Title of Papers Presented at the 147th Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 Heading gene analysis for breeding early-heading rice lines in Saitama prefecture

☆Nakamura, Y., H. Koyama (Saitama Agricultural Technology Research Center)

---

102 Comparative analysis of SNPs detected by three genome-wide genotyping technologies, ddRAD-Seq, GRAS-Di, and MIG-Seq

○Shirasawa, K.[1], K. Mishima[2], T. Iki[2], T. Hirao[3] (1.Kazusa DNA Res. Inst., 2.FFPRI FTBC TRBO, 3.FFPRI FTBC)

---

103 A novel Fusarium head blight resistance allele derived from Japanese landrace at 2DL located QTL is more valuable than that derived from Sumai 3

○Ohnishi, S.[1], K. Horikawa[2], K. Morita[1], N. Yamaguchi[2], C. Souma[2], Y. Sato[1], T. Sonoda[1] (1.HRO Kitami AES, 2.HRO Central AES)

---

104 TE insertion and constitutive expression of *VmSOS1* in salt-tolerant species *Vigna marina*

○Naito, K.[1], Y. Noda[2], F. Wang[1], C. Muto[1], H. Ohashi[3], H. Sakai[4], N. Suzui[2], Y. Yin[2], Y. Miyoshi[2], K. Enomoto[2], N. Kawachi[2], J. Furukawa[5] (1.Res. Cntr. Genet. Resour., NARO, 2.Takasaki Inst. Adv. Quant. Sci., QST, 3.Grad. Sch. Adv. Sci., Univ. Tokyo, 4.Res. Centr. Adv. Anal., NARO, 5.Grad. Sch. Life. Environ. Sci., Univ. Tsukuba)

---

105 Whole genome resequencing analysis of 96 diverse adzuki varieties: A step toward genome breeding in adzuki

☆Adegawa, S.[1], N. Yamaguchi[1], C. Souma[1], K. Shirasawa[2] (1.Central Agr. Exp. Stn., HRO, 2.Kazusa DNA Research Institute)

---

106 Sex determination in *Dioscorea tokoro*, a dioecious wild yam species

☆Kudoh, A.[1], S. Natsume[2], Y. Sugihara[3], H. Katoh[1], A. Abe[2], K. Oikawa[2], M. Shimizu[2], K. Itoh[2], M. Tsujimura[4], T. Terachi[5], T. Sakai[1], A. Ohta[1], R. Terauchi[1] (1.Grad. Agri., Kyoto Univ., 2.IBRC, 3.The Sainsbury Laboratory, 4.Grad. Agri., Ryukoku Univ., 5.Faculty of Life Sciences, Kyoto Sangyo Univ.)

---

107 Whole-genome sequencing of sesame plants

Tanaka, H.[1], E. Ono[2], T. Segawa[2], J. Murata[3], H. Takagi[4], Y. Uegaki[5], H. Toyonaga[3], A. Shiraishi[3], M. Takagi[6], A. Toyoda[7], K. Sato[8], T. Wakasugi[8], M. Horikawa[3], M. Kawase[9], T. Itoh[1], ○M. Yamamoto[8] (1.School of Life Science and Technology, Institute of Science Tokyo, 2.Res. Inst. Suntory Global Innovation Center Ltd. (SIC), 3.Suntory Fdn. Life Sci. (SUNBOR), 4.Fac. Biores. Env. Sci., Ishikawa Pref. Univ., 5.Grad. Sch. Sci. Eng., Univ. Toyama, 6.Suntory System and Technology Ltd. (SST), 7.National Institute of Genetics, 8.Fac. Sci. Acad. Assem., Univ. Toyama, 9.Dep. Agr., Tokyo Univ. Agr.)

---

108 Two QTLs that act additively to accelerate the flowering of Koshihikari and their interactions with meteorological environments.

○Yonemaru, J.[1], K. Wada[1], S. Watanabe[2] (1.NARO-RCAIT, 2.Fukui Pref. Government)

---

109 Candidate genes for ratio of nodule bacteria species on soybean root

○Teraishi, M.[1], K. Sakaguchi[1], T. Tsuchimoto[1], T. Yoshikawa[1,2] (1.Grad. Sch. Agri., Kyoto Univ., 2.Natl. Inst. Genet.)

---

110 Potato blight resistance QTNs revealed by GWAS using a historical phenotype dataset from the HRO breeding program

○Sato, K.[1], Y. Ishikawa[1], T. Wazaki[1], H. Shinada[1], K. Shirasawa[2], N. Yamaguchi[3] (1.Kitami Agri. Exp. Stn., HRO., 2.Kazusa DNA Res. Inst., 3.Chuo Agri. Exp. Stn., HRO.)

---

111 QTL mapping of agronomic traits in true seed- and tuber-derived diploid potatoes

☆Kawamata, M., R. Sanetomo, K. Hosaka (Obihiro University of Agriculture and Veterinary Medicine)

---

112 The effect of *CDF1* alleles on the phenotype of the progeny from a very early-maturing potato cultivar

☆Eguchi, K., R. Sanetomo (Obihiro University of Agriculture and Veterinary Medicine)

---

113 Detection of QTLs associated with anthocyanin content and composition in sweetpotato storage roots

〇Tanaka, M., K. Suematsu, R. Kurata, T. Sakaigaichi (Kyushu Okinawa Agr. Res. Cent., NARO)

---

114 Identification and validation of QTLs controlling southern root-knot nematode (SP6-2) resistance utilized by bulked-segregant analysis

☆Tsuchiya, S.[1], M. Kurihara[2], H. Tabuchi[3], K. Nishimura[4], H. Nishida[4], K. Kato[4], Y. Monden[4] (1.Fac. Agri., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.KARC/NARO, 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

---

115 Genetic analysis of heterosis in culm length of sorghum F_1 hybrid 'Kazetachi'

☆Iri, Y.[1], S. Okada[2], S. Hashimoto[3], S. Nakamura (Araki)[2], K. Shinohara (Omae)[2], S. Kasuga[4], T. Sazuka[2] (1.Grad. Sch. Bioagri., Univ. Nagoya, 2.Biosci. and Biotech. Center, Univ. Nagoya, 3.Grad. Sch. Agric. Life. Sci., Univ. Tokyo, 4.AFC, Fac. of Agri., Univ. Shinshu)

---

116 Yield prediction based on QTLs for yield components using yield dissection models in tomato

☆Tsutsumi-Morita, Y.[1,2,3], E. Heuvelink[2], S. Khaleghi[2], D. Bustos-Korts[3,4], L. Marcelis[2], K. Vermeer[5], H. van Stappen-van Dijk[5], F. Millenaar[5], G. Van Voorn[3], M. Boer[3], F. Van Eeuwijk[3] (1.CCCA, NIES, 2.Horticulture and Product Physiology, Wageningen University & Research, 3.Biometris, Wageningen University & Research, 4.Universidad Austral de Chile, 5.BASF’s vegetable seeds business (Nunhems))

---

117 Comparison of good eating quality QTLs using two recombinant inbred line populations derived from Enrei and Dadachamame.

☆Shioya, N.[1], Y. Takagi[2], E. Ogiso-Tanaka[3], T. Hoshino[1,2] (1.Grad. Sch. Agr., Iwate Univ., 2.Grad. Sch. Agr., Yamagata Univ., 3.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci.)

---

118 Verification of QTLs and prediction of candidate genes associated with grain yield-related traits in a pyramidale wheat (*Triticumturgidum* L.)

☆Chen, T.[1], K. Nishimura[2], K. Murata[1], K. Nagasaka[1], Y. Iwahashi[1], T. Maki[1], Y. Kinoshita[1], H. Inoue[1], R. Nakano[1], T. Nakazaki[1,3] (1.Grad. Sch. Agr., Kyoto Univ, 2.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ, 3.IAC, Kyoto Univ)

---

119 Identification of genetic loci associated with awn length in *Aegilops sharonensis* Eig, a wild relative of wheat

☆Ye, K.[1], R. Terauchi[1,2], A. Ohta[1] (1.Grad. Sch. Agri., Kyoto Univ., 2.Iwate Biotechnology Research Center)

---

120 Analysis of the genetic basis for heading date of African cultivated rice *Oryza glaberrima* for utilization in temperate regions

☆Fujii, M.[1], A. Hirao[1], H. Yasui[2], Y. Yamagata[2] (1.Grad. Sch. Bioresour. Environ. Sci, Kyushu Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ.)

---

121 Exploration of quantitative trait loci for grain shape and weight in *Triticum timopheevii* and its ancestral species, *T. araraticum*

☆Hayashi, K.[1], R. Terauchi[1,2], A. Ohta[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.IBRC)

---

201 Prototype of Generative AI to Plant Breeding Data.

○Kajiya-Kanegae, H.[1,2], J. Yonemaru[1] (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)

---

202 The Activation of Transposons Under Environmental Stress and Their Potential Applications in Breeding

○Ito, H. (Grad. Sch. Sci., Univ. Hokkaido)

---

204 Narrowing down the CAD, casual gene of orange lemma mutation in barley

☆Kako, R.[1], M. Morita[2], N. Yamaji[2], H. Hisano[2], K. Sato[1,2] (1.Grad. Sch. Agr., Setsunan Univ., 2.IPSR, Okayama Univ.)

