Title of Papers Presented at the 127th Meeting of The JAPANESE SOCIETY Oral presentations

Oral Presentations

101 Study of Polish soybean cultivars: Development of early-maturing and chilling-tolerant lines, and estimation of a candidate genomic region for early maturity

☆Yamaguchi, N. [1], H. Kurosaki [2], S. Aoyama [3], M. Ishimoto [4], T. Miyoshi [1], M. Senda [5] (1.Tokachi Agr. Exp. Sta., HRO, 2.Central Agr. Exp. Sta., HRO, 3.Kitami Agr. Exp. Sta., HRO, 4.NIAS, 5.Fac. Agric. Life Sci., Hirosaki U.)

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102 Time of initiation of low temperature treatment for producing cracking seeds in soybean

○Senda, M. [1], M. Hiraoka [1], N. Yamaguchi [2] (1.Fac. Agric. Life Sci., Univ. Hirosaki, 2.Tokachi Agr. Exp. Sta., HRO)

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103 Characterization of Afghanistan wheat landraces for adaptation to high Ca^{2+} and pH condition

Haque, M., M. Alagu, ☆T. Ban (Kihara Institute for Biological Research, Yokohama City University)

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104 Drought resistance of upland NERICA transformed with *AtGolS2*

○Ishizaki, T. [1], K. Maruyama [1], T. Ogata [1], M. Kusano [2,3,4], M. Kobayashi [2], K. Saito [2,5], K. Shinozaki [2], K. Nakashima [1] (1.JIRCAS, 2.RIKEN, 3.Grad. Sch. Life. Environ. Sci., Univ. Tsukuba, 4.PRESTO, 5.Grad. Sch. Pharm., Chiba Univ.)

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105 Effect to the cold tolerance of the heat shock transcription factor which express in cold acclimation of rice

☆Sagehashi, Y., H. Yasuda, Y. Sato (NARO Hokkaido Agr Res Cent)

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106 Identification of a seed dormancy gene *Phs1* in wheat

○Torada, A. [1], M. Koike [1], T. Ogawa [2], Y. Takenouchi [1], J. Wu [2], K. Tadamura [1], T. Matsumoto [2], K. Kawaura [3], Y. Ogihara [3] (1.HOKUREN Agric.Res.Inst., 2.National Inst. of Agrobiol. Sci., 3.Kihara Inst. for Biol. Res., Yokohama City Univ.)

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107 Map-based cloning of the causal gene for barley seed dormancy QTL *SD2*

○Nakamura, S. [1], M. Pourkheirandish [1], H. Morishige [1], Y. Kubo [2], M. Nakamura [2], K. Ichimura [2], S. Seo [3], H. Kanamori [3], J. Wu [3], T. Ando [3], G. Hensel [4], M. Sameri [3], N. Stein [4], K. Sato [5], T. Matsumoto [3], M. Yano [1], T. Komatsuda [3] (1.NICS, 2.Fac. of Agr., Kagawa Univ., 3.NIAS, 4.IPK, 5.IPSR, Okayama Univ.)

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108 Map-based cloning and characterization of rice preharvest sprouting resistance gene, *Sdr1* derived from Kasalath

Takeuchi, Y. [1], ○K. Sugimoto [2], U. Yamanouchi [2], M. Yano [1] (1.NARO Institute of Crop Science, 2.National Institute of Agrobiological Science)

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109 Expression of serotonin biosynthesis pathway genes in halo lesions of rice blast

○Hayashi, K. [1], Y. Hayano_Saito [1], Y. Hujita [2], T. Ashizawa [1], Y. Nagamura [3], H. Suzuki [1] (1.NARO/ARC, 2.NUBS, 3.Natl. Inst. Agr. Sci)

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110 Blast resistance gene, *Pi40*(t), originated from *Oryza austrialiensis* is same as *Piz-t* in *Oryza sativa*

☆Hashimoto, S. [1,2], M. Telebanco-Yanoria [1,3], K. Jena [3], N. Kobayashi [4], Y. Koide [1], Y. Fujita [1], Y. Fukuta [1] (1.Japan International Research Center for Agricultural Science, 2.University of Tsukuba, 3.International Rice Research Institute, 4.Japan National Institute of Crop Science)

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111 Resistance to bacterial blight in rice cultivar Asominori. II. Rough mapping of resistance gene *Xa17* using a cross of its segregated line and Koshihikari

○Taura, S. [1], C. Kwilasa [2], H. Tsuneyoshi [2], K. Kawabe [1], K. Ichitani [2] (1.Div. Gene Res., Kagoshima U., 2.Fac. Agri., Kagoshima U.)

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112 Estimation of the QTL associated with stiff culm in rice, using Takanari and Koshihikari chromosome segment substitution lines

☆Hattori, T. [1], T. Yamamoto [2], R. Aoba [1], T. Hirasawa [1], T. Ookawa [1] (1.Fac. of Agr., Tokyo Univ. of Agri. and Tech., 2.National Institute of Agrobiological Sciences)

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113 Genome-wide association studies of low-P tolerance related traits using Japanese rice varieties 1. -solubilization of unavailable P by root secretion

☆Tabata, Y. [1], F. Fujita [3], M. Yamasaki [2], A. Shimizu [1] (1.Grad.Sch. Environ. Sci.,Univ. Shiga Pref., 2.Food Resources Education and Research Center, Graduate School of Agricultural Science, Kobe University, 3.Environ. Sci.,Univ. Shiga Pref.)

