFTWARE CO.,LTD.)

106 Development of marker database for barley breeding

○Sato, K., Y. Motoi (IPSR, Okayama Univ.)

107 Genome wide analysis of gene expression changes during the course of allopolyploidization and genome stabilization in hexaploid wheat

○Jung, Y. ¹, K. Kawaura ¹, K. Mishina ², S. Sakuma ¹, M. Kishii ³, Y. Ogihara ¹ (1.Kihara Institute for Biological Research, Yokohama City University, 2.National Institute of Agrobiological Sciences (NIAS), 3.International Maize and Wheat Improvement Center (CIMMYT))

108 Genomic prediction and selection trials of complex agronomic traits in recombinant inbred lines from the cross between Japanese soybean cultivars

☆Tsuda, M. ¹, T. Shimizu ¹, K. Machita ¹, M. Saruta ², T. Yamada ³, M. Ishimoto ¹, A. Kaga ¹ (1.NIAS, 2.NARO/WARC, 3.NARO/NICS)

109 QTL analysis of biomass-related traits using RILs derived from a cross between high-yielding rice varieties, 'Tachisugata' and 'Hokuriku 193'

○Matsubara, K. ¹, E. Yamamoto ^{2,3}, R. Mizobuchi ², J. Yonemaru ², T. Ishii ¹, J. Tanaka ¹, H. Tsunematsu ¹, T. Yamamoto ², N. Kobayashi ¹, H. Kato ², M. Yano ¹ (1.NICS, 2.NIAS, 3.NIVTS)

110 65 QTLs control genetic variation of rice grain shape between Koshihikari and IR64

☆Nagata, K. ¹, T. Ando ¹, Y. Nonoue ^{1,2}, T. Mizubayashi ¹, N. Kitazawa ¹, A. Shomura ¹, M. Yano ^{1,3}, S. Fukuoka ¹ (1.Natl. Inst. Agrobiol. Sci., 2.Iwate Agric. Res. Ctr., 3.NARO Inst. Crop Sci.)

111 Complete mitochondrial genome sequence of *Brassica nigra*

○Yamagishi, H. ¹, Y. Tanaka ², T. Terachi ¹ (1.Fac. Life Sci., Kyoto Sangyo U., 2.Grad. Sch. Environ. Life Sci., Okayama U.)

112 QTL analysis for rice grain size and white core using crossed populations between Koshihikari and Yamadanishiki

☆Okada, S. ¹, M. Suehiro ¹, K. Ebana ², K. Hori ², A. Onogi ³, H. Iwata ³, M. Yamasaki ¹ (1.Food Resources Education and Research Ctr., Grad. Agric. Sci., Kobe, 2.Natl. Inst. Agrobiol. Sci, 3.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

113 Genetic analysis of gibberellin deficient mutant appeared during potato breeding

☆Asano, K. ¹, M. Kojima ², H. Sakakibara ², S. Tamiya ¹ (1.NARO Hokkaido Agricultural Research Center, 2.RIKEN, PSC)

114 Establishment of the high-throughput genotyping system by SNP

☆Kurokawa, Y., T. Noda, K. Doi, M. Ashikari (Grad. Sch. Bioagri. Sci., Univ. Nagoya)

115 Pipeline development for comprehensive mining of cis-elements in the large scale data of nucleotide sequences

☆Sasaki, Y. ¹, N. Yamamoto ¹, H. Ohyanagi ¹, M. Kobayashi ¹, T. Takano ¹, S. Terashima ¹, E. Nannbara ², M. Ohtani ², k. Yano ¹ (1.Sch.Agr.,Meiji Univ., 2.Sch. of Cell & Systems Biology.,Toronto Univ.)

116 Identification of a nuclear genomic region that alters mitochondrial genome type in tetraploid wheats

☆Tsuji-mura, M. ¹, N. Mori ², H. Yamagishi ³, T. Terachi ³ (1.Kyoto Sangyo Univ. Plant Organelle Genomics R.C., 2.Grad. Sch. Agric. Sci., Kobe Univ., 3.Fac. Life Sci., Kyoto Sangyo Univ.)

201 Trial for development construction of outcrossing populations using the recessive male-sterility induced by rice retrotransposon *Tos17*

○Tanaka, J. ¹, M. Akasaka ¹, M. Oshima ², K. Abe ², Y. Taniguchi ¹, T. Ishii ¹, Y. Tabei ² (1.NARO Institute of Crop Science, 2.National Institute of Agrobiological Sciences (NIAS))

202 A database PODC for multi-species comparisons of large-scale gene expression networks and high-quality annotations

☆Takano, T. ¹, S. Terashima ¹, M. Kobayashi ¹, Y. Sasaki ¹, H. Matsumura ¹, K. Morimoto ¹, M. Kanno ¹, H. Chiba ², Y. Tada ², A. Shimizu ³, K. Aya ⁴, M. Matsuoka ⁴, M. Watanabe ⁵, K. Suwabe ⁶, K. Yano ¹ (1.Sch. Agri., Meiji Univ., 2.TOHOKU CHEMICAL Co., Ltd.,

3.Sch. of Environmental Sci., Univ. of Shiga pref., 4.Bioscience and Biotechnology Center, Nagoya Univ., 5.G. Sch. of Life Sci., Tohoku Univ., 6.G. Sch./Fac. of Bioresources, Mie Univ.)

203 A new statistical model unifying a crop model and a genome-wide prediction model: application to prediction of flowering time in rice

☆Onogi, A. ¹, M. Watanabe ¹, T. Mochizuki ², T. Hayashi ³, H. Nakagawa ⁴, T. Hasegawa ⁴, H. Iwata ¹ (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Fac. Agr., Kyushu U., 3.NARO/NARC, 4.NIAES)

204 EasyPCC: A tool for high-throughput measurement of canopy coverage ratio applicable to time series images taken under various light conditions

☆Guo, W., S. Ninomiya (Grad. Sch. Agric. Life. Sci, U. Tokyo)

205 Construction of a sorghum HapMap for genomics-assisted breeding

Kanegae, H. ¹, T. Mochizuki ², E. Kaminuma ², M. Minamikawa ¹, M. Kobayashi ^{3,4}, H. Toyoshima ^{3,4}, H. Ohyanagi ^{3,4,5}, H. Takanashi ^{1,4}, A. Nagano ^{6,7}, T. Tokunaga ^{4,8}, T. Sazuka ^{4,9}, K. Yano ^{3,4}, Y. Nakamura ², N. Tsutsumi ^{1,4}, ○H. Iwata ^{1,4} (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Genome Info. Lab., Natl. Inst. of Genet., 3.Fac. Agr., Meiji Univ., 4.CREST, JST, 5.Mitsubishi Space Software Co., Ltd., 6.Cent. Ecol. Res., Kyoto Univ., 7.PREST, JST, 8.EARTHNOTE Co., Ltd., 9.Biosci. Biotech. Cent., Nagoya Univ.)

206 A QTL analysis of the progeny population of "Tentak", an F1 hybrid cultivar with strong heterosis of sorghum

Yamaguchi, M. ¹, S. Araki-Nakamura ², Y. Ito ², K. Ohmae-Shinohara ², M. Matsuoka ², H. Kitano ², S. Kasuga ³, ○T. Sazuka ² (1.Fac. of Agr., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.AFC, Fac. of Agri., Shinshu Univ.)

207 A genetic study of panicle structure of broomcorn (*Sorghum vulgare*)

○Hosaki, T. ¹, S. Araki-Nakamura ², M. Matsuoka ², H. Kitano ², T. Sazuka ² (1.Fac. Agr., Nagoya Univ., 2.Biosci. Biotec. Ctr., Nagoya Univ.)

208 High-density SNP typing of RILs derived from a cross between Japanese and European commercial F1 hybrids for trial of genomic selection in tomato

○Fukuoka, H. ¹, A. Ohyama ¹, E. Yamamoto ¹, T. Hayashi ², S. Negoro ¹, K. Miyatake ¹, H. Yamaguchi ¹, T. Nunome ¹ (1.NIVTS, NARO, 2.NARO/ARC)

209 Heap: a SNPs detection tool by using high-throughput sequencing data for GWAS and GS

☆Kobayashi, M. ^{1,2}, H. Ohyanagi ^{1,2,3}, H. Toyoshima ^{1,2}, H. Takanashi ^{2,4}, A. Nagano ^{5,6}, H. Tainaka ^{2,4}, T. Tokunaga ^{2,7}, T. Sazuka ^{2,8}, H. Iwata ^{2,4}, N. Tsutsumi ^{2,4}, K. Yano ^{1,2} (1.Sch. of Agri., Meiji Univ., 2.JST, CREST, 3.Mitsubishi Space Software Co., Ltd., 4.Agri. and Life Sci., The Univ. of Tokyo, 5.Center for Ecological Research, Kyoto Univ., 6.JST, PRESTO, 7.Earth Note Co. Ltd., 8.Bioscience and Biotechnology Center, Nagoya Univ.)

210 Signatures of artificial selection and local adaptation in the maize genome

☆Takuno, S. (Graduate University for Advanced Studies)

211 Syntenic relationships between the spinach sex chromosome and autosomal regions of sugar beet

☆Takahata, S. ¹, T. Yago ², Y. Honma ¹, T. Kubo ³, Y. Onodera ³ (1.Grad. Sch. Agr., Hokkaido Univ., 2.Sch. Agr., Hokkaido Univ., 3.Res. Fac. Agr., Hokkaido Univ.)