---

205 Characterization of an A-to-G base editor in the Arabidopsis chloroplast genome

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

---

206 Base editors using CRISPR-Cas3 in rice

○Saika, H.[1], K. Yoshimi[2] (1.Inst. Agrobiological Sci., 2.Inst. Med. Sci., Univ. Tokyo)

---

207 Exploration of rice genes targeted by MEL1, a germ cell-specific Argonaute protein

○Nonomura, K.[1,2], H. Liu[3], M. Mimura[4], W. Wu[3], R. Hiratsuka[5], K. Tanaka[6], M. Ohtani[7], T. Demura[8], S. Liu[3], T. Sasaki[9] (1.Plant Cytogen., Natl. Inst. Genet., 2.Genet. Program, SOKENDAI, 3.Zhejiang A&F Univ., 4.Grad. Sch. Agr. Life Sci, Univ. Tokyo, 5.Jikei Univ. Sch. Med., 6.Dept.

Informatics, Tokyo univ. Info. Sci., 7.Grad. Sch. Front. Sci., Univ. Tokyo, 8.Div. Bio. Sci., Nara Inst. Sci. Tech., 9.NODAI Res. Inst., Tokyo Univ. Agr.)

---

208 Functional analysis of a *KNOTTED1*-like gene, a candidate for a gene regulating flowering in pearl millet

☆Kambara, K.[1], S. Gupta[2], T. Takano[1], D. Tsugama[1] (1.Grad. Sch. Agr., Univ. Tokyo, 2.ICRISAT)

---

209 A CMF gene specific for sweetpotato and its wild relative are involved in storage roots formation in sweetpotato

☆Suematsu, K.[1], R. Morita[2], M. Otani[3], R. Suzuki[2], M. Tanaka[1] (1.Kyushu Okinawa Agr. Res. Cent., NARO, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Fac. Biores. Env. Sci., Ishikawa Pref. Univ.)

---

210 Prediction of targets for the *Rf-like* PPR gene cluster in the fertility-restored line RT98C derived from wild rice *Oryza rufipogon* W1109.

☆Igarashi, K., A. Kobayashi, K. Toriyama (Grad.Sch. Agri. Sci., Tohoku Univ.)

---

211 Development of genomic information on wild soybean mini-core collection and its application to gene identification using GWAS

○Li, F.[1], R. Yano[2], R. Nakata[1], K. Kanako[1], M. Hashiguchi[3], R. Akashi[4], H. Tanaka[4], K. Takagi[1], S. Hiraga[1], M. Ishimoto[1] (1.Inst. Crop. Sci., NARO, 2.Res. Cent. Adv. Anal.,NARO, 3.Fac. Reg. Innov., Miyazaki Univ., 4.Fac. Agric., Miyazaki Univ.)

---

212 Collecting genome sequences, phenotypes and pedigree information in 104 Sake brewing rice cultivars.

○Hori, K.[1], K. Ebana[2], S. Matthew[1], N. Tanaka[1], K. Ishimaru[1], H. Hirabayashi[1], Y. Kawahara[3], H. Kajiya-Kanegae[1,4], T. Okunishi[5], K. Sugimoto[1] (1.Inst. Crop Sci., NARO, 2.Res. Cent. Genet. Resources, NARO, 3.Res. Cent. Adv. Anal., NARO, 4.Res. Cent. Agric. Info. Tech., NARO, 5.Inst. Food Res., NARO)

---

213 Genetic diversity and genome-wide association analysis of grain quality and starch traits in sake rice cultivars

○Shenton, M.[1], K. Ishimaru[1], H. Hirabayashi[1], N. Tanaka[1], K. Ebana[3], K. Sugimoto[2], K. Hori[1] (1.Institute of Crop Science, NARO, 2.Institute of Crop Science, NARO, 3.Research Center of Genetic Resources, NARO)

---

214 Construction of genomic prediction models for 100-seed weight in natto soybean

○Yamaguchi, N.[1], K. Shirasawa[2], H. Igarashi[3], T. Yamada[4] (1.Central Agr. Exp. Sta., HRO, 2.Kazusa DNA Res. Inst., 3.Tokachi Agr. Exp. Sta., HRO, 4.Res. fac. Agr., Hokkaido Univ.)

---

215 Development of NARO Open Rice Collection (NRC) and seed ionome analysis

○Tanaka, N.[1], Y. Kawahara[2], K. Ebana[3], M. Shenton[1] (1.NARO, NICS, 2.Research Center for Advanced Analysis, NARO, 3.Research Center of Genetic Resources, NARO)

---

216 Genetic control of seed iron and zinc concentration in Rwandan common bean population revealed by the Genome Wide Association Study (GWAS)

☆Mukamuhirwa, F.[1,2], K. Shirasawa[3], K. Naito[4], E. Rurangwa[2], V. Ndayizeye[2], A. Nyombayire[2], J. Muhire[2], M. Govindaraj[5], N. Ohtake[1], K. Okazaki[1], M. Okada[1], E. Fukai[1] (1.Grad.Sch.Sci.Tec., Niigata Univ., 2.Crop In.Tec.Trans, Rwanda Agri. Anim.Res.Dev. Board, 3.Kazusa DNA Res.Inst., 4.Research Cen.Gen.Res., Nat.Agri.Fo.Res.Org. (NARO), 5.Alliance of Bio.Int.and Int.Cen.Trop.Agri. (CIAT))

---

217 Comparative analysis of genetic loci related to carotenoid accumulation in sweetpotato flesh using GRAS-Di and dpMIG-seq and identification of the genetic loci

☆Horita, N.[1], Y. Okada[2], H. Kanzaki[1], M. Kurihara[3], K. Nishimura[1], H. Nishida[1], K. Kato[1], Y. Monden[1] (1.Grad. Sch. Env. Life. Nat. Sci. Tech., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Env. & Life Sci., Okayama Univ.)

---

218 Attempts at genetic analysis of various agronomic traits in sweetpotato using image analysis

☆Tanaka, S.[1], H. Tabuchi[2], K. Nishimura[3], H. Nishida[3], K. Kato[3], Y. Monden[3] (1.Fac. Agri., Okayama U., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

---

219 Loss of function haplotype of *R* and *T* were selected for improving seed appearance

☆Suganami, M.[1], S. Kojima[2], M. Kamakura[3], M. Shiraishi[3], K. Beppu[3], H. Yoshida[1], N. Nihei[1,4], H. Takahashi[1,4], S. Masumoto[1,4], T. Waki[5], T. Nakayama[5], K. Yoshida[6], T. Matsuda[1,4], M. Watanabe[7], M. Matsuoka[1] (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Graduate School of Agricultural Science, Tohoku University, 3.Ehime Prefectural Saijo Agricultural High School, 4.Faculty of Food and Agricultural Sciences, Fukushima University, 5.Graduate School of Engineering, Tohoku University, 6.Faculty of Food and Health Sciences, Aichi Shukutoku University, 7.Graduate School of Life Sciences, Tohoku University)

---

220 Exploration and validation of allele dosage estimation method for simplified selection of sweetpotato low pasting temperature lines.

☆Nakahara, T.[1], M. Tanaka[2], A. Kobayashi[2], Y. Kawata[2], K. Nishimura[1], H. Nishida[1], K. Kato[1], Y. Monden[1] (1.Grad. Sch. Environ. Life Sci. Tech., Okayama U., 2.KARC/NARO)

---

221 GenEditScan: a fast and efficient analysis tool to detect foreign DNA in the genome-edited agricultural products using high-throughput sequencing data

○Sakai, H.[1], T. Sato[2], T. Itoh[3], R. Onuki[4], Y. Tabei[5] (1.Research Center for Advanced Analysis, NARO, 2.Mizuho Research & Technologies, Ltd., 3.National Taiwan University, 4.Saitama Cancer Center, 5.Faculty of Food and Nutritional Sciences, Toyo University)

---

301 Estimation of tolerance to heat-induced quality decline of rice during ripening in a uniform temperature

☆Nakaoka, F.[1,2], A. Kobayashi[1], G. Chaya[1], S. Watanabe[1], Y. Morozumi[1], H. Nakagawa[3], M. Yamasaki[3] (1.Fuku Agriculture Experimental Station, 2.Niigata University, 3.Reserch Center for Agricultural Information Technology, NARO)

---

302 Constructing prediction models for wheat yield by employing chronological transcriptome data and mining of yield-predictive genetic components

☆Kojima, H.[1], S. Yoshioka[1], S. Kimura[2], S. Kinoshita[2], K. Kuroki[3], H. Iwata[2], S. Nasuda[1] (1.Grad. Sch. Agric., Kyoto Univ., 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.Grad. Sch. Sci., Univ. Tokyo)

---

303 Genomic prediction of stalk lodging resistance and the associated intermediate phenotypes in maize

○Morota, G.[1], C. Machado e Silva[2], B. Kunduru[3], C. McMahan[3], D. Robertson[4], R. Sekhon[3] (1.Grad. Sch. Agr. Life Sci. Univ. Tokyo, 2.Federal University of Viçosa, 3.Clemson University, 4.University of Idaho)

---

304 Estimation of known gene effects via analysis of historical rice field experiment data

☆Chigira, K.[1], E. Yamamoto[1], A. Goto[1], T. Ikegaya[1], N. Suzuki[1], Y. Kawahara[2], M. Yamasaki[3], K. Sugimoto[1], K. Hori[1] (1.Institute of Crop Science, NARO, 2.Research Center for Advanced Analysis, NARO, 3.Faculty of Agriculture, Niigata University)

---

305 Development of a predicting model for the quality of brown rice based on genomic information and the temperature during the ripening period.