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114 QTL analysis for tolerance to rice kernel cracking using moisture absorption method and late harvest method

☆Hayashi, T., A. Kobayashi, K. Tomita, T. Shimizu (Fukui Agri. Cul. Exp. Stn.)

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115 Development of late harvest Chinese cabbage F_1 variety harboring two clubroot resistance genes, *Crr1* and *Crr2*

○Matsumoto, S. [1], K. Hatakeyama [1], S. Takashita [2], T. Miyazaki [2], T. Kondo [2] (1.NARO Institute of Vegetable and Tea Science, 2.Nippon Norin Seed Corporation)

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116 The microscopic analysis of cadmium resistance mechanism of root in *Athyrium yokoscense*

☆Ukai, Y. [1,2], K. Kitazaki [2], S. Hashida [2], K. Shoji [2], F. Goto [2], H. Shimada [1], T. Yoshihara [1,2] (1.Tokyo Univ. of Sci., Fac. of Ind. Sci. and Technol, 2.CRIEPI)

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117 Development of Soybean Breeding Lines with Resistance to Soybean Mosaic Virus, Soybean Cyst Nematode and Soybean Dwarf Virus

☆Kato, S. [1], K. Hirata [1], S. Shimamura [1], Y. Takada [2], A. Kikuchi [1] (1.NARO Tohoku Agricultural Research Center, 2.NARO Western Region Agricultural Research Center)

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118 A selection of standard varieties for evaluating the field resistance to brown spot in rice

☆Matsumoto, K. [1], S. Seta [1], C. Ota [2], T. Yamakawa [1], Y. Nakayama [1], H. Sato [3] (1.Mie Pref. Agri. Res. Inst., 2.Mie Pref. Ise Agri. Forestry Fisheries Office, 3.NARO/KARC)

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119 Varietal difference of field resistance to brown spot in Japanese and world rice core collections

☆Seta, S. [1], K. Matsumoto [1], T. Yamakawa [1], Y. Nakayama [1], H. Sato [2] (1.Mie Pref. Agri. Res. Inst., 2.NARO / KARC)

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120 Study of root system of Afghanistan wheat local variety under mid and late drought condition

☆Ahmadi, S. [1], A. Osmani [1,2], M. Haque [1], M. Alagu [1], T. Ban [1] (1.Kihara Institute for Biological Research, Yokohama City University, 2.Ministry of Agriculture, Irrigation and Livestock, Afghanistan)

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201 Plant Omics Data Center : An Integrated Web Repository for gene expression networks and accurate functional annotations

☆Takano, T. [1], S. Terashima [1], T. Kudo [1], M. Kanno [1], K. Morimoto [1], H. Kanegae [1], Y. Sasaki [1], M. Kobayashi [1], S. Ozaki [1], M. Saito [1], S. Asano [1], K. Yokoyama [1], K. Aya [2], K. Suwabe [3], G. Suzuki [4], M. Watanabe [5], M. Matsuoka [2], H. Ohyanagi [1,6], K. Yano [1] (1.Sch. of Agri., Meiji Univ., 2.Bioscience and Biotechnology Center., Nagoya Univ., 3.Graduate School of Bioresources, Mie Univ., 4.Division of Natural Science, Osaka Kyoiku Univ., 5.Graduate School of Life Sciences, Tohoku Univ., 6.Mitsubishi Space Software Co., Ltd.)

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202 Data mining with gene expression network involving molecular chaperone and protein disulfide isomerase genes in Plant Omics Data Center

☆Kudo, T. [1], T. Takano [1], S. Terashima [1], M. Kanno [1], K. Morimoto [1], H. Kanegae [1], S. Ozaki [1], Y. Sasaki [1], M. Saito [1], S. Asano [1], K. Yokoyama [1], K. Aya [2], K. Suwabe [3], G. Suzuki [4], M. Watanabe [5], M. Matsuoka [2], M. Kobayashi [1], H. Ohyanagi [1,6], K. Yano [1] (1.Sch. of Agri., Meiji Univ., 2.Bioscience and Biotechnology Center., Nagoya Univ., 3.Grad. Sch. Bioresorces., Mie Univ., 4.Sch. Division of Natural Science, Ohsaka Kyoiku Univ., 5.Grad. Life Sci., Tohoku Univ., 6.Tsukuba Division, Mitsubishi Space Software Co., Ltd)

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203 Heap: A high-sensitive SNPs Detection Tool for GWAS and GS

☆Kobayashi, M. [1,2], S. Asano [1,2], H. Ohyanagi [1,2,3], T. Kudo [1,2], S. Ozaki [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.)