212 Historical view of Amylose content in rice breeding program

☆Ikegaya, T. ¹, K. Koyanagi ², T. Shimizu ², H. Shinada ³, T. Nishimura ⁴, Y. Hirayama ⁴, H. Kiuchi ⁴, T. Maekawa ⁴, T. Sato ⁴, K. Fujino ¹ (1.NARO Hokkaido Agr Res Cent, 2.Grad Sch IST Hokkaido U, 3.HRO Tokachi Agr Exp Stn, 4.HRO Kamikawa Agr Exp Stn)

213 Sequence analysis of mitochondrial genome of an alloplasmic male-sterile radish line with the cytoplasm of *Brassicca maurorum*

☆Okabe, S. ¹, S. Bang ³, H. Yamagishi ², T. Terachi ² (1.Grad.Sch.Eng.,kyoto Sangyo U, 2.Fac.Life Sci.,Kyoto Sangyo U, 3.Fac.Agric.,Utsunomiya U)

214 Comparison of (*msh1*) sequence among radish varieties

☆Yamamoto, I. ¹, T. Terachi ², H. Yamagishi ² (1.Grad. Sch. Eng., Kyoto Sangyo U, 2.Fac Life Sci., Kyoto Sangyo U)

215 Analysis of genome-wide polymorphisms in Japanese pears

Onuki, R. ¹, ○T. Tanaka ¹, S. Terakami ², N. Urasaki ³, K. Tarora ³, S. Goeku ³, M. Shoda ³, T. Yamamoto ², T. Itoh ¹ (1.NIAS, 2.NIFTS, 3.OPARC)

216 Genome sequence and high-density linkage map of the salt tolerant species *Vigna marina*

○Naito, K. ¹, C. Sompong ², E. Ogiso ¹, K. Iseki ¹, C. Muto ¹, N. Tomooka ¹, H. Sakai ¹ (1.NIAS, 2.Kasetsart University)

217 Comparative transcriptome analysis between azuki bean and wild relative *Vigna riukiensis* using RNA sequencing method

☆Ogiso, E. ¹, K. Naito ^{1,2}, H. Sakai ¹, N. Tomooka ¹ (1.National Institute of Agrobiological Sciences, 2.JST PREST)

301 Generation mechanism of novel, huge protein bodies containing wild type or hypoallergenic derivatives of birch pollen allergen Bet v 1 in rice endosperm

☆Ogo, Y. ¹, H. Takahashi ², S. Wang ¹, F. Takaiwa ¹ (1.NIAS, 2.NAIST)

302 Studies on the variegated tobacco plants appeared in the chloroplast transformation experiment. I. Temperature-sensitive variegation

☆Tsuji, M. ¹, K. Uemura ², S. Morita ³, M. Yamamoto ⁴, T. Terachi ² (1.Grad.Fac.Eng.,Kyoto SangyoU., 2.Fac.Life Sci.,Kyoto Sangyo U., 3.Grad.Sch.Life and Envi.,Kyoto PrefU., 4.Kansai U. Welf.Sci.)

303 Development of wild barley mutant population induced by gamma chronic irradiation

☆Sakuma, S. ^{1,2}, M. Pourkheirandish ², H. Nakagawa ², T. Komatsuda ² (1.KIBR/YCU, 2.NIAS)

304 Genetic basis of antibiosis to brown planthopper, *Nilaparvata lugens* (Stål), derived from indica cultivar ASD7 in rice, *Oryza sativa* L.

☆Mai, V. ¹, T. Sonoda ¹, A. Yoshimura ¹, M. Matsumura ², H. Yasui ¹ (1.Faculty of Agriculture, Graduate school, Kyushu University, 2.NARO Kyushu Okinawa Agricultural Research Center)

305 Mechanisms of cortical cell-specific expansion of adventitious root under oxygen-deficient conditions in rice

☆Yamauchi, T. ¹, A. Tanaka ¹, N. Nishizawa ^{2,3}, M. Nakazono ¹ (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Res. Inst. Biores. Biotech., Ishikawa Pref. U., 3.Grad. Sch. Agric. Life Sci., U. Tokyo)

306 POPEYE transcription factor responding iron deficiency is involved in the regulation of photosynthesis in Arabidopsis

☆Araki, R. ¹, T. Suzuki ^{2,3}, T. Higashiyama ^{2,3}, T. Shikanai ¹ (1.Grad. Sch. Sci., Kyoto Univ., 2.Grad. Sch. Sci., Nagoya Univ., 3.JST ERATO)

307 Phytic acid transporter OsABCC13 is involved in the regulation of phosphorus homeostasis in rice

☆Usui, Y. ¹, T. Matsubara ¹, O. Yato ², K. Yoshida ¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NARC)

308 Analysis of cis regulatory elements in a pathogen-inducible synthetic promoter and transcription factors in rice

○Morino, K., M. Kimizu, K. Saito (NARO Agric.Res.Ctr.)

309 Bacterial blight (BB) resistance in PI231129 variety with BB resistance gene, *xa8*.
1. Prospects of several resistance genes conferring resistance to PI231129

○Taura, S. ¹, K. Ichitani ², H. Tsuneyoshi ², K. Kawabe ¹ (1.Division of Gene Research, Kagoshima University, 2.Faculty of Agriculture, Kagoshima University)

310 Identification of a *R. solani* resistance gene, *OsPSR1*, by screening rice-FOX *Arabidopsis* lines

☆Maeda, S. ¹, J. Dubouzet ¹, Y. Kondou ², K. Oda ³, M. Matsui ², H. Hirochika ¹, M. Mori ¹ (1.National Institute of Agrobiological Sciences, 2.RIKEN,PSC, 3.RIBS Okayama)

311 Screening of rice cultivars for resistance to rice-ear bugs

○Sugiura, K. ¹, M. Nakamura ², M. Kato ¹, A. Ito ¹, T. Nonoyama ¹, Y. Nakajima ¹ (1.Aichi Agri. Res. Cent., 2.Aichi Agri. Res. Cent. Mount. Reg. Agri. Res. Inst.)

312 Decrease of pecky rice and its factors in rice line "CRR-99-95W" with resistance to rice-ear bugs

○Nakamura, M. ¹, K. Sugiura ², A. Ikeda ¹, T. Suzuki ¹ (1.Mt. Reg. Agric. Inst., Aichi Agric. Res. Ctr., 2.Aichi Agric. Res. Ctr.)

313 Isolation and characterization of heat tolerant mutant lines from Micro-Tom mutant collections

☆Fukumoto, S. ¹, S. Ooshima ², M. Aiba ², K. Hoshikawa ³, H. Ezura ³ (1.Grad. Sch. Life Environ. Sci., Univ. Tsukuba, 2.Central Japan Railway Co., Ltd., 3.Fac. Life Environ. sci., Univ. Tsukuba)

314 Differences of resistance among alleles of the clubroot resistance gene, *Crr1a*, in *Brassica rapa*

○Hatakeyama, K., S. Matsumoto (NARO Institute of Vegetable and Tea Science)

315 Metabolites analysis for cold acclimation of rice

☆Sagehashi, Y., Y. Sato (NARO Hokkaido Agricultural Research Center)

316 Estimation of true blast resistance genes in feed rice varieties by using international differential fungal isolates

○Hayashi, N. ¹, T. Ishii ², H. Kato ¹, Y. Fukuta ³ (1.NIAS, 2.NICS, 3.JIRCAS)

401 Induction of protocorm-like bodies from cultured plantlets in vitro of *Phalaenopsis* and attempt to identify responsible genes for coerulea flower

○Toyama, M., Y. Takahara (Grad. Sch. Bio., Univ. Nagaoka)

402 Evaluation of self-compatibility by detection of a duplicated S-haplotype by TaqMan qPCR in the progeny of a pollen-part self-compatible mutant of Japanese pear

○Mase, N. ^{1,2}, Y. Sawamura ¹, S. Nishio ¹, N. Takada ¹, T. Saito ¹, T. Yamamoto ^{1,2}, H. Iketani ^{1,2} (1.NARO Inst. Fruit Tree Sci., 2.Grad. Sch. Life & Envi. Sci., Univ. Tsukuba)

403 The fertility restorer gene, *Rf4*, for Wild Abortive type cytoplasmic male sterile rice encodes pentatricopeptide repeat containing protein

☆Kazama, T., K. Toriyama (Grad. Sch. Agri. Sci. Tohoku Univ.)

404 Analysis of the RF2 complex mediating fertility restoration for LD-type cytoplasmic male sterile in rice

☆Fujii, S. ¹, T. Kazama ¹, M. Fujiwara ², K. Toriyama ¹ (1.Laboratory of Environmental Plant Biotechnology, Graduate School of Agricultural Science, Tohoku University, 2.Laboratory of Plant Protein Analysis, Plant Education Unit, Nara Institute of Science and Technology)

405 Fine mapping of a restorer of fertility gene for RT98-type cytoplasmic male sterility in rice

☆Igarashi, K. ¹, T. Kazama ¹, K. Motomura ², K. Toriyama ¹ (1.Graduate School of Agricultural Science, Tohoku University, 2.Faculty of Agriculture, University Ryukyus)

406 Fine mapping a restorer of fertility gene for RT102-type cytoplasmic male sterility in rice

☆Okazaki, M. ¹, H. Murata ¹, T. Kazama ¹, K. Motomura ², K. Toriyama ¹ (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Fac. Agri., Univ. Ryukyus)

407 Evaluation of processing suitability of new daidagon-azuki bean Beni Maiko Daidagon

○Furutani, N. ¹, Y. Shizukawa ², K. Ohtani ³, M. Matsui ³ (1.Kyoto Pref. Inst. of Agri. Biotech., 2.Kyoto Pref. Inst. of Agri. Kyoto. Exten.Center., 3.Kyoto Pref. Univ.)

408 Phylogenetic relationships among cultivated and wild common buckwheat based on nucleotide sequences of nuclear DNA

Horiuchi, N. ¹, C. Li ², ○T. Ohsako ¹ (1.Grad. Sch. Live Env. Sci., Kyoto Pref. Univ., 2.Yunnan Agr. Univ.)

409 Morphological and genetic characterization in *Cucumis* species of Laos

☆Tanaka, K. ¹, M. Sugiyama ², A. Saito ², K. Vilayheuang ³, D. Chanthanom ³, H. Matsunaga ², T. Saito ², Y. Sakata ², K. Kato ⁴ (1.Fac. Humanit., Hirosaki U., 2.NARO/NIVTS, 3.NAFRI, 4.Grad. Sch. Environ. Life Sci., Okayama U.)