☆Suzuki, N.[1], S. Taniguchi[2], T. Hayashi[2], K. Matsushita[1], H. Kanegae[1,2], H. Nakagawa[2], A. Goto[1,2] (1.Inst. Crop Sci., NARO, 2.Res. Ctr. Agric. Info. Tech., NARO)

---

306 Evaluation of Segregation Prediction Accuracy for Aboveground Traits Using Soybean RILs and Subsequent Progeny Populations

☆Sakurai, K.[1], Y. Toda[2], H. Tsujimoto[3], A. Kaga[4], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Inst. Agro-Env. Sci., NARO, 3.Arid Land Res. Ctr., Tottori Univ, 4.Inst. Crop Sci., NARO)

---

307 Application of Random Forest in a Bayesian Optimization Framework: To propose optimal rice genotype and environment combinations

☆Mochizuki, H.[1], K. Hamazaki[2], C. Sato[3], A. Abe[4], C. Kim[5,6], H. Shimono[5], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ., 2.Adv. Int. Proj., RIKEN, 3.Ifu-Rinrin, 4.Iwate Biotechnology Research Center, 5.Iwate University, 6.Sky Ocean Technology Co., Ltd. Sky Ocean Technology Co., Ltd.)

---

308 Potential assessment of genomics-assisted breeding using fruit morphological features of citrus

☆Hironaga, K.[1], T. Seino[2], K. Nonaka[3], T. Shimizu[3,4], M. Minamikawa[5] (1.Fac. Hort., Chiba Univ., 2.Grad. Sch. Hort., Chiba Univ., 3.NIFTS, NARO, 4.Kazusa DNA Res. Inst., 5.IAAR, Chiba Univ.)

---

309 Prediction of wheat milling yield based on the combination of multispectral image analysis, near-infrared spectrometry and morphometrics of grains

☆Yoshioka, M., T. Ikeda, Y. Ban, M. Ito, K. Kawaguchi, T. Sugita, K. Kato (Western Region Agricultural Research Center, NARO)

---

310 Identification and application of non-shattering genes in the mutant lines induced from an Indica Group variety, Nan-jing11

Nagano, N.[1], ○Y. Fukuta[1,2] (1.Univ. Ryukyu, Fac. Agr., 2.JIRCAS)

---

311 Development of transformation protocols in Brassicaceae and points to be resolved

○Koizuka, N. (Coll. Agr., Tamagawa Univ.)

---

312 Reconstitution of the stigma-side dominance relationship in *Brassica s*elf-incompatibility using transgenic *Arabidopsis thaliana*

☆Chen, J., h. kitashiba, m. yamamoto (Grad. Sch. Agric. Sci., Tohoku Univ)

---

313 Identification of mutations repressing the unstable self-incompatibility of *Arabidopsis thaliana* transformant expressing AlSRKb(S367L) under high temperature

☆Yokosawa, S., H. kitashiba, M. Yamamoto (Grad. Sch. Agri., Tohoku Univ.)

---

314 Recognition specificity analysis of *Brassica* and *Raphanus S* genes showing highly homology using *Arabidopsis thaliana* transformants.

☆Suzuki, T.[1], M. Ogura[1], T. Makino[2], H. Kitashiba[1], M. Yamamoto[1] (1.Grad. Sch. Agrisci., Univ. Tohoku, 2.Grad. Sch. Sci., Univ. Tohoku)

---

315 Which S haplotypes are used in Japanese Brassica F1 varieties?

☆Kato, R., J. Ji, X. Zhu, M. Yamashita, S. Miyashita, M. Yamamoto, H. Kitashiba (Grad. Sch. Agri. Sci., Tohoku Univ.)

---

316 Development of the digital PCR analysis method for estimation of selfing seed contamination rate in strawberry F_1 seed production

○Ishimori, M.[1], S. Kataoka[2], T. Sueyoshi[3], S. Nagamatsu[3], M. Tanaka[3], M. Ogura[2], Y. Noguchi[2], Y. Higuchi[1], S. Isobe[1] (1.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 2.NIVFS, NARO, 3.Fukuoka Agr. Forest Res. Cent.)

---

317 Exploration of genes regulating grass-clump dwarf in synthetic hexaploid wheat.

☆Nakanishi, S.[1], K. Nishimura[1], M. Okada[2], T. Nakazaki[3,4], Y. Monden[1], K. Kato[1], H. Nishida[1] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. Sci. Tech., Niigata Univ., 3.Grad. Sch. Agr., Kyoto Univ., 4.IAC, Kyoto Univ.)

---

318 Functional analysis of a fertility restorer gene for Tadukan-type cytoplasmic male sterile rice

☆Takatsuka, A.[1], Y. Iwai[1], H. Mireau[2,3], T. Kazama[4], K. Igarashi[1], K. Toriyama[1] (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.IJPB, INRAe Versailles, 3.AgroParisTech, Paris-Saclay Univ., 4.Grad. Sch. Biores. Environment. Sci., Kyushu)

---

319 Exploration of PPR genes that regulate the expression of *orf288,* a CMS-causing gene in *japonica* rice mitochondria

○Toriyama, K.[1], Y. Iwai[1], K. Igarashi[1], T. Kazama[2] (1.Grad. Sch. Agri. Sci. Tohoku. Univ., 2.Grad Sch. Biores. Environment. Sci., Kyushu Univ.)

---

320 Increased glucoraphanin content in intergeneric hybrid between *Brassica oleracea* var. *italica* and *Diplotaxis tenuifolia*

☆Odashima, K.[1], T. Suzuki[2], T. Ohnishi[1], S. Bang[1] (1.Grad. Sch. Agr., Utsunomiya U., 2.Center for Bioscience research and Education, Utsunomiya U.)

---

321 Optimizing visualization of pollen tubes in wide hybridization of wheat

〇Sakuma, S., K. Mishina, M. Morita, S. Matsumoto (Faculty of Agriculture, Tottori University)

---

401 Analysis of starch structure in different organs of rice with loss of starch synthase (SS) IIb function generated using CRISPR-Cas9 genome editing.

〇Miura, S.[1,2], H. Odajima[1], S. Hirata[3], N. Crofts[4], R. Morita[3], N. Fujita[1,2] (1.Faclt. Biores., Akita Pref. Univ., 2.Starch Tecnologies Co., LTD, 3.The University of Tokyo, 4.National Institute of Technology, Akita College)

---

402 Isoflavone content in seeds of soybean introduced with *Soybean dwarf virus* resistance gene *Rsdv1*

☆Takahashi, H.[1], H. Maeda[2], N. Yamaguchi[3] (1.Kamikawa Agr. Exp. Sta., HRO, 2.Hirosaki University, 3.Central Agr. Exp. Sta., HRO)

---

403 Screening and evaluation of high protein content lines from a soybean mutant population.

〇Ashikaga, N.[1], H. Igarashi[1], S. Kobayashi[2], H. Takahashi[3], K. Sato[4], Y. Hosokawa[2], N. Yamaguchi[2] (1.Tokachi Agri. Exp. Stn., HRO, 2.Central Agri. Exp. Stn., HRO, 3.Kamikawa Agri. Exp. Stn., HRO, 4.Kitami Agri. Exp. Stn., HRO)

---

404 Genotype-by-environment interaction (GEI) and yield stability of soybean genotypes in Hokkaido

☆Igarashi, H.[1], N. Yamaguchi[2] (1.Tokachi Agr. Exp. Stn., HRO, 2.Central Agr. Exp. Stn., HRO)

---

405 Genotype by environment interactions for grain yield observed among adzuki bean cultivars in Hokkaido

☆Hosokawa, Y.[1], H. Nagasawa[2], N. Yamaguchi[1], Y. Horiuchi[2] (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO)

---

406 Development of ‘Kitahonami’-derived wheat lines with breaking the linkage of resistance to wheat yellow mosaic disease and high-activity polyphenol oxidase.