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204 Validation of image based method for automated detecting of paddy rice flowering in the field

☆Guo, W. [1], T. Fukatsu [2], S. Ninomiya [1] (1.Grad. Sch. Agric. Life. Sci, U. Tokyo, 2.NARO)

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205 Functional extension and improvement of gsWizaRd software for genomic selection

○Iwata, H. [1], B. Galliot [1], Y. Takase [2], K. Kamatsuki [2], H. Ohyanagi [2], T. Hayashi [3] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Tsukuba Div., Mitsubishi Space Software Co., Ltd., 3.NARC, NARO)

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206 Simulation of the impact of mis-labeling on genomic selection

☆Yabe, S. [1], H. Iwata [1], J. Jannink [2] (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.USDA-ARS)

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207 Effect of population size and number of markers on the selection efficiency of genomic selection in tomato : a simulation study

☆Yamamoto, E. [1], H. Matsunaga [1], M. Minamikawa [2], H. Kanegae [2], A. Onogi [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)

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208 Genotype imputation using whole genome sequences of a sorghum reference panel

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

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209 Linkage mapping, molecular cloning and functional analysis of soybean gene *Fg3* encoding flavonol 3- *O*-glycoside:2"- *O*-glucosyltransferase

☆Di, S. [1], F. Yan [1], F. Rojas Rodas [1], T. Rodriguez [1], Y. Murai [2], T. Iwashina [2], S. Sugawara [3], T. Mori [3], R. Nakabayashi [3], K. Yonekura-Sakakibara [3], K. Saito [3], R. Takahashi [1,4] (1.Graduate School of Life and Environmental Sciences, University of Tsukuba, 2.Department of Botany, National Museum of Nature and Science, 3.RIKEN Center for Sustainable Resourse Science, 4.National Insititute of Crop Science)

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210 CACTA-superfamily transposable element is inserted in MYB transcription factor gene of soybean line producing variegated seeds

☆Yan, F. [1], S. Di [1], R. Takahashi [1,2] (1.Grad. Sch. Life Environ. Sci., Univ. of Tsukuba, 2.Natl. Inst. Crop Sci.)

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211 Gene expression analysis for anthocyanin synthesis in strawberry fruits

Hirakawa, H. [1], K. Tasaki [2], K. Namai [2], T. Ohashi [2], F. Maeda [3], M. Watanabe [3], T. Wada [4], K. Hirashima [4], K. Shimomura [4], K. Shirasawa [1], ○S. Isobe [1] (1.Kazusa DNA Research Institute, 2.Tochigi Prefectural Agricultural Experiment Station, 3.Chiba Prefectural Agriculture and Forestry Research Center, 4.Fukuoka Agriculture and Forestry Research Center)

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212 Transcriptome analysis of combined stress responses between drought and high salinity in maize

☆Kamara, M. [1,2], Y. Kobayashi [1], R. Sakran [1,3], Y. Kobayashi [1], Y. Yamamoto [1], H. Koyama [1] (1.Faculty of Applied Biological Sciences, Gifu University, Japan., 2.Faculty of Agriculture, Kafrelsheikh University, Egypt., 3.Rice Research and Training Center, Field Crop Research Institute, ARC, Egypt.)

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213 COMET; A sensitive and accurate tool for rapid identification of conserved cis-element motifs on the basis of large-scale gene expression and sequence data

☆Sasaki, Y. [1], M. Ohtani [2], N. Yamamoto [1], T. Takano [1], S. Terashima [1], M. Kobayashi [1], H. Ohyanagi [1], E. Nambara [2], K. Yano [1] (1.Bioinformatics Laboratory, Department of Life Sciences, School of Agriculture, Meiji University, 2.Sch. of Cell & Systems Biology.,Toronto Univ.)

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214 A genome-wide association study (GWAS) in *japonica* rice

☆Yano, K. [1], K. Aya [1], H. Takeuchi [1], M. Inari-Ikeda [1], M. Yamasaki [2], S. Yoshida [3], H. Kitano [1], K. Hirano [1], M. Matsuoka [1] (1.Bioscience and BIothechnology Ctr., Nagoya U., 2.Food Resources Education and Res. Ctr., Grad. Sch. Agric. Sci., Kobe U., 3.Hyogo Agric. Forest. Fish. Res. Ctr.)

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301 Identification of salt tolerant accessions in Vigna nakashimae and their genetic diversity analysis using RADseq

☆Ogiso-Tanaka, E. [1], C. Sompong [2], C. Rusama [3], H. Sakai [1], K. Naito [1], A. Baba [1], K. Iseki [1], Y. Takahashi [1,4], N. Tomooka [1] (1.National Institute of Agrobiological Sciences, 2.Kasetsart University, THAILAND, 3.Mie University, 4.JSPS research fellow)

---

302 Genetic variations for salt tolerance among populations of wild *Vigna* growing in South Asia

☆Iseki, K. [1], E. Ogiso-Tanaka [1], Y. Takahashi [1,2], C. Muto [1], H. Sakai [1], K. Naito [1], N. Tomooka [1] (1.National Institute of Agrobiological Sciences, 2.JSPS Reseach Fellow)

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303 Neo-domestication and Re-domestication

☆Takahashi, Y. [1,2], C. Muto [1], K. Iseki [1], E. Ogiso-Tanaka [1], T. Isemura [1], H. Sakai [1], K. Naito [1], S. Natesan [3], P. Muthaiyan [3], A. Kaga [1], N. Tomooka [1] (1.NIAS, 2.JSPS, 3.Tamil Nadu Agr. Univ.)