410 Genetic studies on Bambuseae species in Japan. XXXVI. Further observations on the flowering aspect and seedlings of Ginmeisuo, a cultivar of *Bambusa multiplex*

○Muramatsu, M. (none)

411 Phylogenetic relationships between common buckwheat and wide relative *Fagopyrum homotropicum* based on nuclear DNA sequences and cross compatibility

☆Yamamoto, Y. ¹, C. Li ², T. Ohsako ¹ (1.Grad. Sch. Life Env. Sci., Kyoto Pref. Univ., 2.Yunnan Agr. Univ.)

412 Breeding of a rice near-isogenic line "Hitomebore" with QTL for cold tolerance at booting stage derived from Bhutanese variety, Kuchum

○Endo, T. ¹, K. Saeki ¹, T. Ando ², A. Shomura ², T. Mizubayashi ², T. Yamamoto ² (1.Miyagi Prefectural Furukawa Agricultural Experiment Station, 2.National Institute of Agrobiological Sciences)

413 Reciprocal translocation identified in *Vigna angularis* dominates the wild population in East Japan

Wang, L. ¹, S. Kikuchi ², ☆C. Muto ³, K. Naito ³, T. Isemura ³, S. Isobe ⁴, A. Kaga ³, N. Tomooka ³ (1.Chinese Academy of Agri. Sci., 2.Grad.Sch. Hort. Chiba U., 3.National Institute of Agrobiological Sciences, 4.Kazusa DNA Res. Inst.)

414 Molecular phylogeny of the genus *Vigna*

☆Takahashi, Y. ^{1,2}, C. Muto ¹, K. Iseki ¹, K. Naito ¹, N. Tomooka ¹ (1.National Institute of Agrobiological Sciences, 2.Research Fellow of the Japan Society for the Promotion of Science)

415 Multiple origins of the genomic and genic structure of the local rice variety Kitaake from the northern limit of rice cultivation in the world

○Fujino, K., M. Obara, K. Tamura, K. Sato (NARO Hokkaido Agr Res Cent)

416 Genetic analyses of grain size and shape among hexaploid wheat accessions

☆Yoshioka, M., N. Mizuno, S. Takenaka, M. Nitta, J. Li, S. Nasuda (Grad. Sch. Agri., Kyoto Univ.)

417 Development of a 10K SNP array for Japanese soybeans

○Kaga, A. ¹, T. Shimizu ¹, T. Matsumoto ¹, H. Ohyanagi ², S. Watanabe ^{1,3}, H. Kanamori ¹, N. Namiki ², M. Shimomura ², H. Uenishi ¹, Y. Katayose ¹, M. Ishimoto ¹ (1.National

418 Construction of a high-density genetic map of common wheat by Genotyping-by-Sequencing

☆Kobayashi, F., H. Kanamori, T. Tanaka, Y. Katayose, J. Wu, H. Handa (NIAS)

501 Comparison of quality-related alleles among Australian and North American wheat classes exported to Japan

○Ikeda, T., M. Yanaka, K. Takata (Western Reg. Agri. Res. Cent.,NARO)

502 RNAi expression analyses in hybrid of low glutelin mutant rice variety and trial of becoming it low phosphorus

○Hashizume, F., Y. Mori, M. Hara (Mie Pref.Agr.Res.Inst.)

503 Estimation of major triacylglycerol lipase candidate genes in rice grain and isolation of candidate rice mutants by TILLING method

Hasegawa, Y. ^{1,2}, S. Hamada ^{1,3}, T. Kumamaru ⁴, H. Matsusaka ⁴, ☆Y. Suzuki ¹
(1.NARO, Inst. Crop Sci., 2.Inst. Wood Tech., Akita Pref. Univ., 3.Fac. Agri. and Life Sci., Hirosaki Univ., 4.Fac. Agri., Kyushu Univ.)

504 Inheritance of panicle shape and grain color in common millet (*Panicum miliaceum* L.)

○Nakajo, S. (Iwate Agric. Res. Ctr.)

505 Genetic study of quantitative and qualitative traits of DDMP saponin in wild soybean seeds

☆Katsuki, R. ¹, S. Watanabe ², A. Kaga ³, T. Shimizu ³, M. Ishimoto ³, K. Harada ³, C. Tsukamoto ⁴, J. Abe ¹, T. Yamada ¹ (1.Grad. Sch. Agric., Univ. Hokkaido, 2.Fac. Agric., Univ. Saga, 3.NIAS, 4.Fac. Agric., Univ. Iwate)

506 Isoflavone content and composition in response to temperature during soybean seed filling

☆Sugisawa, S., A. Torii, J. Abe, T. Yamada (Grad. Sch. Agric., Univ. Hokkaido)

507 Genetic and physiological analyses of varietal difference in chlorophyll content of stay-green soybean seeds

○Tsuchida, M. ¹, E. Ohashi ¹, H. Kobayashi ¹, M. Kusaba ², J. Abe ¹, T. Yamada ¹
(1.Grad.Sch.Agr.,Univ.Hokkaido, 2.Grad.Sch.Sci.,Hiroshima)

508 Genetic control of saponin components by using natural mutants in soybean

Yano, R. ¹, S. Tochigi ¹, Y. Takada ², Y. Takahashi ³, C. Tsukamoto ³, ○M. Ishimoto ¹
(1.National Institute of Agrobiological Sciences, 2.NARO Western Region Agricultural Research Center, 3.Graduate School of Agriculture, Iwate University)

509 Characterization of rice *camel* mutant showing abnormal apical meristems and identification of its responsible gene

☆Kobayashi, K., K. Hibara, J. Itoh, Y. Nagato (Grad. Sch. Agric. Life Sci., U. Tokyo)

510 Molecular dissection of rice leaf development in wild type and various morphogenetic mutants

☆DECHKRONG, P., J. Itoh (Grad.Sch.Agric.Life Sci.,U.Tokyo)

511 Functional analysis of a gene that regulates axillary meristem initiation in rice

☆Tanaka, W. ^{1,2}, Y. Ohmori ¹, T. Ushijima ³, H. Matsusaka ³, T. Matsushita ³, T. Kumamaru ³, S. Kawano ², H. Hirano ¹ (1.Department of Biological Sciences, Graduate School of Science, The University of Tokyo, 2.Department of Integrated Bioscience, Graduate School of Frontier Science, The University of Tokyo, 3.Faculty of Agriculture, Kyushu University)

512 Gene Body Methylation in rice

○Tsuji, H. ¹, N. Saihara ¹, Y. Higashi ¹, F. Miura ², T. Kurata ³, T. Ito ³, K. Shimamoto ¹
(1.Lab. Plant Mol. Genet., Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol., 2.Grad. Sch. Med.Sci., Kyushu Univ., 3.Plant Global Education Project, Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol.)

513 The deletion wheat mutant of clock-related gene, *Wheat PHYTOCLOCK 1*, disrupts the short day response, resulting in extra early-flowering

Nishiura, A. ¹, Y. Kazama ², T. Abe ², N. Mizuno ³, S. Nasuda ³, ○K. Murai ¹ (1.Dep. Biosci., Fukui Pref. Univ., 2.RIKEN Nishina Cent., 3.Grad. Sch. Agr. Sci., Kyoto Univ.)

514 Analysis of a novel flowering time gene in rice on the chromosome 9

☆Yoshitsu, Y., Y. Takahata, S. Yokoi (Fac. Agr., Iwate Univ.)

515 Genetic mapping of the earliness gene on chromosome 3B detected in the wheat breeding line "Chogokuwase"

Yamashita, H. ¹, M. Takeguchi ¹, ○H. Nishida ¹, N. Mizuno ², M. Nitta ², M. Fujita ³, S. Nasuda ², K. Kato ¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Grad. Sch. Agr., Kyoto U., 3.NARO/NICS)

516 Analysis of onion4, a rice shoot development mutant associated with biosynthesis of very-long-chain fatty acids

☆Kogure, K., Y. Ito (Grad. Sch. Agri. Sci. , Univ. Tohoku)

517 Effect of Vernalization genes and Photoperiodic Response genes on heading date of wheat in southern part of Japan

○Matsunaka, H. ¹, K. Kato ², H. Nishida ², K. Nakamura ¹, M. Okami ¹, M. Fujita ³ (1.NARO/KARC, 2.Grad. Sch. Environ. Life Sci., 3.NARO/NICS)

601 Relationship between phytic acid synthesis-related gene, *OsPGK1*, and the homeostasis of phosphorus in seeds

☆Tagashira, Y. ¹, T. Shimizu ¹, O. Yatou ², K. Yoshida ¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NARC)

602 Chromosomal inversion caused by gamma irradiation contributes to downregulation of a WBC11 homolog in bloomless sorghum

○Mizuno, H. ¹, H. Kawahigashi ¹, H. Kanamori ¹, H. Minami ², J. Ogata ¹, H. Nakagawa ³, T. Matsumoto ¹ (1.NIAS, 2.MSS, 3.JIRCAS)

603 Genome-wide transcriptome analysis under phosphate starvation in wheat

○Oono, Y., F. Kobayashi, Y. Kawahara, T. Yazawa, H. Kanamori, H. Sasaki, S. Mori, J. Wu, T. Itoh, T. Matsumoto, H. Handa (National Institute of Agrobiological Sciences)

604 Analysis of auxin or cytokinin responsive gene expression on protonema cells in *Physcomitrella patens*, *Racomitrium japonicum* and *Pohlia flexuosa*

☆Ueno, H. ¹, Y. Takahara ² (1.Grad. Sch. Bio., Nagaoka University of Technology, 2.Bio., Nagaoka University of Technology)

605 Rare allele of a novel histone H4 acetyltransferase enhances grain weight, yield and plant biomass presumably through the regulation of transcription

☆Nagai, K. ¹, T. Kuroha ¹, X. Song ^{1,2}, M. Ayano ¹, A. Minami ¹, M. Ashikari ¹ (1.Biosci. Biotec. Cent., 2.Chin. Acad. of Sci.)