○Kiuchi, H.[1], T. Sonoda[1], S. Adegawa[2], N. Yamaguchi[2], C. Souma[2], S. Ohnishi[1] (1.HRO Kitami AES, 2.HRO Central AES)

---

407 Variation in rice bran lipid content in high-yielding rice varieties and genetic resource lines

○Araki, E.[1], T. Miyazawa[2], T. Miyazawa[2], R. Sogame[2], Y. Ito[3], K. Ebana[4], K. Toriyama[3] (1.Inst. Food Res., NARO, 2.New Indust. Creat. Hatchery Cent., Tohoku Univ., 3.Grad. Sch. of Agri. Sci., Tohoku Univ., 4.Inst. Gen. Resources Cent., NARO)

---

408 Trait analysis of the AGPase gene *OsAGPL1* mutation in Non-Flowering Rice

☆Miyazaki, K., M. Suzuki, N. Nishide, S. Hashimoto, R. Morita, N. Aoki, T. Izawa (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

---

409 A new medium early maturing potato variety “Shinsei” suitable for long-term storage with good chipping quality

○Shimosaka, E.[1], S. Tamiya[1,2], K. Asano[1,3], S. Tsuda[1], M. Nishinaka[1,4], M. Mori[1,5], A. Kobayashi[1,6], N. Mukojima[1,7], K. Akai[1], S. Okamoto[1,8], A. Takada[1,9] (1.Hokkaido Agri. Res. Cent., NARO, 2.Tohoku Agri. Res. Cent., NARO, 3.AFFRC, MAFF, 4.Central Region Agri. Res. Cent., NARO, 5.Calbee Potato, Inc, 6.Kyushu Okinawa Agri. Res. Cent., NARO, 7.Nagasaki Agri. For. Dev, 8.Cent. for Seeds and Seedlings, NARO, 9.Headquarters, NARO)

---

410 Approach to melon breeding from Miyazaki - Development of high-sugar and high-flavor F1 melon strains -

○Chen, L.[1,2], K. Hahismoto[1], A. Yamaguchi[1], R. Watanabe[1], R. Watanabe[1], A. Hironaka[1] (1.Fac. Envir. Hort. Sci., Minami Kyushu Univ., 2.Grad. Sch. Hort. & Food Sci., Minami Kyushu Univ.)

---

411 Estimating fruit traits QTLs in two Japanese melon landraces of Makuwa and Conomon and their origin

○Tanaka, K.[1], K. Nakajima[1], G. Shigita[2,3], M. Okuma[4], R. Ishikawa[1], H. Nishida[4], K. Kato[4] (1.Fac. Agr. Life Sci., Hirosaki Univ., 2.Tech. U. Munich, 3.Life Environ. Sci., Univ. Tsukuba, 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

---

412 Phylogenetic analysis based on the chloroplast genome in sweetpotato

☆Kurihara, M., M. Nishinaka, K. Taguchi (NARO・CARC)

413 Towards the utilization of genetic resources in the original countries by using local rice varieties collected more than half-century ago

○Ishii, T.[1], S. Lim[1], C. Orn[2], R. Ishikawa[1], H. Saito[3], Y. Sato[4] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodian Agr. Res. Dev. Inst., 3.Trop. Agr. Res. Front, JIRCAS, 4.Natl. Inst. Genet.)

---

414 Genetic variation of heading date in rice germplasm from Zambia

○Oshiro, K.[1], T. Sato[2], K. Triyama[3], S. Komatsubara[4], R. Mulenga[5], M. Chitambi[5], G. Munkombwe[5], M. Chinji[5], E. Musabula[5], N. Museta[5], L. Kamguya[5], J. Njobvu[5], Y. Fukuta[6] (1.Grad. Sch. Agr., Univ. Ryukyus, 2.Fac. Agr., 3.Grad. Sch. Agr. Sci., 4.JICA, 5.ZARI, 6.Univ. Ryukyus)

---

415 Relationship between agronomic traits and QTL for hybrid weakness in RILs derived a cross between Milyang 23 and Akihikari

☆Kobayashi, H.[1], Y. Fukuta[1,2] (1.Faculty of Agriculture of University of the Ryukyus, 2.JIRCAS)

---

416 Origin of crop varieties by cultivar-wild species hybridizations: a case study of yams (*Dioscorea* spp.) in Japan

☆Minoji, K.[1], A. Ohta[1], T. Sakai[1], Y. Sugihara[2], A. Kudoh[1], R. Terauchi[1,3] (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.IBRC)

---

417 Analysis of starch granule size diversity in t in *Vigna* species

○Matsushima, R.[1], J. Kim[1,2], T. Ishii[3], J. Yamashita[1] (1.Institute of Plant Science and Resources, Okayama University, 2.RIKEN Center for Sustainable Resource Science, 3.Arid Land Research Center, Tottori University International Platform for Dryland Research and Education)

---

418 Growth characteristics under subtropical environmental conditions of barley genetic resources collected from Taiwan

○Saisho, D.[1], Y. Okada[2], T. Suzuki[2], H. Lin[3], W. Chiou[4] (1.IPSR, Okayama Univ., 2.Kyushu Okinawa Agricultural Research Center, NARO, 3.Taichung DARES, MOA, 4.Dept. Agronomy, National Chung Hsing University)

---

419 Development and interlaboratory validation of a cultivar-specific identification method for 'Shine Muscat' using loop-mediated isothermal amplification (LAMP)

○Takabatake, R.[1], Y. Monden[2], A. Shindo[2], Y. Minegishi[3], F. Taniguchi[4], Y. Hashimoto[1], T. Takeuchi[5], K. Takasaki[5], S. Isobe[6] (1.Institute of Food Research, National Agriculture and Food

Research Organization, 2.Graduate School of Environmental, Life, Natural Science, and Technology, Okayama University, 3.Nippon Gene Co., Ltd., 4.Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization, 5.FASMAC Co., Ltd., 6.Kazusa DNA Research Institute)

---

420 Secretory production of lysostaphin, an antimicrobial protein, from rice suspension cells

☆Yahara, T., G. Watarai, A. Ohtawara, S. Shimoda, H. Yoneyama, Y. Ito (Grad. Sch. Agri., Tohoku Univ.)

---

421 A population of diploid interspecific hybrids between Asian and African rice reveals variations of pollen fertility associated with meiotic abnormalities

☆Zahidah, Q.[1], M. Ishihara[1], Y. Minouchi[1], D. Kuniyoshi[2], T. Yamamoto[3], K. Nagaki[3], Y. Kishima[1] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Tropical Agriculture Research Front, JIRCAS, 3.IPSR, Okayama Univ.)

---

501 Genetic analysis of resistance to green rice leafhopper in the backcross progenies with the genetic background of African cultivated rice, *Oryza glaberrima*

☆Hironaka, R.[1], T. Thein[1], Y. Yamagata[2], H. Yasui[2] (1.Grad. Sch. Bioresour. Environ. Sci., Kyushu Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ.)

---

502 Functional analysis of quantitative blast resistance gene *Pid3-I1* in rice

☆Abe, K., T. Ishihara, T. Inukai (Grad. Sch. Agric., Univ. Hokkaido)

---

503 Fine Mapping and Identification of a Locus Conferring Resistance to Cucumber Mosaic Virus in Spinach

☆Wu, Y.[1], H. Hirakawa[2], C. Masuta[3], Y. Onodera[3] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Res. Fac. Agr., Kyushu Univ., 3.Res. Fac. Agr., Hokkaido Univ.)

---

504 Dominant genes encoding resistance to soil-borne wheat mosaic virus in barley (*Hordeum vulgare* L.)

○Komatsuda, T. (Shandong Academy of Agricultural Sciences (SAAS) Crop Research Institute)

---

505 Mixed infections of wheat yellow mosaic virus (WYMV) and soil-borne wheat mosaic virus (SBWMV) reduce wheat yields.

○Kurushima, M.[1], T. Todai[1], T. Sonoda[2], S. Ohnishi[2], M. Ishikawa[3], H. Ishimura[4] (1.Tokachi Agricultural Experiment Station, Hokkaido Research Organization, 2.Kitami Agricultural Experiment Station, Hokkaido Research Organization, 3.Tokachi Agricultural Extension Center, Hokkaido, 4.Agricultural Technologies and Extension Division, Hokkaido)

---

506 The establishment of a method for inducing clubroot disease by local heating

☆Haraguchi, K., S. Bang, T. Koyama, T. Ohnishi (Sch. Agr., Univ. Utsunomiya)

---

507 Response to low-fertilizer in the panicle architectures of cultivated rice

☆Ito, H.[1], T. Mori[1], K. Hasegawa[1], M. Amano[1], H. Yoshida[2], S. Nishiuchi[1], J. Murase[1], M. Matsuoka[2], H. Takahashi[1], M. Nakazono[1] (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.IFeS, Fukushima Univ.)

---

508 Disruption of lipid-related gene alters pollen fertility, lipid accumulation, and cold tolerance in rice

☆Lubba, K.[1], K. YAMAMORI[2], Y. KISHIMA[1] (1.Hokkaido University Graduate School of Agriculture, 2.Kyoto University Graduate School of Agriculture)

---

509 Effects of interaction between red rice genes *Rd* and *Rc* common to weedy rice on seed freezing tolerance

☆Takama, R.[1,2], J. Tanaka[2,3] (1.Inst. Plant Protection, NARO, 2.Univ. Tsukuba, Grad. Sch. Sci. Tech., 3.Headquaters, NARO)

---

510 Elucidating salt-tolerant mechanisms in *Vigna luteola* by grafting and identifying salt tolerant gene candidates via root transcriptome

☆Iki, Y.[1], F. Wang[2], K. Ito[1], T. Wakatake[3], K. Tanoi[4], K. Naito[2] (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO, 3.Grad. Sch. Sci. and Technol, NAIST, 4.Grad. Sch. Agri. and Life. sci., Univ. Tokyo)

---

511 Decoding Plant Stress Communication: VOC-Induced *HsfA2* Expression and Heat Stress Tolerance in *Arabidopsis thaliana*

☆Barbaruah, B.[1], F. Shuo[1], H. Ito[2] (1.Grad. Sch. Life Sci., Hokkaido Univ., 2.Fac. Sci., Hokkaido Univ)

---

512 Investigation on Drought Stress Effect on Four Japanese Chili Pepper Varieties

☆Airlangga, R.[1], H. Ito[2] (1.Grad. Sch. Life Sci., Hokkaido Univ., 2.Fac. Sci., Hokkaido Univ.)