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304 Breeding of a new lodging-resistant soybean cultivar "Hatsunagaha"

○Kono, Y. [1], M. Takahashi [1], N. Oki [1], M. Takahashi [1], K. Komatsu [2], Y. Nakazawa [1] (1.NARO,KARC, 2.NARO,HARC)

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305 Genetic studies on Bambuseae species in Japan. XXXVII. About an aspect of the propagation and a distribution boundary, particularly *Nezasa* line

○Muramatsu, M. ()

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306 *Brassica* vegetables called Inly found in the northern part of main Okinawa island

○Egashira, H. [1], Y. Takaesu [2], S. Yamamoto [3], M. Takeya [3] (1.Fac. Agr., Yamagata Univ., 2.Okinawa Pref. Agr. Res. Cen., 3.NIAS)

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307 Candidate of the original 'Somei-yoshino' tree in the Ueno Park

○Nakamura, I., A. Tsuchiya, H. Takahashi, S. Makabe (Grad. Sch. Hort., Chiba U.)

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308 A challenge to overcome graft-incompatibility using Nicotiana plants

☆Notaguchi, M. [1,2], Y. Sato [3], T. Higashiyama [1,2,3] (1.Graduate School of Science, Nagoya University, 2.JST ERATO Higashiyama Live-Holonics Project, 3.Institute of Transformative Bio-Molecules, Nagoya University)

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309 Evaluation of wild rice resources using NGS in Viet Nam

Tamura, N. [1], S. Saito [1], H. Pham [2], T. Nguyen [2], D. Lam [3], B. Bui Chi [3], ○R. Ishikawa [1] (1.Fac. of Agri. and Life Sci. Hirosaki Univ., 2.Cuu Long Delta Rice Res. Inst., Viet Nam, 3.Inst. of Agri. South. Viet Nam)

310 Distribution of *Hwa1-1* and *Hwa2-1*, complementary genes causing a hybrid weakness phenomenon, in NIAS global rice core collection

○Ichitani, K. [1], T. Koga [1], E. Sakaguchi [1], S. Taura [2], R. Ishikawa [3], T. Tezuka [4], T. Kuboyama [5] (1.Fac. Agr., Kagoshima Univ., 2.Inst. Gene Res., Kagoshima Univ., 3.Fac. Agri. and Life Sci., Hirosaki Univ., 4.Grad. Sch. Life Envi. Sci., Osaka Pref. Univ., 5.Col. Agr., Ibaraki Univ.)

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311 Genetic polymorphism of Japanese landraces of rice revealed by SSR, RAPD and SCAR

☆Ishida, M., M. Yanase, T. Tezuka, T. Morikawa (Grad. Sch. Life and Envi. Sci., Osaka Pref. Univ.)

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312 Canceled

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313 The effect of glutenin subunits introduced from common wheat to durum wheat on the semolina dough properties

○Funatsuki, W. [1], H. Okusu [2], M. Yanaka [1], T. Ikeda [1], K. Takata [1] (1.NARO Western Region Agricultural Research Center, 2.Nippon Flour Mills Co., Ltd.)

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314 Variations of HMW-glutenin subunits in wheat landraces stocked in the National Agrobiodiversity Center, RDA-Korea

Yoko, K. [1], S. Lee [2], Y. Jung [2], K. Kawaura [1], M. Lee [2], ☆Y. Ogihara [1] (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.Natl. Acad. Agr. Sci., Korea)

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315 Progress in breeding soft wheat for cold tolarance

☆Himi, E. [1], H. Ito [1], S. Ikenaga [1], M. Taira [1,2], K. Nakamura [1,3], Y. Taniguchi [1] (1.NARO Tohoku Agr. Res. Cent., 2.NARO Inst. of Crop Sci., 3.NARO Kyushu Okinawa Agr. Res. Cent.)

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316 Breeding of a new malting barley cultivar “Tochigi-Nijo45” with null LOX-1

○Oozeki, M. [1], T. Sotome [2], N. Haruyama [3], M. Yamaguchi [1], H. Watanabe [4], T. Okiyama [4], T. Takayama [5], T. Nagamine [6], M. Ooyama [1], Y. Suzuki [7], T. Toyoshima [8], T. Sekiwa [1], T. Kato [1] (1.Tochigi Agr. Exp. Stn., 2.Ansoku Agr. Pro. Office, 3.Tochigi Pref. Sus. Agr. Ext. Cen., 4.Tochigi Pref. Dep. Of Agr., 5.NARO Natl.Inst.Crop.Sci., 6.NARO NARCT., 7.Kamitsuga Agr. Pro. Office, 8.Shimotsuga Agr. Pro. Office)

317 Chloroplast DNA variation within two natural populations of wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) in southern Turkey