606 Phylogenetic networks of sweet potato (*Ipomoea batatas* L.) through South-America to Oceania based on genome-wide analysis of retrotransposon insertions

☆Monden, Y. ¹, K. Taharadani ¹, M. Intoh ^{2,3}, N. Saitou ^{4,5,6}, M. Tahara ¹ (1.Grad. Sch. Env. & Life Sci., Univ. Okayama, 2.National Museum of Ethnology, 3.SOKENDAI, Cul. & Soc. Stud., 4.National Institute of Genetics. Population Genetics, 5.SOKENDAI, Life Sci., 6.Grad. Sch. Sci., Univ. Tokyo)

607 Analysis of an active transposon in rice during callus induction and regeneration

○Habu, Y., H. Saika, H. Numa (Agrogenomics Res Center, NIAS)

608 Epigenome editing in potato by hetero-grafting

☆Kasai, A., H. Hojo, T. Harada (Fac. Agric. Life Sci., Hirosaki Univ.)

609 Growth pattern and morphogenesis at the rhizome bud of *Oryza longistaminata*, wild rice species in Africa, which can do vegetative reproduction by rhizome

☆UEHARA, K., M. ASHIKARI (Grad. Sch. Agr., Univ. Nagoya)

610 The trade-off between cleistogamy and fertility modulated by B-class mutations in rice

○Yoshida, H. ^{1,2}, M. Kuroki ³, S. Yao ², F. Lombardo ¹, H. Shimizu ³, T. Ikegaya ³, M. Kimizu ², S. Ohmori ², T. Akiyama ¹, T. Hayashi ⁴, S. Koike ⁴, O. Yatou ² (1.NARO Inst. Crop Sci., 2.NARO Agric. Res. Ctr., Hokuriku Res. Ctr., 3.NARO Hokkaido Agric. Res. Ctr., 4.NARO Tohoku Agric. Res. Ctr.)

611 Genetic analysis of wheat spike compactness mutants

☆Uchiyama, H., S. Sakuma, K. Kawaura, Y. Ogihara (KIBR, YCU)

612 Toward identification of the substrate of CYP78 regulating leaf and embryo size

☆Mizuno, I., M. Mimura, J. Itoh, K. Hibara (Grad. Sch. Agric. Life Sci., U.Tokyo)

613 QTL analysis for cooked rice properties using RILs derived from a cross between 'Hinohikari' and 'Nikomaru'

○Kobayashi, A. ¹, T. Kataoka ², Y. Kogi ¹, K. Tamura ², K. Tomita ¹ (1.Fukui Agr. Exp. Stn., 2.NARO/KARC)

614 Evaluation for agronomic traits and processing suitability of rice inbred lines derived from a cross between a seed storage protein mutant *esp2* and Koshihikari

☆Hori, K. ¹, Y. Kawagoe ¹, K. Nakamura ², N. Tsuge ², T. Okunishi ³, T. Ishii ⁴, T. Ikka ¹, T. Yamamoto ¹ (1.NIAS, 2.Nisshin Flour Milling Inc., 3.NARO NFRI, 4.NARO NICS)

615 Natural variation of glucose content in rice straw using liquid hydrolysate after dilute sulfuric acid pretreatment

☆Goda, T. ¹, H. Teramura ², M. Suehiro ¹, K. Kanamaru ³, M. Maeda ¹, S. Okada ¹, H. Kawaguchi ², C. Ogino ², A. Kondo ², M. Yamasaki ¹ (1.Food Resources Education and Research Center, Graduate School of Agricultural Science, Kobe University, 2.Graduate School of Engineering Kobe University, 3.Graduate School of Agricultural Science, Kobe University)

616 QTL analysis of the hybrid vigor in the commercial F1 hybrid cultivar W77 of Chinese cabbage

☆Abe, H. ¹, T. Kawanabe ², N. Saeki ¹, M. Shimizu ¹, S. Konno ³, A. Nagano ^{4,6}, M. Honjyo ⁴, M. Yasugi ⁴, H. Kudoh ⁴, K. Hatakeyama ⁵, S. Matsumoto ⁵, K. Okazaki ¹, M. Kaji ³, R. Fujimoto ^{2,6} (1.Grad. Sch. Agric. Sci, Niigata Univ., 2.Grad. Sch. Agric. Sci, Kobe Univ., 3.Watanabe Seed Co., Ltd, 4.Cent. of Ecol. Res., Kyoto Univ., 5.NARO, NIVTS, 6.PRESTO, JST)

Poster presentations

P001 Building genomic selection models for fruit traits using multiple F1 families in Japanese pear

☆Minamikawa, M. ¹, A. Onogi ¹, S. Terakami ², N. Takada ², T. Saito ², T. Hayashi ³, T. Yamamoto ², H. Iwata ¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Natl. Inst. Fruit Tree

P002 Constructing a crowd participant system and scale-out for breeding science

○Kaminuma, E. ¹, T. Fujisawa ¹, Y. Baba ^{2,3}, H. Kashima ⁴, Y. Nakamura ¹ (1.NIG, 2.NII, 3.JST, ERATO, 4.Kyoto Univ)

P003 Development of the *Vigna* Genome Server, 'VigGS'

○Sakai, H., K. Naito, T. Itoh, N. Tomooka (National Institute of Agrobiological Sciences, Japan)

P004 Development of high-throughput phenotyping system using an unmanned helicopter

☆Watanabe, K. ¹, K. Arai ², M. Usami ², W. Guo ¹, H. Kanegae ¹, M. Minamikawa ¹, T. Hakoyama ¹, K. Yamazaki ¹, H. Takanashi ^{1,6}, M. Fujimoto ^{1,6}, T. Sazuka ^{3,6}, T. Tokunaga ^{4,6}, R. Sugiura ⁵, S. Ninomiya ¹, T. Fujiwara ¹, N. Tsutsumi ^{1,6}, H. Iwata ^{1,6} (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Air4D Co., Ltd., 3.Biosci. Biotech. Cent., Nagoya Univ., 4.EARTHNOTE Co., Ltd., 5.NARO, HARC, 6.CREST, JST)

P005 Development of digital application for supporting phenotyping in field using tablet device

○Tanabata, T. ¹, T. Kataoka ², A. Kobayashi ³, K. Hori ⁴ (1.RIKEN CSRS, 2.NARO KARC, 3.Fukui Agr. Exp. Stn., 4.NIAS)

P006 The evaluation of environmental stability for agronomic traits in the original rice cultivar and its isogenic lines of complete blast resistance

○Kanbe, T. ¹, N. Hashimoto ¹, H. Kasaneyama ¹, T. Matsui ¹, E. Nara ¹, K. Ishizaki ¹ (1.Niigata Crop Res. Cent., 2.Niigata Crop Res. Cent., 3.Niigata Crop Res. Cent., 4.Niigata Crop Res. Cent., 5.Niigata Crop Res. Cent.)

P007 Fast estimation of model parameters for predicting rice phenological development: the application of particle swarm optimization (PSO) and GPU computing

☆Aoike, T. ¹, M. Watanabe ², A. Onogi ², O. Ideta ³, T. Yoshioka ⁴, K. Eban ⁵, H. Yamasaki ⁶, H. Iwata ² (1.Faculty of Agriculture, U. Tokyo, 2.Grad. Sch. Agric. Life Sci., U. Tokyo, 3.Natl. Agr. Res. Ctr., Western Region, 4.Food Resources Education and Research Ctr., Grad. Sch. Agric. Sci., Kobe U., 5.Natl. Inst. Agrobiological Sci., 6.NARO/NARC)

P008 Novel methods for evaluating genotype x environmental interaction in multiple traits: application of tensor principal component analysis

☆Hori, T. ¹, D. Montcho ², C. Agbangla ³, K. Futakuchi ², H. Iwata ⁴ (1.Faculty of Agriculture, Univ. Tokyo, 2.Africa Rice Center, 3. Université d'Abomey-Calavi, 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P009 Evaluation of the UK wheat varieties as a high-yield germplasm in the warm region of Japan

○Fujita, M., T. Takayama, C. Kiribuchi-Otobe, H. Kojima, S. Oda (NARO/NICS)

P010 Development of a new soybean cultivar "Kanto 115" with small black seeds

○Takahashi, K. ¹, T. Yamada ¹, A. Hishinuma ¹, M. Hajika ¹, K. Hirata ², N. Yamada ³, N. Oki ⁴ (1.NARO Inst. Crop Sci., 2.NARO Tohoku Agri. Res. Ctr., 3.Nagano Pref. Vegetable and Ornamental Crops Exp. Stn., 4.NARO Kyushu Okinawa Agri. Res. Ctr.)

P011 A new soybean cultivar "Sachiyutaka A1" with shattering resistance

○Hishinuma, A. ¹, K. Takahashi ¹, T. Yamada ¹, M. Hajika ¹, K. Hirata ², N. Yamada ³, N. Oki ⁴, H. Funatsuki ⁵ (1.NARO Inst. Crop Sci., 2.NARO Tohoku Agri. Res. Ctr., 3.Nagano Pref. Vegetable and Ornamental Crops Exp. Stn, 4.NARO Kyushu Okinawa Agri. Res. Ctr., 5.NARO Western Agri. Res. Ctr.)

P012 Breeding of a new soybean line "Hitachi No.2" with SMV and SCN resistance

☆Ikeda, C. ¹, M. Iwahashi ¹, K. Kosuge ², M. Miyamoto ³, K. Okano ³, M. Hirayama ⁴, M. Hajika ⁵, K. Takahashi ⁵, T. Yamada ⁵, M. Ishimoto ⁶, T. Sayama ⁶, K. Okamoto ¹ (1.Plant Biotech. Inst., Ibaraki Agri. Cent., 2.Rokkou Agri. & For. Management Office, 3.Agri. Res. Inst., Ibaraki Agri. Cent., 4.Ibaraki Pref., 5.NARO Nat. Inst. Crop. Sci., 6.Nat. Inst. Agrobiol. Sci.)