---

513 Response of tomato plants to salt stress, waterlogging and their combination

☆ANEE, T.[1], N. Suzuki[2] (1.Graduate School of Green Science and Engineering, Sophia University, 2.Faculty of Science and Technology, Sophia University)

---

514 *RbohD*, an ROS-producing gene, regulates memory of short-term heat stress and responses to flooding with physical flow in *Arabidopsis thaliana*

○Suzuki, N.[1], M. Yunose[2], K. Katano[3], R. Shimizu[2], C. Sumi[1], M. Kaji[4], S. Shigaki[5], H. Suzuki[6] (1.Faculty of Science and Technology, Sophia University, 2.Graduate School of Science and Technology, Sophia University, 3.College of Life Sciences, Ritsumeikan University, 4.Division of Environmental Design, Graduate School of Science and Engineering, Kanazawa University, 5.Principles of Informatics Research Division, National Institute of Informatics, 6.Faculty of Engineering, Hokkai-Gakuen University)

---

515 Analysis of rice lateral root formation mechanism by WOX gene cluster.

☆Kushida, S.[1], Y. Dong[1], P. LIPIO[1], M. Inari-Ikeda[2], Y. Inukai[3] (1.Grad. Sch. Bioagr., Nagoya U., 2.Sch. Hel. Nut., U. Tokaigakuen., 3.ICREA, Nagoya U.)

---

516 Growth analysis of all cells of the rice leaf primordium by live imaging

☆Taguchi, M.[1], Y. Tokuyama[2], R. Kelly-Bellow[3], R. Smith[3], Y. Kishima[2], Y. Koide[2] (1.Sch. Agr., Hokkaido Univ., 2.Grad. Sch. Agr., Hokkaido Univ., 3.Department of Computational and System Biology, JIC)

---

517 Genetic analysis of a spontaneous mutant, dwarf and short panicle

Le, T.[2], D. Lam[1], E. Fukai[3], ○R. Ishikawa[1] (1.Fac. Agri. Life Sci., Hirosaki Univ., 2.Climate Change Institute, An Giang University, 3.Fac. Agri., Niigata Univ.)

---

518 Variation of thermo-sensitivity of heading date found in Hokkaido rice varieties affect heading synchrony and premature heading

☆Hoque, M.[1], S. Sakaguchi[1], M. Takatori[1], M. Kinoshita[2], H. Shinada[3], N. Yamaguchi[4], T. Nishimura[4], Y. Kishima[1] (1.Grad. Sch. Agr., Hokkaido. Univ., 2.Kamikawa Agricultural Experimental Station, Hokkaido Research Organization, 3.Kitami Agricultural Experimental Station, Hokkaido Research Organization, 4.Central Agricultural Experimental Station, Hokkaido Research Organization)

---

519 Analysis of the transcription factor SlMYB21 involved in jasmonate-mediated fruit set in tomato

☆Nomura, Y.[1], Y. Lu[2], Y. Shinozaki[2], T. Kawakatsu[3], K. Harada[1], R. Yano[4], M. Kojima[5], Y. Takebayashi[5], H. Sakakibara[6], H. Ezura[2,7], T. Ariizumi[2,7] (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Institute of Agrobiological Sciences., NARO, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)

---

520 Identification of a novel heading time-related gene *HvHY2* in barley using MutMap approach

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

---

521 Diversity in the juvenile-to-adult phase transition of six common wheat cultivars with different winter-spring growth habits

☆Senoo, K.[1], T. Yoshikawa[2], S. Nasuda[1] (1.Grad. Sch. Agric., Kyoto Univ., 2.Natl. Inst. Genet.)

Poster Presentations

P001 Rapid Screening of Genome-Edited Plantlets Using High-Resolution Melting

☆Kawauchi, T., N. Nishide, T. Izawa (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P002 Efficient field crop phenotyping using the laser distance measurer and mobile device

〇Yamashita, Y., H. Sato, N. Junsai, T. Igarashi (Central Agr. Exp. Stn., HRO)

P003 Visible-near infrared spectral analysis for identification of physiological and genetic features in rice

〇Sato, Y.[1], H. Takehisa[1,2], I. Nagaoka[3], A. Ikehata[4] (1.Inst. Crop Sci., NARO, 2.Inst. Fruit Tree and Tea Sci., NARO, 3.Central Region Agric. Res. Cent., NARO, 4.Inst. Food Res., NARO)

P004 Regeneration of sorghum using cullus derived from mature seeds

〇Hattori, E. (Toyota Motor Corporation)

P005 Phenotypic analysis using UAV images for selection of eraly maturing rice lines

〇Suzuki, Y.[1], T. Nakano[1], D. Ogawa[2], T. Sakamoto[3] (1.Plant Biotechnology Institute , Ibaraki Agricultural Center, 2.Institute of Crop Science,NARO, 3.Institute for Agro-Environmental Science,NARO)

P006 Development of a KASP marker set for high-throughput genotyping in Japanese barley breeding programs with various end-use purposes

☆Shimizu, H.[1], G. Ishikawa[2], H. Aoki[3], M. Nakata[1], T. Tonooka[4], A. Takahashi[2], J. Tanaka[4] (1.Kyushu Okinawa Agricultural Research Center, NARO, 2.Institute of Crop Science, NARO, 3.Hokkaido Agricultural Research Center, NARO, 4.NARO Headquarters)

P007 *in planta* Particle bombardment (iPB） revolutionizes soybean genome editing

〇Imai, R., K. Fujii, T. Ogawa, K. Kuriyama, Y. Hirayama, K. Sasaki (Inst. Agrobiol. Sci., NARO)

P008 Simulation Study on Genomic Prediction for Intercropping

☆Kinoshita, S.[1], H. Takanashi[1], Y. Ohmori[1], H. Takahashi[2], Y. Ichihashi[3], Y. Fuji[4], M. Tsuda[5], T. Ishii[6,7], W. Guo[1], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Grad. Sch. Bioagri. Sci., Nagoya Univ., 3.RIKEN BioResource Res. Ctr., 4.RIKEN Ctr. for Sustainable Sci., 5.Faculty of Food and Nutritional Sci., Toyo Univ., 6.Arid Land Res. Ctr. (ALRC), Tottori Univ., 7.Int. Platf. Dryland Res. Educ. (IPDRE), Tottori Univ.)

P009 Research on grain skinning in barley: QTL analysis and the relation with malt extract.

☆Sasaki, S., R. Kanatani, N. Hirota, M. Nanamori, T. Hoki (Crop Research Laboratories, SAPPORO BREWERIES LTD.)

P010 Verification of the effectiveness of generative AI in 3D plant reconstruction

〇Kodama, K., J. BURRIDGE, P. BLOK, W. Guo (Univ. Tokyo)

P011 Estimation of Missing Genomic Information in Soybean Crossing Populations and Haplotype-Based Genomic Prediction

☆Okabe, R.[1], K. Sakurai[2], M. Inamori[2], H. Igarashi[3], N. Yamaguchi[4], A. Kaga[5], H. Iwata[2] (1.Fac. Agr., Univ. Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Tokachi Agr. Exp. Sta., HRO, 4.Central Agr. Exp. Sta., HRO, 5.Inst. Crop Sci., NARO)

P012 Relationships of heading period and various characteristics in rice.

○Fukui, K. (The Research Center of Genetic Resources, NARO)

P013 Rice production and climate in Niigata Prefecture and development of a new line

○Yamasaki, M., K. Ishii, T. Sato (Fac. Agr., Niigata Univ.)

P014 New durum wheat cultivar ‘Setodure R5’ with good pasta making quality

○Keita, K.[1], Y. Ban[1], M. Ito[1], K. Kawaguchi[1], H. Okusu[2], T. Tanaka[2], H. Kawakami[2], M. Yamaguchi[2], K. Takata[1,3], M. Yanaka[1,4], W. Funatsuki[1,5] (1.WARC, NARO, 2.Central Laboratory, NIPPN Corporation, 3.Obihiro University of Agriculture and Veterinary Medicine, 4.KARC, NARO, 5.TARC、NARO)

P015 Development of a new winter wheat cultivar, ‘Setonohohoemi’ with good bread-making quality and resisntance to wheat yellow mosaic virus for western Japan

○Ito, M.[1], Y. Ban[1], K. Kato[1], K. Kawaguchi[1], K. Takata[2], M. Yanaka[3], W. Funatsuki[4], T. Ikeda[1], N. Ishikawa[1] (1.Western Region Agricultural Research Center, NARO, 2.Obihiro University of Agriculture and Veterinary Medicine, 3.Kyushu Okinawa Agricultural Research Center, NARO, 4.Tohoku Agricultural Research Center, NARO)

P016 Development of perennial crops (Development and evaluation of inter-specific breeding line of buckwheat)

○Suzuki, T.[1], K. Matsusima[2], A. Matsuura[2], K. Tsujimoto[3], R. Kurokoh[3], S. Murakami[3], N. Takahashi[3], K. Murata[3], K. Katsu[1], M. Katsuta[1] (1.KARC., NARO, 2.Inst. Agric., Acad. Assembly Fac., Shinshu Univ., 3.Univ. Tokai)

P017 Development of a new winter wheat cultivar, “Tatsukirari” with good bread-making and soy sauce-brewing quality for western Japan.