○Mori, N. [1], T. Shizuka [1], H. Ozkan [2], S. Ohta [3] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Fac. Agr., Dpt. Field Crops, Univ. Cukurova, 3.Dpt. Biosci., Fukui Pref. University)

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318 Exploration and collection of wheat landraces and wild Triticeae genetic resources in Georgia

○Sasanuma, T. [1], H. Nishida [2], Z. Asanidze [3], T. Bragvadze [3], O. Kovaleva [4], T. Smekalova [4] (1.Fac. Agr., Yamagata Univ., 2.Grad. Sch. Environ. Life Sci., Okayama Univ., 3.Ilia State Univ., 4.VIR)

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319 Impact of wild relatives on wheat adaptation to heat stress

☆Mohammed, Y. [1,2], I. Tahir [2], N. Kamal [1,2], A. Eltayeb [1], A. Ali [3], H. Tsujimoto [1] (1.Arid Land Res. Center, Tottori U., 2.Agric. Res. Corp., 3.Plant Breeding and Genetics Laboratory, FAO/IAEA Joint Division)

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320 Population structure analysis for selection of core-collection on the entire diploid wheat accessions conserved by NBRP-Wheat

☆Takenaka, S., M. Nitta, T. Kawahara, S. Nasuda (Grad. Sch. Agri., Kyoto Univ.)

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401 Marker candidates for barley breeding developed by RNA-Seq analysis

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

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402 Restriction-site associated DNA sequencing for crops at different ploidy and zygosity levels

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

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403 Identification of novel QTLs for compactness, threshability, and rachis fragility in common wheat

☆Katkout, M. [1], M. Kishii [2], K. Kawaura [1], K. Mishina [3], S. Sakuma [1], K. Umeda [1], S. Takumi [4], M. Nitta [5], S. Nasuda [5], Y. Ogihara [1] (1.KIBR, Yokohama City U., 2.CIMMYT, 3.NIAS, 4.Grad. Sch. Agric. Sci., Kobe U., 5.Garad. Sch. Agri., Kyoto Univ.)

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404 QTL analysis of leaf morphological traits in Japanese traditional leafy vegetables, Mizuna and Mibuna

☆Kawakatsu, Y. [1], K. Kaminoyama [1], K. Igarashi [2], H. Nakayama [1,3], M. Yasugi [4], H. Kudoh [4], A. Nagano [4,5], K. Yano [2], N. Kubo [6], S. Kimura [1] (1.Fac. Life Sci., Kyoto Sangyo Univ., 2.Fac. Agri., Meiji Univ., 3.Japan Society for the Promotion of Science, 4.Center for Ecological Research, Kyoto Univ., 5.JST PRESTO, 6.Grad. Sch.Life Environ. Sci., Kyoto Pref. Univ.)

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405 Map-based cloning of a QTL for pod dehiscence conditioning shattering resistance in soybean

○Funatsuki, H. [1,2], M. Suzuki [3], A. Hirose [1], H. Inaba [3], T. Yamada [4], M. Hajika [4], K. Komatsu [1], T. Katayama [5], T. Sayama [1,6], M. Ishimoto [1,6], K. Fujino [6] (1.NARO/HARC, 2.NARO/WARC, 3.Grad. Sch. Agr., Hokkaido Univ., 4.NARO/ICS, 5.Fac. Agr., Kagawa Univ., 6.Natl. Inst. Agrobiol. Sci.)

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406 Detection of QTL for heading date under short day conditions and evaluation of QTL by QTLSeq

○Tanaka, T. [1], E. Ogiso-Tanaka [1], H. Saito [2], K. Tanaka [3], T. Sasaki [4], M. Yano [5] (1.NIAS, 2.Kyoto University, 3.Tokyo University of Agriculture, 4.NODAI Research Institute, 5.NICS)

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407 Genome wide association studies for yield components in a collection of Afghan wheat local varieties

☆Maqsodi, A., M. Alagu, T. Ban (Kihara Institute for Biological Research,Yokohama City University)

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408 Genetic diversity among the local population from Hokkaido evaluated by genome sequences of 21 rice varieties

○Fujino, K., T. Ikegaya (Hokkaido Agr Res Cent)

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409 Chromosomal regions of the adaptability derived from Akage

☆Ikegaya, T., K. Fujino (NARO Hokkaido Agr Res Cent)

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410 Phenotypic changes and progression in population structure from landraces to the current varieties during 100-year rice breeding programs in Hokkaido

☆Nishimura, T. [1], H. Kiuchi [1], Y. Hirayama [1], K. Fujino [2], T. Sato [1] (1.HRO/Kamikawa Agri.Exp.Sta., 2.NARO/HARC)

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411 Exploring genetic factors for cold tolerance at the booting stage of rice by using multiple progeny populations derived from a local strain in Hokkaido

☆Ishiguro, S. [1], Y. Sone [1], S. Kamidai [1], K. Onishi [2], M. Ezawa [1], K. Fujino [1], T. Sato [3], Y. Kishima [1] (1.Res. Fac. Agric., Hokkaido U., 2.Obihiro U. Agr. & Vet. Med., 3.H. R. O. Kamikawa Agr. Exp. Sta.)