P013 Breeding of new common millet cultivar 'Kibi Iwate Mochi 1' with large blackish brown grain and high-yielding ability

○Takakusagi, M. ¹, S. Nakajo ², A. Nakanishi ¹ (1.Iwate Agric. Res. Cent. Northern Region Agricultural Institute, 2.Iwate Agric. Res. Cent.)

P014 "Satsuiku 2", the first LOX-less (with no lipoxygenase-1 activity) malting barley variety in Japan

○Kanatani, R. ¹, W. Saito ¹, T. Hoki ¹, T. Iimure ², N. Hirota ¹, M. Kihara ¹, K. Takoi ³, T. Shinkai ³, A. Tanigawa ³, T. Watanabe ², K. Takazumi ², K. Ogushi ¹ (1.BRDD, Sapporo Brew. Ltd., 2.Frontier Laboratories of Value Creation, Sapporo Brew. Ltd., 3.Product & Technology Innovation Department, Sapporo Brew. Ltd.)

P015 A new soybean cultivar 'Toyomizuki' with processing suitability for tofu and chilling tolerance

☆Yamaguchi, N. ¹, T. Miyoshi ¹, S. Hagihara ^{1,2}, C. Suzuki ^{1,3}, S. Koyano ^{3,4}, S. Shirai ^{1,3}, S. Yumoto ^{1,5}, Y. Tanaka ¹, H. Kurosaki ^{1,3}, H. Yamazaki ^{1,6}, S. Ohnishi ^{1,2} (1.Tokachi Agr. Exp. Sta., HRO, 2.Kitami Agr. Exp. Sta., HRO, 3.Central Agr. Exp. Sta., HRO, 4.Hokkaido Nucl. Energy Environ. Res. Ctr., 5.Natl. Inst. Crop Sci., 6.Agr. Res. Dep., HRO)

P016 Variation in morphology, heading date and B-chromosome frequency in the rye populations at sand dune fields in Fukui Prefecture

Iwasaki, R., ○S. Ohta (Dep. Biosci., Fukui Pref. Univ.)

P017 Development of seed cleaner

Okuizumi, H. ¹, ☆T. Fujita ^{1,2}, R. Yazawa ¹, S. Hirashima ¹, E. Iizumi ¹, M. Akiba ¹, T. Iizumi ¹, H. Nakazawa ¹, Y. Ito ¹, E. Nonaka ¹, J. Inoue ¹ (1.National Institute of Agrobiological Sciences, 2.Tokyo University of Science)

P018 Variation in *SiDREB2* gene of foxtail millet and diversity of landraces from India

Suehiro, S. ¹, E. Domon ², ○K. Fukunaga ¹ (1.Fac. Life Environ. Sci., Pref. U. Hiroshima, 2.NIAS)

P019 Genetic analysis on wheat A genome ortholog of rice shattering related gene *qSH1*

☆Arai, Y., T. Sasanuma (Fac. Agr., Yamagata Univ.)

P020 Genetic analysis on fruit color variation in *Capsicum baccatum*

☆Matsumoto, Y., Y. Inaba, T. Sasanuma (Fac. Agr., Yamagata Univ.)

P021 Genetic interaction at two seed shattering loci and their effect on abscission layer formation in the genetic background of wild rice, *Oryza rufipogon*

☆Inoue, C., T. Htun, K. Inoue, K. Ikeda, T. Ishii, R. Ishikawa (Grad. Sch. Agr. Sci., Kobe Univ.)

P022 Genetic variation of Khao Kai Noi, Lao rice landrace, (*Oryza sativa* L.), examined by simple sequence repeat markers

☆Vilayheuang, K. ^{1,4}, R. Machida-Hirano ², C. Bounphanousay ⁴, K. Watanabe ^{2,3}
(1.Grad. Sch. LES., Univ. Tsukuba, 2.Gene Res. Cen., Univ. Tsukuba, 3.Fac. LES., Univ. Tsukuba, 4.ARC, NAFRI, Vientiane, Lao P.D.R)

P023 Genetic analysis of domestication traits in emmer wheat using backcross inbred lines

○Mori, N. ¹, P. Ngoc ¹, C. Vladutu ¹, P. Thanh ², P. Thanh ¹, T. Ishii ², S. Kianian ³
(1.Lab. Plant. Genet., Grad. Sch. Agr. Sci., Kobe Univ., 2.Lab. Plant. Breed., Grad. Sch. Agr. Sci., Kobe Univ., 3.USDA-ARS Cereal Disease Lab., Univ. Minnesota, U. S. A.)

P024 Entering into force of the Nagoya Protocol to the Convention on Biological Diversity

○Yamamoto, A. (Environment Policy Div., Minister's Secretariat, MAFF)

P025 Evaluation of petal harvesting related traits in safflower genetic resources

☆Aoyagi, S., Y. Takahashi, Y. Aizawa, T. Abe, T. Sasanuma (Fag. Agr., Yamagata Univ.)

P026 What we can see through an educational program 'Kitchen PCR'

○Asakura, N., R. Kikuchi (Kanagawa Univ. Fac. Eng.)

P027 Seed production potential of wild soybean under cultivated condition

☆Aoki, D. ¹, A. Mizuguti ¹, A. Arie ², K. Takamoto ², D. Stojšin ³, M. Horak ³, M. McPherson ³, S. Nakai ² (1.Fukui Prefecture University Faculty of Biotechnology, 2.Monsanto Japan Limited, 3.Monsanto Company)

P028 Analysis of phenomenon of multiple embryo sac formation and multiple embryogenesis in Arabidopsis transformants of ASG-1

○Chen, L. ¹, Y. Nishimura ¹, K. Yoshida ², T. Tetsumura ³, T. Sugita ⁴, D. Kurihara ⁵, T. Higahsiyama ⁵ (1.Fac. Environ. Hort. Sci., Minami Kyushu U., 2.Fac. Agri., U. of Tokyo, 3.Fac. Agri., U. of Miyazaki, 4.Miyazaki Pref. Agri. Experi. Sta., 5.Fac. Sci., Nagoya U.)

P029 Genes modifying the effect of ion-beam induced late heading mutant gene in a extremely late-heading mutant KGM27 in rice

○Ichitani, K. ¹, E. Sakaguchi ¹, T. Koga ¹, D. Yamaguchi ¹, S. Taura ², M. Sato ¹ (1.Fac. Agri., Kagoshima Univ., 2.Inst. Gene Res., Kagoshima Univ.)

P030 Characterization of a *SICCD8* detective mutant line 5291 in tomato

☆Tsutsumi, T. ¹, S. Fukushima ¹, Y. Okabe ², T. Arizumi ², H. Ezura ², M. Umehara ¹ (1.Dept. Appl. Biosci., Fac. Life Sci., Toyo Univ, 2.Grad. Sch. Life Env. Sci., Univ. Tsukuba)

P031 Narrowing down the apomixis-controlling gene region utilizing deletion mutants induced by heavy ion-beam irradiation

○Takahara, M. ¹, M. Ebina ¹, R. Morita ², Y. Kazama ², T. Abe ², T. Takamizo ¹, H. Nakagawa ³ (1.NILGS, 2.RIKEN Nishina Center, 3.JIRCAS)

P032 Characteristics of hybrid seedlings in crosses of *Nicotiana nesophila* Johnston × *N. tabacum* L. and *N. nesophila* × the progenitors of *N. tabacum*

○Muraida, N., W. Marubashi (Sch.Agr.Meiji U.)

P033 Transfer of early flowering alleles from *Aegilops tauschii* to Japanese common wheat cultivar

○Takumi, S. ¹, T. Nguyen ¹, K. Murai ² (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Fac. Biosci., Fukui Pref. Univ.)

P034 Studies on the variegated tobacco plants appeared in the chloroplast transformation experiment. II. Molecular nature of chloroplast DNA

☆Uemura, K. ¹, M. Tsuji ², S. Morita ³, M. Yamamoto ⁴, T. Terachi ¹ (1.Fac.Life Sci., Kyoto Sangyo Univ., 2.Grad. Sch. Fac. Eng., Kyoto Sangyo Univ., 3.Grad. Sch. Life and Envi., Kyoto Pref Univ., 4.Kansai Univ. Welf. Sci.)

P035 Modification of fatty acid composition of rapeseed (*Brassica napus*) by ACP-thioesterase (Cle-FatB2) gene of *Cuphea leptopoda*

Nishida, M., Y. Kakizaki, H. Doi, H. Akiyama, S. Yokoi, ○Y. Takahata (Fac. of Agri., Iwate Univ.)

P036 Functional analysis of apomixis specific gene: ASG-1 gene transformation to gramineous plants

○Nishimura, Y. ¹, K. Yoshida ², T. Sugita ³, D. Kurihara ⁴, T. Higashiyama ⁴, L. Chen ¹ (1.Fac. Environ. Hort., Minami Kyushu U., 2.Fac. Agri., U. Tokyo, 3.Miyazaki Pref. Agri. Experi. Sta., 4.Fac. Sci., Nagoya U.)

P037 Investigation of male sterility and female fertility in transgenic male sterile rice plants using promoters of anther-specific expressed gene in rice

☆Akasaka, M. ¹, Y. Taniguchi ¹, M. Oshima ², K. Abe ², Y. Tabei ², J. Tanaka ¹ (1.NARO, 2.NIAS)

P038 Flowering habits and seed productivity in progenies from dominant male sterile rice plants with tapetum-specific expression of *barnase* gene

○Abe, K. ¹, M. Oshima ¹, J. Tanaka ², M. Akasaka ², Y. Taniguchi ², F. Hirose ¹, H. Ichikawa ¹, Y. Tabei ¹ (1.NIAS, 2.NARO)

P039 Confirming a major QTL and finding additional loci conditioning to Brown spot field resistance in rice

○Sato, H. ¹, K. Matsumoto ², C. Ota ², T. Yamakawa ², J. Kihara ³, R. Mizobuchi ⁴ (1.Kyushu Okinawa Agriculture Research Center, 2.Mie Prefecture Agricultural Research Institute, 3.Shimane University, 4.National Institute of Agrobiological Sciences)

P040 QTL analysis of blast field resistance in a Japanese domestic rice cultivar, "Ouu357"

○Kataoka, T. ¹, S. Fukuoka ², T. Mizubayashi ², M. Yamaguchi ³, T. Endo ⁴, K. Nakagomi ⁵, H. Sato ¹ (1.NARO/KARC, 2.Natl. Inst. Agrobiol. Sci., 3.NICS, 4.Miyagi Pref. Furukawa Agri. Exp. Stn., 5.NARO/WARC)

P041 Genetic analysis of net blotch resistance derived from wild barley

Sato, K., ○K. Sakamoto, H. Hisano (Institute of Plant Science and Resources, Okayama University)

P042 Screening of cucurbitaceous plants for resistance to root-knot nematodes

○Iwahori, H. ¹, H. Watanabe ², Y. Hoshi ², K. Uesugi ¹, Y. Tateishi ¹ (1.Kyushu Okinawa Agr. Res. Ctr., NARO, 2.Sch. Agr., Tokai Univ.)