○Ban, Y.[1], K. Kato[1], M. Ito[1], N. Tokuriki[2], Y. Nakagaki[2], M. Hirose[2], K. Kawaguchi[1], T. Ikeda[1], K. Takata[1,3], M. Yanaka[1,4], W. Funatsuki[1,5], N. Ishikawa[1] (1.Western Region Agr. Res. Cent., NARO, 2.Higashimaru Shoyu Co., Ltd., 3.Obihiro Univ. Agric. Vet. Med., 4.Kyushu Okinawa Agr. Res. Cent., NARO, 5.Tohoku Agr. Res. Cent., NARO)

P018 Research on fruit traits and population structure analysis of East Asian eggplant genetic resources, focusing on Mizunasu (*Solanum melongena* L.)

○Segami, S.[1], K. Nishimura[2] (1.Res. Inst. Env. Agr. Fish., Osaka Pref., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P019 New hull-less barley cultivar 'Sun-Sun Fiber' with extremely high beta-glucan content.

○Sugita, T.[1], M. Ito[1], Y. Ban[1], K. Kato[1], Y. Nogata[1], D. Abe[1], T. Yoshioka[2], A. Takahashi[3], t. Yanagisawa[3], T. Nagamine[4] (1.WARC/NARO, 2.BRAIN/NARO, 3.NICS/NARO, 4.CARC/NARO)

P020 Mapping of Sarude gene in foxtail millet using dpMIG-seq

○Fukunaga, K.[1], Y. Satani[1], K. Nishimura[2] (1.Fac. Biores. Sci., Pref.U.Hiroshima, 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P021 Development of a new high-yielding soybean cultivar “Sorahibiki” for Tohoku and Hokuriku regions of Japan by crossing Japanese and U.S. soybean cultivars.

○Hishinuma, A.[1], S. Shimamura[2], E. Sasatani[1], Y. Nanjo[1], T. Sayama[1], K. Hirata[3], A. Kikuchi[1], S. Kato[3], T. Matsumoto[1], T. Yamada[4], M. Hajika[5], K. Takahashi[3], N. Yamada[6], Y. Kono[7], Y. Shinoto[1], M. Furuhata[1] (1.TARC, NARO, 2.KARC, NARO, 3.NICS, NARO, 4.RCAIT, NARO, 5.Kubota, Corp., 6.Nagano Pref. Agr. Expt. Sta., 7.CARC, NARO)

P022 Development of “HYBRID TOGO 2GO S/4GO S”, the Early-Ripening Varieties of Improved Hybrid Togo series.

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

P023 Basic research on yield estimation of wild rice using phytolith analysis (III) field trial to collect data for yield estimation using phytolith in archeology

☆Sakamoto, T.[1], T. Kojo[1], R. Takahashi[1], K. Shimizu[2], R. Ishikawa[3], T. Udatsu[4], K. Ichitani[2] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima U., 2.Fac. Agr., Kagoshima U., 3.Fac. Agri. Life Sci., Hirosaki U., 4.Fac. Agri., U. Miyazaki)

P024 Evaluation of genetic diversity and the development of quasi-natural populations of wild emmer wheat populations in southern Turkey

○Mori, N.[1], S. Takenaka[2], K. Tanno[3], H. Ozkan[4], S. Ohta[5] (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Fac. Agric., Ryukoku Univ., 3.Fac. Litl., Ryukoku Univ., 4.Fac. Agric., Univ. Cukurova, Turkey, 5.Prof. emeritus, Fukui Pref. Univ.)

P025 Whole genome analysis of late-flowering, resilient, and tillering isogenic lines of Koshihikari

☆Sugihara, H., M. Tomita (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

P026 Characterization of a large tomato mutant pools induced by fast-neutron and heavy ion beam irradiation in National BioResource Project-Tomato.

○Sugimoto, K.[1], T. Shimokawa[2], N. Kikuchi[3], M. sweet[3], H. Ezura[1] (1.Univ. Tsukuba, T-PIRC, 2.QST, Institute for Quantum Medical Science, 3.Quantum Flowers & Foods Co., Ltd.)

P027 Investigation of intraspecific variation, geographic differentiation, and differentiation among taxonomic groups in daylilies based on morphological characters

○Sasanuma, T.[1,2], K. Tamagawa[2], N. Saito[1], Y. Sato[1], S. Asami[1], Y. Osafune[3], T. Sugawara[3], S. Kishimoto[3,4] (1.Fac. Agr., Yamagata Univ., 2.Grad. Sch. Agr., Yamagata Univ., 3.Mt. Chokai and Tobishima island Geopark Promotion Council, 4.Fac. Life Design, Tohoku Inst. Tech.)

P028 Investigation for development of wheat varieties adapted to west coast area of Northeast Japan. 2

☆Sasaki, M.[1], R. Ogata[1], H. Nagaya[1], H. Kamata[1], K. Hatta[2], H. Aoki[2], Y. Terasawa[2], H. Matsunaka[2], A. Matsuoka[3], A. Nakamaru[3], H. Ito[3], S. Ikenaga[3], A. Nakatsubo[1], T. Sasanuma[1] (1.Fac. Agr., Yamagata Univ., 2.Hokkaido Agr. Res. Cent., NARO, 3.Tohoku Agr. Res. Cent., NARO)

P029 Soybean lines relatively hard to reduce in low-yield year at Hokuriku region.

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

P030 Genetic diversity of local *Brassica juncea* populations in the eastern Shan State of Myanmar

☆Nohara, T.[1], S. Yoshida[2], A. O. M[3], K. Irie[4], K. Wakui[2] (1.Agri. Science. Grad.Agri., Tokyo Univ. of Agri., 2.Dept. of Bio. Res. Dev., Grad. Agri., Tokyo Univ. of Agri., 3.Dept. of Agri. Res., Min. of Agri., Livest. and Irrig., Myanmar, 4.Fac. of Intl. Agri. and Food. Stud., Tokyo Univ. of Agri.)

P031 Evaluation of Inbreeding Depression in Citrus Breeding Population and Its Application to Breeding

☆Kimura, S.[1], M. Minamikawa[2], K. Nonaka[3], T. Shimizu[3], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ, 3.NIFTS, NARO)

P032 Development of a novel visualization tool "GenoSee" for graphical genotypes

☆Hashimoto, S.[1,2] (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.JSPS Research Fellow PD)

P033 Genotypes of rice heading date genes in rice flour lines for the northern Tohoku region

〇Ohmori, S.[1], S. Kanda[2], W. Sunaga[2], Y. Taniguchi[1], J. Tanaka[1] (1.Crop Sci., NARO, 2.Aomori Pref. Indust. Tech. Res. Cent. Agric. Res. Inst.)

P034 Genetic analysis of potato late bright resistance and development of DNA markers by Polyploid QTL-seq

☆Nakajima, H.[1], T. Mizubayashi[2], H. Yamakawa[2], K. Akai[1] (1.Hokkaido Agricultural Research Center, NARO, 2.Institute of Crop Science, NARO)

P035 A comparison of scaffolding methods in the *de novo* genome assembly of peach

☆Nishimura, K.[1], K. Ushijima[1], M. Amamori[2], S. Nakanishi[1], Y. Monden[1], K. Kato[1], H. Nishida[1], F. Fukuda[1], A. Toyoda[3], R. Nakano[2] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.National Institute of Genetics)

P036 Virome analysis for evaluation of infected wheat samples

〇Tanaka, T.[1], S. Takata[2], H. Kojima[2], E. Yazaki[1], F. Kobayashi[2] (1.NAAC, NARO, 2.NICS, NARO)

P037 QTL Mapping of Important Agronomic Traits in Grain Amaranth (*Amaranthus hypochondriacus*)

☆Zaelani, A.[1], S. Isobe[2], K. Shirasawa[2], Y. Yoshioka[3] (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.Kazusa DNA Research Institute, 3.Inst. Life & Env. Sci., Univ. Tsukuba)

P038 Detection of genes involved in rice grain chalkiness using Genome-wide association study

☆Fujii, E.[1], E. Yamamoto[1], M. Yamasaki[2], K. Hori[1] (1.Inst. Crop Sci., NARO, 2.Grad. Sch. Sci. Tech., Niigata Univ.)

P039 Genome sequence and gene annotation of a durum wheat cultivar Langdon

☆Ohta, A., K. Yoshida, T. Sakai, M. Nitta, S. Nasuda, R. Terauchi (Grad. Sch. Agri., Kyoto Univ.)

P040 Characterization of DNA rearrangements in Arabidopsis M1 plants irradiated at the seed and seedling stages with ion beams

〇Kitamura, S.[1], K. Satoh[1], Y. Hase[1], R. Yoshihara[2], Y. Oono[1], N. Shikazono[3] (1.QST-Takasaki, 2.Grad. Sch. Sci. & Eng., Saitama Univ., 3.QST-Kansai)

P041 Purification of high-molecular-weight DNA using polysaccharide hydrolase.