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412 Azuki bean genome sequenced by single molecule real time sequencing technology

○Naito, K. [1], H. Sakai [2], E. Ogiso-Tanaka [1], Y. Takahashi [1], K. Iseki [1], C. Muto [1], K. Sato [3], K. Teruya [3], A. Shiroma [3], M. Shimoji [3], T. Hirano [3], T. Itoh [2], N. Tomooka [1] (1.Genetic Resource Center, NIAS, 2.Agrogenomics Res. Center, NIAS, 3.OIAS)

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414 Survey sequence of the del(3CL) chromosome derived from *Aegilops triunicialis*

☆Mizuno, N. [1], T. Tanaka [2], V. Jan [3], K. Marie [3], J. Dolezel [3], T. Endo [1,3], S. Nasuda [1] (1.Grad. Sch. Agri., Kyoto Univ, 2.NIAS, 3.Institute of Experimental Botany, Czech Republic)

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415 Nucleotide sequence analysis of BAC clones for the male-specific region of the spinach Y chromosome

☆Kudo, T. [1], S. Fujito [1], A. Toyoda [2], Y. Suzuki [3], Y. Onodera [4] (1.Grad. Sch. Agr., Hokkaido Univ., 2.National Institute of Genetics, 3.Grad. Sch. Frontier Sciences., The Univ. of Tokyo, 4.Res. Fac. Agr., Hokkaido Univ.)

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416 Screening of a salt-tolerant rice mutant and rapid identification of the candidate gene by MutMap

☆Takagi, H. [1], A. Abe [1], T. Muluneh [1], K. Yoshida [2], K. Oikawa [1], A. Uemura [1], H. Yaegashi [1], R. Trauchi [1] (1.Iwate Biotech. Res. Cent., 2.Koube U.)

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417 Identification of a gene encoding a glucoraphasatin synthase in radish

○Kakizaki, T. [1], H. Kitashiba [2], F. Li [2], Z. Zou [2], N. Fukino [1], T. Ohara [1], T. Nishio [2], M. Ishida [1] (1.NARO Institute of Vegetable and Tea Science, 2.Grad. Sch. Agric. Sci., Tohoku Univ.)

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418 Genetic diversity in barley (Hordeum vulgare L.) during salinity stress based on simple sequence repeats SSR-markers

☆ELakhdar, A. [1,2,3], A. Ahmed [2], A. Khairy [3], T. Kumamaru [1] (1.Plant Gen., Lab., Fac., Agric., Kyushu Univ., 2.Fac., Agric., Alexandria Univ., Egypt., 3.Field Crops Res. Inst., Agric. Res. Center, Egypt.)

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501 Molecular genetic analysis of novel gene named *VRN-D4* in chromosome 5D on heading characteristics in wheat

○Kato, K. [1], H. Harada [2], H. Nishida [1] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Fac. Agr., Okayama U.)

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502 Identification of a mitochondrial gene associated with the delayed flowering in alloplasmic wheat lines

Narita, K. [1], M. Ozeki [1], K. Kato [1], S. Kitagawa [1], Y. Gyawali [2], T. Terachi [2], ○K. Murai [1] (1.Dep. Biosci., Fukui Pref. Univ., 2.Fac. Life Sci., Kyoto Sangyo Univ.)

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503 Genetic mapping of a novel heading-time gene detected in 2H chromosome in barley

Tanabe, R. [1], ○H. Nishida [1], E. Aoki [2], K. Kato [1] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.NICS/NARO)

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504 Effects of a recessive spring growth habit gene and its linkage relations with marker genes located in the distal region of barley 4HL arm

○Taketa, S., Y. Kikuchi (Institute of Plant Science and Genetic Resources)

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505 Promotion of leaf senescence by the two step regulation involving biosynthesis of ethylene and strigolactone

☆Ueda, H. [1], M. Kusaba [1,2] (1.Grad. Sch. Sci., Hiroshima U., 2.CREST)

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506 Involvement of VIP1 in regulation of root tropisms of Arabidopsis

☆Tsugama, D. [1,2], T. Takano [3] (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.JSPS Research Fellow (PD), 3.ANESC., Univ. Tokyo)

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507 Fine mapping of qDsf1 which controls flowering time of soybean

☆Takeshima, R. [1], N. Yamaguchi [2], T. Sayama [3], M. Ishimoto [3], S. Watanabe [4], T. Yamada [1], J. Abe [1] (1.Grad. Sch. Agric., Hokkaido U., 2.Hokkaido Research Organization Tokachi Agricultural Experiment Station, 3.Agrogenomics Research Center, National Institute of Agrobiological Sciences, 4.Fac. Agr. Saga U.)