P043 Screening of resistance for *Meloidgyne graminis* in *Zoysia* species

○Matsuda, Y. ¹, Y. Kitajima ¹, H. Kaneko ¹, H. Iwahori ², T. Murata ¹ (1.Sch. of Agri. Tokai U., 2.NARO/KARC)

P044 Effects of alleviation of low-oxygen stress and rapid-imbibition on QTLs controlling pre-germination flooding tolerance in soybean

☆Nishida, M., R. Shirai, M. Teraishi, T. Tsukiyama, Y. Okumoto (Grad. Sch. Agri., Kyoto Univ.)

P045 Positive correlation between seedling vigor and expression of genes for ABA catabolic enzymes and GA biosynthesis enzymes under low temperatures

○Ohashi, M., A. Endo, Y. Sato (NARO Hokkaido Agricultural Research Center)

P046 Improving low temperature germinability in rice by QTL pyramiding

☆Satoh, T. ¹, K. Tezuka ¹, T. Kawamoto ², S. Shibata ², K. Katoh ², R. Takahashi ², N. Satoh ³, K. Sakurai ³, A. Watanabe ³, H. Takahashi ³, H. Akagi ³ (1.Grad. Sch. Biores. Sci. Akita Pref. Univ., 2.Akita Pref. Agri. Exp. Sta., 3.Akita Pref. Univ.)

P047 Cadmium uptake characters of wild rice strains of *Oryza glumaepatula*

☆Miyakawa, N. ¹, E. Fujieda ², N. Satoh ², K. Sakurai ², H. Takahashi ², A. Watanabe ², H. Akagi ² (1.Grad. Sch. Biores. Sci. Akita Pref. Univ., 2.Akita Pref. Univ.)

P048 Importance of ABA, GA and oxygen-scavenging system in recovery of radish seedlings after osmotic stress

○Yoshino, Y., M. Saito, T. Ito, J. Nakamura, A. Tateishi, S. Kubota, K. Nomura (Coll. Bioresource Sci., Nihon U.)

P049 Rice ABC transporter RCN1 is required for stomatal closure

☆Matsuda, S. ¹, Y. Tokuji ¹, M. Nakazono ², I. Takamura ³, K. Kato ¹ (1.Obihiro Univ. Agric. & Vet. Med., 2.Grad. Sch. Agric., Nagoya U., 3.Res. Fac. Agric. Hokkaido Univ)

P050 Analyses of functions of Arabidopsis VIP1 and its close homologs

☆Tsugama, D. ^{1,2,3}, M. Kobayashi ¹, T. Takano ¹ (1.ANESC., Univ. Tokyo, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.JSPS Research Fellow (PD))

P051 Analysis of iron toxicity tolerant cultivars selected from Rice Core Collection

☆Hirakawa, T. ¹, H. Takahashi ¹, Y. Inukai ², M. Nakazono ¹ (1.Grad. Sch. Bioagr. Sci., Univ. Nagoya, 2.ICCAE, Univ. Nagoya)

P052 Response of Arabidopsis to a combination of heat stress and drought

☆Fukui, G., M. Endo, N. Suzuki (Sophia University, Faculty of Science and Technology)

P053 Global gene expression analysis of a bicarbonate-tolerant species *Puccinellia tenuiflora* and its related sensitive species *Poa annua* under NaHCO₃ treatment

☆Kobayashi, S. ¹, H. Kurokochi ¹, H. Satone ², E. Tang ², S. Asakawa ², T. Takano ¹ (1.ANESC, Univ. Tokyo, 2.GSALS, Univ. Tokyo)

P054 Evaluation on overwintering ability of F9 RIL between "Fuyugoshi", a domestic rice strain and "Hoshinoyume", a commercial rice variety in Hokkaido

○Ushiki, J. ¹, S. Matsuba ¹, F. Sasaki ^{1,2}, S. Hayashi ¹, K. Okazaki ¹ (1.Hokkaido Agr. Exp. Stn., 2.Aomori Pref. Industrial Technology Res. Cent.)

P055 Mapping of QTLs controlling cool temperature tolerance on chromosome 4 in rice and breeding of near isogenic lines

○Kon, C. ¹, S. Kanda ¹, T. Ono ², M. Suto ¹, S. Moriyama ¹ (1.AITC Agric. Res. Inst., 2.Aomori Prefecture Seihoku District Administration Office)

P056 Varietal characteristics of extensograph, farinograph and mixograph values at hard wheat cultivar of Nagano

○Uehara, Y. ¹, H. Maejima ¹, T. Ushiyama ² (1.Nagano Agr.Exp.Stn., 2.Nagano Nansahin Agr.Exp.Stn.)

P057 Natural variation in ABA sensitivity of hexaploid wheat seedlings and its effect on seed dormancy

☆Yokota, H. ¹, M. Iehisa ¹, S. Nasuda ², S. Takumi ¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Grad. Sch. Agr., Kyoto Univ.)

P058 Genetic analyses of seed lignan content in sesame

○Yamamoto, M. ¹, S. Yoroizuka ¹, N. Goto ², K. Masuda ², T. Wakasugi ¹, K. Yamada ¹
(1.Grad. Sch. Sci. Eng., Univ. Toyama, 2.Fac. Sci., Univ. Toyama)

P059 Quality and processing suitability of soft winter wheat line with glutenin subunits derived from a club wheat

○Yoshimura, Y. ¹, M. Sato ², H. Jinno ¹, M. Ikeda ³, T. Abe ² (1.Kitami Agri. Exp. Stn., HRO, 2.Central Agri. Exp. Stn., HRO, 3.Western Reg. Agri. Res. Cent.,NARO)

P060 Varietal difference of ash content in barley flour

○Maeijma, H., Y. Uehara (Nagano Agri.Exp.Stn.)

P061 Quality of flour and noodle making in barley lines with different contents of amylose and β -glucan

○Takahashi, A., T. Yoshioka (NARO/WARC)

P062 Characterization and rough mapping of the responsible gene using endosperm mutant of rice

☆Doi, M. ¹, T. Hobo ², S. Ota ³, H. Kitano ² (1.Fac. Agr., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.Grad. Sch. Bioagr. Sci., Nagoya U.)

P063 Gene expression of anthocyanidin reductase (ANR) and leucoanthocyanidin reductase (LAR) and accumulation of proanthocyanidins in buckwheat seedlings

○Matsui, K. ¹, Y. Yasui ², M. Mori ³, Y. Nishiba ¹, A. Walker ⁴, T. Hisano ¹ (1.NARO/KARC, 2.Grad. Sch. Agric. Kyoto Univ., 3.Res. Inst. Biores. Biotec. Ishikawa Pref. Univ., 4.CSIRO)

P064 Expression analysis of seed storage proteins in alien chromosome addition lines of common wheat with weak dough

○Tanaka, H. ¹, T. Kodani ¹, T. Arakawa ¹, H. Tsujimoto ² (1.Fac. Agr., Tottori Univ., 2.ALRC, Tottori Univ.)

P065 Additional nitrogen fertilization at heading time of rice down-regulates cellulose synthesis in seed endosperm

○Kuroda, M. ¹, K. Midorikawa ², K. Terauchi ², M. Hoshi ², S. Ikenaga ³, Y. Ishimaru ², K. Abe ^{2,4}, T. Asakura ² (1.NARO Agric. Res. Cent., 2.The Univ. Tokyo, 3.NARO Tohoku Agric. Res. Cent., 4.Kanagawa Sci. Acad. Technol.)

P066 Analysis of qSRN7 affecting higher order branching of panicle in rice increasing grain number

○Hobo, T. ¹, Y. Fujishiro ², R. Ishihara ², Y. Takeda ², T. Kunishima ², S. Ota ², M. Ikeda ¹, J. Kyojuka ³, H. Kitano ¹ (1.Biosci. Biotech. Ctr., Nagoya U., 2.Grad. Sch. Bioagr. Sci., Nagoya U., 3.Grad.Sch. Agric. Life Sci., U.Tokyo)

P067 Genetical analysis for panicle traits in rice using NERICA's parental line, WAB181-18

☆Agata, A. ¹, T. Hobo ³, Y. Takeda ², R. Ishihara ², T. Kunishima ², Y. Fujishiro ², S. Ota ², M. Doi ¹, K. Doi ², Y. Inukai ⁴, D. Makihara ⁴, H. Kitano ³ (1.Fac. Agr., Nagoya U., 2.Grad. Sch. Bioagr. Sci., Nagoya U., 3.Biosci. Biotec. Ctr., Nagoya U., 4.ICCAE, Nagoya U.)

P068 QTL analysis on the branching structure of rice panicle using an indica type multi-grain cultivar, VT-101

☆Ota, S. ¹, T. Hobo ², T. Touyama ¹, D. Tran ³, D. Tran ⁴, H. Le ⁴, H. Kitano ² (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.Grad. Sch. IDEC, Hiroshima U., 4.Dep. Mol. Biol. Agric. Genet. Inst., Ha Noi, Vietnam)

P069 Characterization of a rice line displaying abundant tillers under sparse planting condition isolated from Koshihikari/ *Oryza rufipogon* CSSL (2)

○Inagaki, N. (Div Plant Sci, Natl Inst Agrobiol Sci)

P070 Is circadian rhythm involved in hybrid vigor in *Arabidopsis thaliana*

Kawanabe, T. ¹, N. Saeki ², H. Abe ², ○R. Fujimoto ¹ (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Grad. Sch. Sci. Tech., Niigata Univ.)