☆Nakagawa, K.[1], H. Matsumura[3], N. Hayashida[2] (1.Master's Program, Shinshu University, 2.Division of Applied Biology, Faculty of Textile, Shinshu University, 3.Gene Research Center, Shinshu University)

P042 Identification of SNP alleles associated with flowering time in small spray-type chrysanthemum varieties by Genome-wide association study.

☆Inazaki, F.[1], K. Shirasawa[2], S. Kurihara[1,3], T. Gounai[1] (1.Plant Biotech. Inst., Ibaraki Agri Cent., 2.Kazusa DNA Res. Inst., 3.Hitachiomiya Dist. Agri. Dev. Ext. Cent.)

P043 Site-directed mutagenesis of CENH3 genes for the development of the haploid-inducers in barley

○Hisano, H., H. Munemori, M. Hamaoka, N. Yamaji (IPSR, Okayama Univ.)

P044 Chromosomal structural changes responsible for rice albino mutants obtained by neutron irradiation using J-PARC accelerator

☆Nakayama, Y.[1], K. Kojima[1], N. Kikuchi[2], T. Kuboyama[1] (1.Col. Agr., Ibaraki U., 2.QFF)

P045 Genome editing techniques for controlling gene copy number variations in rice using multiple nucleases

☆PARK, H., H. SAIKA, T. KUROHA, H. YOSHIDA (Inst. Agro. Sci., NARO)

P046 Efficiency of mutant detection from bulked wheat seeds by digital PCR

☆Kanda, Y.[1], K. Takagi[1], N. Yamaji[2], F. Abe[3], M. Kaboshi[1], K. Sato[1,2,4] (1.Kazusa DNA Research Inst., 2.IPSR, Okayama U., 3.Inst. Crop Sci., NARO, 4.Grad. Sch. Agr., Setsunan Univ.)

P047 Evaluation of antioxidant capacity in leaves of high carotenoid tobacco mutants

○Mikami, M., T. Takeuchi, H. Ayabe, Y. Takakura, H. Magome (Leaf Tobacco Research Center, JAPAN TOBACCO INC.)

P048 Evaluation of grain dormancy on genome edited wheat with *TaQsd1* triple mutations for multiple years.

○Kishi-Kaboshi, M.[1,2], F. Abe[2], M. Chono[2], N. Yamaji[3], H. Hisano[3], K. Sato[1,3,4] (1.Kazusa DNA Res. Inst., 2.NICS, NARO, 3.IPSR, Okayama U., 4.Grad. Sch. Agr., Setsunan Univ.)

P049 Effects of ectopic expression of the phosphate transporter AtPHO1 on phosphate acquisition and transportation

☆Shimizu, A.[1], H. Suzuki[2], Y. Tada[2] (1.Bionics, Grad. Sch., Tokyo Univ. of Technol., 2.Sch. Biosci, Biotechnol., Tokyo Univ. of Technol.)

P050 Effects of overexpressing potassium transporter AtHAK5 on low potassium tolerance in transgenic Arabidopsis

Watanabe, K., Y. Watanabe, Y. Fujishiro, ○Y. Tada (Sch Biosci Biotechnol, Tokyo Univ Technol)

P051 Insight into the molecular evolution of glutamine synthetase gene family of *Arabidopsis*

○Watanabe, A.[1], H. Takahashi[2] (1.Fac. Bioresource Sci., Akita Pref. Univ., 2.Cluster of Agricultural Sci., Fukushima Univ.)

P052 Analysis of a semi-dwarf mutant of rice induced by carbon-ion irradiation.

○Morita, R.[1], H. Ichida[1], Y. Hayashi[1], Y. Shirakawa[1], K. Ichinose[1], T. Sato[1,2], K. Toriyama[2], T. Abe[1] (1.RIKEN, Nishina Cent., 2.Grad. Sch. Agri. Sci., Tohoku Univ.)

P053 Functional analysis of the rice large grain mutation-causing gene LGG and its orthologous genes

○Tsugane, K.[1], M. Tsugane[1], W. Chiou[2], M. Maekawa[3] (1.National Institute for Basic Biology, 2.National Chung Hsing University, 3.Okayama University)

P054 Effects of yield-related genomic regions pyramided in the rice cultivar 'Hitomebore' on yield

☆Takasago, H.[1], T. Fujioka[2], M. Terata[1], Y. Yoshitsu[1], C. Nomura[3], Y. Ogasawara[3], H. Utsushi[3], M. Watanabe[1], A. Abe[3] (1.Iwate Agric. Res. Cent., 2.Presnt affiliation: Iwate Pref. Agri. College, 3.Iwate Biotech. Res. Cent.)

P055 Chronological observation of anther morphology in CMS eggplant showing anther indehiscence

☆Miyata, A.[1], M. Tsujimura[2], T. Shizuka[3], S. Arimura[4], S. Isshiki[5], T. Terachi[1] (1.Fac. Life Sci., Kyoto Sangyo Univ., 2.Fac. Agr., Ryukoku Univ., 3.Cent. Plant Sci., Kyoto Sangyo Univ., 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo., 5.Fac. Agr., Saga Univ.)

P056 Dose the mutation of the SLO1 PPR protein binding site influece efficiency of the RNA editing?

☆Sugimoto, H.[1], I. Nakazato[2], S. Arimura[2] (1.Fac. Agr., Univ. Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P057 Alteration of seed size by rice OsSub53 gene editing

☆Yamaguchi, t., M. Kawabe, Y. Saitoh (Grad. Sch. Agri., Univ. Iwate)

P058 Comprehensive analysis of metabolites and genes involved in common scab resistance

☆Fujiwara, Y.[1], K. Asano[2], Y. Sekiyama[1] (1.Research Center for Advanced Analysis, NARO, 2.Hokkaido Agricultural research Center, NARO)

P059 Meta-analysis to identify cis-elements inducing rice bran-specific gene expression

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

P060 'OneWheatData', French-Japanese collaboration for the utilisation of wheat genetic resources data

○Ishikawa, G.[1], H. Kajiya-Kanegae[1,2], C. Pommier[3], C. Debiton[4] (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agri. Info. Tech., NARO, 3.INRAE - URGI, 4.INRAE - GDEC)

P061 Exploring Automated Curation of Plant Genome Information from Digital Files.

○Ichihara, H.[1], Y. Nakamura[1,2], S. Isobe[1,3] (1.Kazusa DNA Res. Inst., 2.Nat. Inst. Genet., 3.Grad. Sch. Agr. and Life Sci., Univ. of Tokyo)

P062 Exploration of QTLs for Resistance to Root-Knot Nematode in Rice and Isolation of the *RKNR1* Gene.

○Sunohara, H.[1,2], S. Sawa[1] (1.FAST, Kumamoto Univ., 2.Present address: ECC Co., Ltd.)

P063 Analysis of Disease Responses via Bioactive Small Molecules during Wheat Powdery Mildew Infection

☆SATO, Y.[1,2,3,4], Y. WENG[1,2,3,5], T. SHIMAZAKI[2,3,4], Y. KANNO[1], Y. TAKEBAYASHI[1], K. YOSHIDA[6], K. NIHEI[4], M. OKAMOTO[1,2,7] (1.RIKEN, CSRS, 2.Ctr. for Biosci. Res.&Educ., Utsunomiya Univ., 3.Grad. Sch. Reg. Dev.&Creat., Utsunomiya Univ., 4.Sch. Agri., Utsunomiya Univ., 5.UGSAS, Tokyo Univ. of Agri.&Tech., 6.Grad. Sch. Agri., Kyoto Univ., 7.KIBR, Yokohama City Univ.)

P064 Why has the potato cyst nematode resistance gene *H1* not yet been identified?

○Umemoto, N.[1], H. Hamada[2], Y. Nagira[2], H. Yamada[2], Y. Sakamoto[3], I. Habe[3], K. Naito[4], H. Sakai[4], H. Yamakawa[4], K. Akai[4] (1.RIKEN CSRS, 2.Agri-Bio Res. Cent. Kaneka Co., 3.Nagasaki Agri. Forest. Tech. Dev. Cent., 4.NARO)

P065 Varietal differences of internal browning in sweet potato

○Maeda, S., T. Kawamura, C. Endo (Agricultural Research Institute, Ibaraki Agriculture Center)

P066 Degree of residual leaves at maturity in Hokkaido azuki bean cultivars and trial of a simple quantification method.

☆Doman, K.[1], F. Kousaka[1], H. Nagasawa[2], Y. Horiuchi[2] (1.Central AES, HRO, 2.Tokachi AES, HRO)

P067 Pyramiding effect of two QTLs, *bsr1* and *qBSR3.1-kd*, for brown spot resistance in rice

○Matsumoto, K.[1], S. Ohashi[1], D. Nakamura[1], Y. Honda[1,2] (1.Mie Pref. Agri. Res. Inst., 2.Mie Pref. Government)

P068 Antioxidants have antifungal effects and ability to activate defense responses to rice blast fungus

☆Huang, Y., T. Hikawa, M. Kato, T. Inukai (Grad. Sch. Agri., Univ. Hokkaido)

P069 Establishment of sweet potato transformation system for functional analysis of the root-knot nematode infection-responsive genes

☆Kohyama, T.[1], N. Suwa[1], S. Kanda[2], M. Otani[3], E. Asamizu[2] (1.Graduate school of Agriculture, Ryukoku University, 2.Faculty of Agriculture, Ryukoku University, 3.Institute of Bioresource Engineering, Ishikawa Prefectural University)

P070 Genetic analysis of resistance against bacterial blight of some mutant lines induced by ion beam irradiation in rice

☆Ellewala Kankanamge, E.[1], R. Takahashi[2], Y. Maeda[2], S. Taura[1,3], K. Ichitani[1,4] (1.Uni. Grad. Sch. Agr., Kagoshima Univ., 2.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 3.Inst. Gene Res., Kagoshima Univ., 4.Fac. Agr., Kagoshima Univ.)