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508 The effect of Dt2 for the semi-determinate habit on branching in soybean

☆Hayashi, T., R. Takeshima, C. Zhao, T. Yamada, J. Abe (Grad. Sch. Agr., Univ. Hokkaido)

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509 Analysis of *capricious spikelets1* mutant showing pleiotropic phenotype

☆Sato, D., T. Hirokawa, H. Hirano (Grad. Sch. Sci., Univ. Tokyo)

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510 Analysis of rice washidukami (wad) mutant that shows abnormal spikelet development

☆Sugiyama, S. [1], W. Tanaka [1,2], T. Toriba [3], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Frontier Sci., Univ. Tokyo, 3.Kiseiken)

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511 Analysis of *g1* suppressor and a trial to identify the responsible gene

☆Hirokawa, T. [1], D. Sato [1], T. Toriba [1,2], A. Yoshida [1,3], H. Nagashima [1], I. Takamure [4], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.National Institute for Basic Biology, 3.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 4.Grad. Sch. Agric., Hokkaido Univ.)

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512 Identification of a *fon2* enhancer in rice

☆Suzuki, C. [1], D. Sato [1], W. Tanaka [1,2], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Frontier Sci., Univ. Tokyo)

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513 *RE1* and *RE2* expressing in rice endosperm control embryo-endosperm ratio

☆Kobayashi, H. [1], N. Nagasawa [2,3], Y. Sato [4], J. Itoh [1], H. Sakai [2], Y. Nagato [1], K. Hibara [1] (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.DuPont, 3.Fac. Biores. Sci., Akita Pref. U., 4.NIAS)

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514 *NAL2/3* genes encoding WOX-type transcriptional factor in rice control leaf width

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

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515 Analysis of leaf vein pattern and isolation of a gene responsible for narrow leaf in rice

☆Kubo, F. [1], Y. Yasui [1], Y. Sato [2], T. Kumamaru [3], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Bioagri. Sci., Nagoya Univ., 3.Fac. Agri., Kyushu Univ.)

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516 Collection and phenotypic analysis of Heterotrimeric G-protein related mutants

☆Miura, K. [1], S. Segami [1,2], I. Sugita [1], M. Nakamura [1], I. Takamure [3], Y. Iwasaki [1] (1.Faculty of Biotechnology, Fukui Prefectural University, 2.JSPS Research Fellow, 3.Res. Fac. Agr. Hokkaido Univ.)

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517 Genetic analysis of rice heterotrimeric G-protein γ3,γ4-subunit mutants

☆Segami, S. [1,2], K. Miura [1], I. Sugita [1], M. Nakamura [1], I. Takamure [3], Y. Iwasaki [1] (1.Faculty of Biotechnology, Fukui Prefectural University, 2.JSPS Research Fellow, 3.Res. Fac. Agr., Hokkaido Univ.)

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518 Genetic analysis of rice heterotrimeric G-Protein γ1, γ2-subunit genes suppressed plants

☆Sugita, I. [1], S. Segami [1,2], K. Miura [1], M. Nakamura [1], Y. Iwasaki [1] (1.Faculty of biotechnology, Fukui prefectural university, 2.JSPS Research Fellow)

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601 CRISPR/Cas9-mediated targeted mutagenesis using gRNA expression cassette driven by RNA polymerase II in rice

☆Mikami, M. [1,3], M. Endo [3], S. Toki [1,2,3] (1.Gra. Sch. Nanobiol., Yokohama City Univ., 2.Kihara Inst. Biol. Res., Yokohama City Univ., 3.Natl. Inst. Agrobiol. Sci.)

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602 A quarter of genetic recombination is intragenic in rice, it has the potential of the formations of chimeric genes

○Tanaka, J. [1], J. Yonemaru [2], S. Ogawa [3], T. Ishii [1] (1.NARO Institute of Crop Science, 2.National Institute of Agrobiological Sciences (NIAS), 3.National Institute of Technology, Numazu College)

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603 Linkage analysis of *HLA1*, a causal gene for hybrid lethality in *Nicotiana debneyi*

☆Kitamura, N., T. Morikawa, M. Yanase, Y. Ogata, M. Oda, T. Tezuka (Grad. Sch. Life Envi. Sci., Osaka Pref. U.)

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604 Development of low-calorie rice cultivars. 2. Yield test of BC2F3 generation

○Kawamoto, T. [1], S. Shibata [1], K. Kato [1], R. Takahashi [1], N. Fujita [2] (1.Akita Pref. Agri. Expmt. St., 2.Akita Pref. Univ. Fac. Bio. Sci.)

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605 "Pikamaru", high yielding rice cultivar with low amylose content of grain and disease resistances

○Sato, H. [1], M. Sakai [1], K. Tamura [1], Y. Tamura [1], T. Kataoka [1], R. Kaji [2] (1.NARO/KARC, 2.NARO/TARC)

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606 Mapping and expression analyses of a gene involved in fruit GABA content in tomato

☆Kawamata, T. [1], T. Saito [2], T. Fujii [3], C. Konishi [3], S. Inai [3], N. Fukuda [1], H. Ezura [1], C. Matsukura [1] (1.Grad. Sch. Life. Env. Sci., Univ.Tsukuba, 2.NARO Institute of Vegetable and Tea Science, 3.Nippon Del Monte Co., Ltd.)