P071 Analysis of agronomic performance and practicality of β -glucanless barley lines

○Tonooka, T. ^{1,2}, E. Aoki ¹, T. Yoshioka ^{1,3}, N. Kawada ², H. Araki ² (1.NARO Inst. Crop. Sci., 2.NARO Kyushu Okinawa Agric. Res. Cent., 3.NARO West. Reg. Agric. Res. Cent.)

P072 Identification of genes for annual growth habit derived from African rice (*O.glaberrima* Steud.)

Ozaki, Y. ¹, M. Fujioka ¹, ☆H. Sunohara ¹, T. Takashi ², H. Kitano ³, K. Doi ¹ (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.STAY GREEN Co., Ltd., 3.Biosci. Biotec. Ctr., Nagoya U.)

P073 Characterization of QTLs for hydraulic conductance and maintaining leaf color at ripening stage detected in a high photosynthesis rice cultivar, Akenohoshi

○Yamamoto, T. ¹, T. Suzuki ², K. Suzuki ², S. Adachi ^{1,3}, T. Ookawa ², T. Hirasawa ², M. Yano ^{1,3} (1.National Institute of Agrobiological Sciences, 2.Tokyo University of Agriculture and Technology, 3.NARO Institute of Crop Science)

P074 The analysis of seed longevity focusing on the degradation of the RNA in embryos of rice seed

☆Kumasaka, Y. ¹, N. Sano ^{1,2}, K. Murata ³, T. Yamada ¹, M. Kanekatsu ¹ (1.Grad. Sch. Agr., Tokyo U. Agr. Tec, 2.RIKEN CSRS, 3.Toyama Pref. Agr. Forest. Fish. Res)

P075 Genetic mechanism regulating the number of root cortical cell layers in rice

☆Tasaki, M. ¹, Y. Momiki ², N. Satoh-Nagasawa ³, Y. Kitomi ⁴, M. Takahashi-Nosaka ¹, K. Hibara ⁵, Y. Nagato ⁵, H. Kitano ⁶, Y. Inukai ¹ (1.ICCAE, Nagoya U., 2.Sch. Agr. Sci., Nagoya U., 3.Fac. Biores. Sci., Akita Pref. U., 4.NIAS, 5.Grad. Sch. Agric. Life Sci., U. Tokyo, 6.Biosci. Biotech. Ctr., Nagoya U.)

P076 Analysis of the *rrl3* mutants reveals the importance of arginine biosynthesis in the maintenance of root apical meristem in rice

○Shelley, I. ¹, S. Watanabe ², N. Nagasawa ³, A. Ogawa ³, H. Kitano ⁴, Y. Inukai ¹ (1.ICCAE, Nagoya U., 2.Sch. Agr. Sci., Nagoya U., 3.Fac. Biores. Sci., Akita Pref. U., 4.Biotsci. Biotech. Ctr., Nagoya U.)

P077 Analysis of rice *mkb3* mutant showing pleiotropic abnormalities in above-ground part

☆Shimano, S., K. Hibara, J. Itoh (Grad. Sch. Agric. Life Sci., U. Tokyo)

P078 Expression and DNA methylation pattern analyses of *Wheat PISTILLATA-2* (*WPI2*) in polyploid wheat

☆Tanaka, M., S. Kitagawa, K. Murai (Dep. Biosci., Fukui Pref. Univ.)

P079 A malformed spikelet mutant (mls3) induced by two bases substitution at the zinc finger protein gene on the chromosome 4 in rice

☆Nakada, A., K. Oshima, Y. Kishima, I. Takamure (Res. Fac. Agr. Hokkaidou. Univ)

P080 Searching for interaction proteins and downstream factors of QHB in rice

☆Sibata, A. ¹, K. Sibata ¹, S. Nishiuchi ¹, H. Inahashi ¹, Y. Inukai ² (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.ICCAE, Nagoya U.)

P081 Diallel analysis of bloting time in cabbage (*Brassica oleracea*)

○Kakizaki, T. ¹, T. Ohara ¹, N. Fukino ¹, K. Hatakeyama ¹, S. Matsumoto ¹, H. Hanzawa ², M. Ishida ¹ (1.NARO Institute of Vegetable and Tea Science, 2.KANEKO SEEDS)

P082 Flowering controll of tomato, using auxin biosynthesis inhibitors

○Kikuchi, R. ^{1,4}, T. Higashide ², K. Soeno ³, Y. Shimada ⁴ (1.Kanagawa Univ., 2.NARO, 3.NARO, 4.KIBR, Yokohama city Univ.)

P083 A controlled environment system for agronomic trait analysis in soybean

☆Yokota, Y. ¹, T. Yamada ², K. Takagi ³, M. Kuroda ⁴, M. Ishimoto ¹ (1.National Institute of Agrobiological Sciences, 2.NARO Institute of Crop Science, 3.NARO Agricultural Research Center, 4.NARO/ARC Hokuriku Research Center)

P084 The effect of early- or late- heading *Aegilops tauschii* genotype on the flowering and expression pattern of *VRN1* gene in synthetic hexaploid wheat

☆Yamakage, Y. ¹, Y. Fujiwara ¹, S. Takumi ², K. Murai ¹ (1.Dep. Biosci., Fukui Pref. Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ.)

P085 Effect of hybrid necrosis on grain development in crosses between two wild einkorn wheat species

☆Takamatsu, K. ¹, T. Ikeda ², S. Takumi ¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.NARO West. Reg. Agr. Res. Cent.)

P086 Analysis of the role of SRK N-linked glycosylation in self-incompatibility in transgenic Brassicaceae

○Yamamoto, M. ¹, J. Nasrallah ² (1.Graduate School of Agricultural Science, Tohoku University, 2.Cornell Univ. Department of Plant Biology)

P087 Versatility and cyto- and molecular genetical characterizations of male sterile line of radish carrying *Brassica fruticulosa* cytoplasm

☆Kadota, A., Y. Chen, S. Bang, Y. Kaneko (Fac. Agric., Utsunomiya. U)

P088 Comparative transcriptome analysis of Owen-type cytoplasmic male sterile and fertile anther in sugar beet

☆Honma, Y. ¹, K. Taguchi ², T. Kubo ¹ (1.Grad. Sch. Agr., Hokkaido U., 2.NARO, Hokkaido Agricultural Research Center)

P089 Expression of beech FLOWERING LOCUS T (FT) at the timing of flowering induction

○Akada, S. ¹, M. Nakagawa ², Y. Ohmiya ³ (1.Fac. Agri. and Life Sci., Hirosaki Univ., 2.Office for Promotion of Gender Equality, Hirosaki Univ., 3.Forestry and Forest Products Research Institute)

P090 Sequence variations at the bolting locus B in Japanese sugar beet

○Kuroda, Y., H. Takahashi, K. Okazaki, K. Taguchi (Hokkaido Agr. Res. Cent., NARO)

P091 Callus formation and regeneration with anther culture derived from hybrids between *Oryza sativa* L. and *O. glaberrima* Steud

☆Kuniyoshi, D. ¹, R. Iwashiro ¹, Y. Kanaoka ¹, E. Inada ¹, Y. Okamoto ², Y. Kishima ¹ (1.Res. Fac. Agri., Hokkaido U., 2.Rakuno Gakuen University)

P092 Exploration of male determinant for buckwheat heteromorphic self-incompatibility using RNA-seq analysis

○Aii, J. ¹, S. Sato ¹, A. Tamaki ¹, M. Nagano ², C. Campbell ³, Y. Yasui ⁴, M. Mori ⁵, T. Ota ⁶, H. Tanaka ¹ (1.NUPALS, 2.Canadian Buckwheat International, 3.McKay Seed Company, 4.Grad. Sch. Agr., Kyoto Univ, 5.Res. Inst. Bioresour. Biotech., Ishikawa Pref. Univ, 6.Dep. Evol. Stud. Biosys., Grad. Univ)

P093 Genome-wide association study and accuracy of genomic selection models in Japanese tomato F1 varieties

☆Yamamoto, E. ¹, H. Matsunaga ¹, A. Suzuki ^{2,3}, M. Minamikawa ², H. Kanegae ², T. Nunome ¹, H. Yamaguchi ¹, K. Miyatake ¹, S. Negoro ¹, A. Ohyama ¹, H. Iwata ², H. Fukuoka ¹ (1.NIVTS, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Kaneko Seeds Co., Ltd.)

P094 Development of the Indel markers for the application of chromosomal segment substitution lines (CSSLs) with multiple donor cultivars

☆Choi, S. ¹, H. Sakai ¹, J. Wu ¹, T. Ando ¹, M. Yano ^{1,2}, S. Fukuoka ¹, J. Yonemaru ¹ (1.National Institute of Agrobiological Sciences, 2.NARO Institute of Crop Science)

P095 Search for *spikelet-tipped bristles 1* (*stb1*) gene using QTL-seq analysis in foxtail millet [*Setaria italica* (L.)P.Beauv.]

○Mukainari, Y. ¹, H. Takagi ², R. Terauchi ², K. Fukunaga ³ (1.Grad. Sch. Comprehensive Scientific Research, Pref. Univ. Hiroshima, 2.Iwate Biotech. Res. Cent., 3.Fac. Life and Environ. Sci., Pref. Univ. Hiroshima)

P096 Establishment of a base of inbred lines of Brassica rapa using DNA markers

☆Kamura, K. ¹, M. Yoshida ¹, M. Shimizu ¹, N. Saeki ¹, H. Abe ¹, Y. Ebe ¹, K. Okazaki ¹, R. Fujimoto ², T. Kawanabe ² (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ.)