P071 Verification of QTLs related to WYMV resistance from the resistant cultivar ‘Shunyo’ and genotyping of the resistance alleles in the pedigree

☆Takata, S.[1], G. Ishikawa[1], H. Maejima[2], Y. Uehara[2], K. Tsunekawa[3], R. Suzuki[3], S. Kato[3], N. Saka[3], C. Souma[4], M. Yanaka[1], K. Nakamura[1], H. Matsunaka[1], C. Otobe[1], K. Hatta[1], H. Kojima[1], F. Kobayashi[1] (1.NARO, 2.Nagano Pref. Agri. Exp. Sta., 3.Aichi Agri. Res. Cen., 4.HRO)

P072 Three-year trial for resistance against bacterial blight of rice mutant lines induced by ion beam

☆Takahashi, R.[1], K. Kato[1], Y. Maeda[1], Y. Shibata[1], Y. Gatayama[2], S. Taura[3], K. Ichitani[4] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.KIAD Tokunoshima, 3.Inst. Gene Res., Kagoshima Univ., 4.Fac. Agr., Kagoshima Univ.)

P073 Substitution mapping of QTL for brown planthopper resistance (*qBPH6*) in introgression line of African rice, *Oryza glaberrima*

☆BEGUM, K., K. Baba, D. Fujita (Grad. Sch. Agri., Univ. Saga)

P074 Search for a cis-element responsible for bran-specific expression of rice lipase by the transient expression in immature seeds

Urakawa, M., K. Kuwabara, K. Toriyama, ◯Y. Ito (Grad Sch Agri Sci)

P075 Effects of multiple allelic variations in the *VRN-3* locus on agronomic traits in Hokkaido spring wheat

◯Hayashi, K.[1], R. Saitou[1], T. Sonoda[1], L. Díaz Suárez[2], S. Ohnishi[1], K. Ohnishi[2] (1.HRO Kitami AES, 2.Obihiro University of Agriculture and Veterinary Medicine)

P076 Structural characteristics of plant basic 7S globulin as a target of breeding for protein quality

◯Hirano, H., J. Shirakawa (Inst. Mol. Cell. Regulation, Gunma Univ.)

P077 Designing flag leaf source ability by QTL pyramiding in rice

☆Nomura, C., H. Utsushi, A. Abe (Iwate Biotechnology Research Center)

P078 Comparative QTL analysis of yield-related traits in bidirectional BC_1F_1 populations from the cross showing hybrid vigor at early seedling stage in rice

☆Kojo, T.^{1}, T. Sakamoto^1, M. Higashi^2, S. Taura^3, S. Ogihara^4, T. Kuboyama^5, K. Ichitani^2 (1.Grad. Sch. Agr. Forest. Fish., Kagoshima U., 2.Fac. Agr., Kagoshima U., 3.Gene Res. Inst., Kagoshima U., 4.Grad. Sch. Agr., Ibaraki U, 5.Col. Agri. Ibaraki U.)

P079 Development of multispectral imaging analysis method for objective evaluation of seed quality of wheat and soybean

〇Yamada, T.^{1}, G. Ishikawa^2, K. Nakashima^2, Y. Nanjo^3, H. Nakamura^2, K. Kato^4, T. Okada^2, M. Yoshioka^4, T. Ikeda^4, J. Yonemaru^1 (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO, 3.Tohoku Agric. Res. Cent., NARO, 4.Western Reg. Agric. Res. Cent., NARO)

P080 Study of QTLs responsible for early flowering in the F_2 population derived from the cross *Ipomoea nil*, Q63 x *I. hederacea*, Q65

☆Murakami, K.^{1}, A. Hoshino^{2,3}, E. Nitasaka^4, T. Kuboyama^1 (1.Col. Agr., Ibaraki U., 2.Natl., Inst. Basic Biol., 3.SOKENDAI, 4.Grad. Sch. Sci., Kyushu U.)

P081 Development of PHYTOMap for rice shoot apical meristem

☆Iwama, K.^{1}, Y. Morishita^2, H. Tsuji^{3,4} (1.Sch. Agri., Nagoya Univ., 2.Grad. Sch. Bioagr. Sci., Nagoya Univ., 3.BBC, Nagoya Univ., 4.KIBR, Yokohama City Univ.)

P082 Global transcriptome analysis of *TAB1* and *ASP1*-regulated genes during axillary meristem development in rice

☆Ohyama, A.^{1}, T. Toriba^2, W. Tanaka^1 (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ.)

P083 A novel role of *FINE CULM1* in rice tiller formation

〇Tanaka, W.^{1}, A. Ohyama^1, T. Toriba^2, R. Tominaga^1, H. Hirano^3 (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ., 3.Grad. Sch. Sci., Univ. Tokyo)

P084 Role of class III homeodomain leucine zipper gene family in developing shoot apical meristems in rice

☆Chiba, K.^{1}, S. Kawanabe^2, R. Satoh^1, N. Nagasawa^2, J. Itoh^3, N. Satoh-Nagasawa^2 (1.Grad. Sch. Biores. Sci., Akita Pref. Univ., 2.Fac. Biores. Sci., Akita Pref. Univ., 3.Grad. Sch. Agri. & Life Sci., Univ. Tokyo)

P085 How did multiple male sterility inducing cytoplasm evolve in the course of wild beet mitochondrial diversification?

Kubota, K.[1], M. Oishi[1], E. Taniguchi[1], A. Akazawa[1], K. Matsui[1], K. Kitazaki[1], A. Toyoda[2], H. Toh[2], H. Matsuhira[3], Y. Kuroda[3], ○T. Kubo[1] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Adv. Genomics Ctr., Natl. Inst. Genetics, 3.Hokkaido Agr. Res. Ctr., NARO)

P086 Evaluation of Genetic Diversity and Current Status of On-farm Seed Saving in 'Inekokina', a Local Turnip Variety of Nagano Prefecture

☆Kohara, R.[1], K. Matsushima[2], K. Nemoto[2] (1.Grad. Sch. Sci and Tec., Univ. Shinshu, 2.Inst. Agric. Acad. Assy. Fac., Univ. Shinshu)

P087 Introduction of betalain synthesis genes overexpression system called RUBY to *Chrysanthemum seticuspe* without antibiotic selection

○Matsushita, S., M. Kurao, S. Chokyu (Agr. Tech. Res. Cent., HiTRI)

P088 Visual evaluation of the transformation process in Poncirus trifoliata using the RUBY pigment biosynthesis marker gene.

○Shirakami, N., M. Kurao, J. Kaneyoshi, S. Chokyu, S. Matsushita (Agric. Tech. Res. Cent., Hiroshima Pref. Tech. Res. Inst.)

P089 A QTL associated with bigerm seed rate in sugar beet is located in a genomic region distinct from the Multigerm locus M.

○Matsuhira, H., T. Narihiro, Y. Kuroda (Hokkaido Agri. Res. Cent., NARO)

P090 Diversity of pollen-related traits in the genera *Triticum* and *Aegilops* that include wheat and its wild relatives

☆Kobayashi, S.[1], H. Kojima[2], S. Sakuma[3], H. Kakui[4], S. Nasuda[2] (1.Fac. Agric., Kyoto Univ., 2.Grad. Sch. Agric., Kyoto Univ., 3.Fac. Agric., Tottori Univ., 4.Grad. Sch. Agric. Life Sci., Univ. Tokyo.)

P091 Quantitative evaluation of compatibility of homostyly in *Primula sieboldii* by observing its pollen tube elongation

☆Ueda, Y.[1], T. Yasuda[1], Y. Yoshida[2] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Food Resources Education and Research Center, Grad. Sch. Agr. Sci., Kobe Univ.)

P092 Control culture condition for induction of greening of somatic embryos for differentiation in tea plant and analysis the functional components in embryos.

〇Furukawa, K., H. Sei, S. Yahashi, R. Yoshikawa, H. Segawa (National Institute of technology (KOSEN), Numazu college)

P093 Histological observation and estimation of the causative gene on genic male sterility expressed in "Tennoji-kabu".

☆Ozeki, M.[1], N. Sunagawa[2], K. Komatsu[2], Y. Mitsui[2], K. Wakui[2] (1.NODAI Genome Res. Ctr., Tokyo Univ. of Agri., 2.Fac. Agri. Dept. Bioresource Dev., Tokyo Univ. of Agri.)

P094 Occurrence of doubled haploid plants by crossing *Cymbidium eburneum* with three-way hybrids of *Cymbidium* spp. using early ovary culture method

☆Kokubo, H.[1], K. Mabuchi[1], T. Ishida[2], J. Kato[1] (1.Dept.Biol.Sci.Edu.,Aichi U.Educ., 2.Ishida Cymbidium Nursery)