P097 Efficient screening of novel retrotransposons that show insertion polymorphism among sweet potato cultivars via high-throughput sequencing platform

☆Imai, Y. ¹, Y. Monden ¹, Y. Okada ², O. Jahana ³, A. Kobayashi ², H. Tabuchi ², M. Tahara ¹ (1.Grad. Sch. Env. & Life Sci., Univ. Okayama, 2.KONARC, 3.OPARC)

P098 Transposon insertion on the genes located in the sex determination region of papaya

☆Ueno, H. ¹, N. Urasaki ², S. Natsume ³, K. Yoshida ³, K. Tarora ², A. Shudo ², R. Terauchi ³, H. Matsumura ⁴ (1.Dep. Biosci. Tex. Tech., Shinshu U., 2.Okinawa Pref. Agric. Res. Ctr., 3.Iwate Biotech. Res. Ctr., 4.Gene Res. Ctr., Shinshu U)

P099 Search for pathotype-specific regions of three isolates in the fungal pathogen *Fusarium oxysporum* causing yellow wilt of Brassica crops

☆Funaki, T. ¹, A. Tago ¹, Z. Pu ¹, E. Fukai ¹, Y. Sano ¹, T. Abe ¹, S. Fuji ², R. Fujimoto ³, M. Shimizu ⁴, S. Natsume ⁴, R. Terauchi ⁴, K. Okazaki ¹ (1.Grad. Sch. Sci. Tech., Niigata

P100 Exploration of candidate genes for semi-dwarf mutant *sda* in tartary buckwheat based on *de novo* assembled genome sequences

☆Nakano, A. ¹, T. Morishita ², T. Suzuki ², A. Shimizu ³, J. Aii ¹, H. Tanaka ¹ (1.NUPALS, 2.NARCH, 3.IRB, NIAS)

P101 Characterization of an ion-beam induced semi-dwarf mutant *sdb* in tartary buckwheat

☆Komori, M. ¹, A. Nakano ¹, E. Hashimoto ¹, T. Funaki ², T. Morishita ³, T. Suzuki ³, A. Shimizu ⁴, J. Aii ¹, H. Tanaka ¹ (1.NUPALS, 2.Niigata University, 3.NARCH, 4.IRB, NIAS)

P102 Comparative genome sequence analysis among Koshihikari and its related cultivars

○Kawahara, Y. ¹, N. Tanabe ², T. Itoh ¹, T. Izawa ² (1.Agrogenomics Res. Center, NIAS, 2.Div. of Plant Sci., NIAS)

P103 QTL analysis for capsanthin content in pepper

○Konishi, A. ¹, N. Furutani ¹, A. Ohyama ², H. Fukuoka ² (1.Kyoto Pref. Inst. of Agri. Biotech, 2.NARO Inst. of Vegetable and Tea Sci.)

P104 Comparative mapping of rice QTLs for deep rooting using three F2 populations

○Kawai, S., Y. Kitomi, N. Kanno, T. Mizubayashi, S. Fukuoka, Y. Uga (NIAS)

P105 QTL analysis for leaf senescence in an *indica-japonica* hybrid rice

☆Nishikiori, R. ¹, S. Endo ², Y. Kajiyama ², Y. Matsumoto ², M. Itakura ², T. Osawa ², Y. Kushida ², R. Shishido ¹ (1.Grad. Sch. Bioresource Sci, Nihon U., 2.Coll. Bioresource Sci, Nihon U.)

P106 Earliness genes surpassing an effect of the photoperiod-insensitive allele at *PpdA1* in a tetraploid wheat

☆Nishimura, K., K. Katsura, H. Saito, A. Kitajima, T. Nakazaki (Grad. Sch. Arg.,Kyoto U)

P107 Characterization of a low phytic acid mutant in rice

☆Nakamura, Y. ¹, M. Azuma ¹, Y. Yamagiwa ¹, O. Yato ², J. Aii ¹, H. Tanaka ¹ (1.NUPALS, 2.NARC)

P108 Mapping of resistance to southern bean mosaic virus in soybean-2-

○Saruta, M., Y. Takada (WARC)

P109 Development of InDel markers for Hokkaido rice (*Oryza sativa* L.) cultivars and construction of molecular linkage map of RIL population

Takano, S. ¹, S. Matsuda ¹, ☆N. Kinoshita ¹, N. Shimoda ¹, T. Sato ², K. Kato ¹ (1.Obihiro Univ. Agric. & Vet. Med., 2.H.R.O. Kamikawa Agr. Exp. Sta.)

P110 Application of genotyping by sequencing (GBS) to recombinant inbred lines of rice

☆Zhu, X. ¹, K. Doi ² (1.Biosci. Biotec. Ctr., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U.)

P111 Identification of novel genes controlling flowering time in soybean

○Watanabe, S. ¹, T. Yamada ², T. Anai ¹, M. Ishimoto ³, A. Kaga ³ (1.Fac. Agr., Univ. Saga, 2.Grad. Sch. Agr., Univ. Hokkaido, 3.NIAS)

P112 Chromosomal structure of an awnless gene region in wheat progenitor *Aegilops tauschii* var. *anathera*

☆Nishijima, R., S. Takumi (Grad. Sch. Agr. Sci., Kobe Univ.)

P113 Analysis of the dwarfing gene *dw1* that is used in sorghum breeding and its ortholog of rice

☆Fujimoto, H. ¹, S. Nakamura ², K. Shinohara ², S. Kasuga ³, Y. Ito ², M. Matsuoka ², H. Kitano ², T. Sazuka ² (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.AFC, Fac. of Agri., Shinshu Univ.)

P114 Genetic mapping and development of near-isogenic lines for the genes determining liguleless phenotype in *Triticum durum*

☆Amagai, Y., T. Kuboyama, N. Watanabe (Col. Agri., Univ. Ibaraki)

P115 Development of dCAPS makers for F1 seed purity test of melon by the analysis of PolA1 gene

☆Tsuchiya, A. ¹, D. Ogawa ², S. Makabe ³, T. Ito ², I. Nakamura ³ (1.Fac. Hort., Chiba U., 2.Inst. Hort. Plant Breed., 3.Grad. Sch. Hort., Chiba U.)

P116 Detection of polymorphisms between common wheat cultivars by RAN-seq analysis

☆Mizuno, N. ¹, K. Sato ², S. Nasuda ¹ (1.Grad.Sch.Agric.Sci., Kyoto U., 2.IPSR, Okayama U.)

P117 Pollen genome sequencing in red clover for SNP discovery

○Isobe, S. ¹, K. Shirasawa ¹, M. Kimura ¹, Y. Hoshino ², H. Hirakawa ¹ (1.Kazusa DNA Res. Inst., 2.Field Sci. Cen. for Northern Biosphere, Univ. Hokkaido)

P118 Construction of high-density map and QTL analysis for contents of bitterness in hop (*humulus lupulus* L.)

○Uemoto, M., N. Suda, K. Ogushi (BRDD, Sapporo Brew. Ltd.)

P119 Molecular characterization of SSR marker associated with early heading date in some rice genotypes

○Khatab, I. ¹, T. Kumamaru ² (1.Kafrelsheikh University, 2.Grad. Sch. Agr., Univ. Kyushu)

P120 Mapping of a QTL controlling grain thickness and yield

☆Yamaguchi, T. ¹, M. Omoteno ², F. Taguchi ³, Y. Iyama ¹, K. Fujita ¹, T. Ebitani ¹ (1.Toyama Pref. Agr. Forest. Fish. Res. Cent, 2.MAFF, 3.NIAS)

P121 Development of high efficient and expression transgenic rice plants using RNA silencing machinery

☆Ozawa, M., Y. Sato (Grad. Sch. Bioagr. Sci., Nagoya Univ.)

P122 Association of genome-wide transcriptional changes and pollen fertilities in rice under the low-temperature stress at the booting stage

☆Ishiguro, S. ¹, K. Fujino ¹, Y. Sato ², Y. Kishima ¹ (1.Res. Fac. Agr., Hokkaido U., 2.NARO Hokkaido Agricultural Research Center)

P123 Genome-wide comparative transcriptional analysis of developing seeds among seven *Oryza sativa* L. subsp. *japonica* cultivars grown northern limit of cultivation

☆Takano, S. ¹, Y. Hirayama ², T. Sato ², K. Kato ¹ (1.Obihiro Univ. Agr. & Vet. Med., 2.H.R.O. Kamikawa Agr. Exp. Sta.)

P124 Proteomic Analysis of Heat Stress Tolerance in Rice Seeds under Treatment of Hot Water Disinfection using Koshihikari / Habataki CSSLs

☆Kashiwagi, M. ¹, K. Izumikawa ¹, K. Murata ², T. Yamada ¹, M. Kanekatsu ¹ (1.Grad. Sch. Agric. Sci., Tokyo U. Agr. & Tec., 2.Toyama Pref. Agr. Forest. Fish. Res. Cen.)

P125 Transposition of fold back element in *Vrn-A1* of wheat- *Leymus racemosus* chromosome introgression lines induced early flowering

☆Mohammed, Y., H. Tsujimoto (Arid Land Res. Center, Tottori Univ.)

P126 Functional analysis of Arabidopsis Dynamin-Related Protein 2 (DRP2) in post-Golgi trafficking

☆Huang, J. ¹, M. Fujimoto ¹, M. Fujiwara ², Y. Fukao ², S. Arimura ¹, N. Tsutsumi ¹ (1.Grad. Sch. Agric. Life. Sci., U. Tokyo, 2.Plant Global Education Project, NAIST)

P127 Floral transcriptome analysis of *Primula sieboldii* E. Morren

○Ueno, S. ¹, D. Mizuta ², R. Ohsawa ² (1.Dept. For. Genet., FFPRI, 2.Grad. Life Env. Sci., Univ. Tsukuba)

P128 Approach for identification of factors controlling transposition activity of the rice transposon *mPing*

☆Teramoto, S. ¹, T. Tsukiyama ¹, T. Tanisaka ^{1,2}, Y. Okumoto ¹ (1.Grad. Sch. Agric., Kyoto Univ., 2.Dep. Agric. Regional Reclamation., Kibi Int. Univ.)