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607 Effect of biochemical factors affecting on maltose production after heat processing in different immature black soybean varieties (Edamame)

○Hirota, T. [1], S. Yoshida [1], T. Sawada [2], Y. Nakamura [2] (1.Hyogo Pref. Tech. Cent. Agr. Forest. Fish., 2.Akita Pref. Univ.)

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608 The analyses of resistant starch in mutant rice lines for low calory rice

☆Tsuiki, K., N. Fujita (Faculty of Bioresource Sciences, Akita Prefectural University)

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609 The analyses of endosperm starch in double mutant rice line having extremely low soluble starch synthase activity

☆Hayashi, M., M. Kodama, Y. Nakamura, N. Fujita (Department of Biological Production, Akita Prefectural University)

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610 Influence of the quantity and quality of the additional protease on swelling of the gluten-free rice bread

○Araki, E. [1], S. Hamada [1,2], K. Suzuki [1], Y. Suzuki [1] (1.NARO, Inst. Crop Sci., 2.Fac. Agri. and Life Sci., Hirosaki Univ.)

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611 Identification of major triacylglycerol lipase candidate genes in rice grain and enzymatic characterization of candidate lipase

Nagata, T. [1,2], Y. Hasegawa [1,3], S. Hamada [1,4], T. Kumamaru [5], H. Matsusaka [5], ○Y. Suzuki [1] (1.NARO, Inst. Crop Sci., 2.Nat. Inst. Agrobiol. Sci., 3.Inst. Wood Tech., Akita Pref. Univ., 4.Fac. Agri. and Life Sci., Hirosaki Univ., 5.Fac. Agri., Kyushu Univ.)

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612 A possible role of chromatin modification control of nucleolar organizing region (NOR) in alignment of meiotic chromosomes in rice

Liu, H. [1], ○K. Nonomura [1,2] (1.Exp. Farm, Natl. Inst. Genet., 2.Dept. Life Sci., Grad. U. Adv. Study/SOKENDAI)

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613 Manipulation of ploidy level overcomes interspecific hybridization barrier in rice endosperm

☆Tonosaki, K. [1], D. Sekine [2], T. Ohnishi [1], H. Furuumi [2], N. Kurata [2], T. Kinosita [2] (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.Grad. Sch. of Nat. Sci. and Tech., Kanazawa Univ., 3.Plant Genet. Lab., Natl. Inst. Genet.)

---

614 LM-RNA-seq analysis of female reproductive tissue on pollination in *Arabidopsis thaliana*

☆Matsuda, T. [1], M. Matsushima [1], M. Nabemoto [2], M. Osaka [2], S. Sakazono [2], H. Masuko-Suzuki [2], M. Sone [2], H. Takahashi [3], M. Nakazono [3], M. Iwano [4], S. Takayama [4], K. Shimizu [5], K. Okumura [1], K. Yano [6], G. Suzuki [7], M. Watanabe [2], K. Suwabe [1] (1.Grad. Sch. Biores., Mie Univ., 2.Grad. Sch. Life Sci., Tohoku Univ., 3.Grad. Sch. Bioagr. Sci., Nagoya Univ., 4.Grad. Sch. Biol. Sci., NAIST, 5.Inst. Evol. Biol. & Env. Studies, Univ. Zurich, 6.Grad. Sch. Agric., Meiji Univ., 7.Div. Nat. Sci. Osaka Kyoiku Univ.)

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615 Screening of the pollen *S* gene candidates by transcriptome analysis in a wild self-incompatible species of barley, *Hordeum bulbosum*

☆Asahara, R., T. Yoneda, S. Hashimoto, K. Kakeda (Grad. Sch. Biores., Mie Univ.)

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616 Molecular analysis of *Rf2*-mediated fertility restoration for Owen cytoplasmic male sterility in sugar beet

☆Honma, Y. [1], K. Taguchi [2], D. Uchiyama [1], T. Kubo [1] (1.Grad. Sch. Agr., Hokkaido U., 2.NARO, Hokkaido Agr. Res. Center)

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617 S^h as an allogamous gene in common buckwheat

○Honda, Y. (NAROTohoku Agricultural Research Center)

Poster presentations

P001 Potential of genomic selection and genome-wide association study for fruit traits in *Citrus*

☆Minamikawa, M. [1], K. Nonaka [2], E. Kaminuma [3], H. Kanegae [1], A. Onogi [1], S. Goto [2], T. Yoshioka [2], A. Imai [2], T. Hayashi [4], Y. Nakamura [3], T. Shimizu [2], H. Iwata [1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Natl. Inst. Fruit Tree Sci., 3.Genome Info. Lab., Natl. Inst. of Genet., 4.Natl. Agri. Res. Cntr.)

P002 UAV remote sensing of sorghum biomass and its application to genomic selection modeling

☆Watanabe, K. [1], K. Arai [2,6], 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)

P003 Consideration of the optimal crop model for heading date prediction in rice

☆Aoike, T. [1], M. Watanabe [2], A. Onogi [2], O. Ideta [3], T. Yoshioka [4], K. Ebana [5], M. Yamasaki [4], H. Nakagawa [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)

P004 DNA genotyping of spring wheat accessions from Kazakhstan

○Turuspekov, Y. [1], J. Plieske [2], M. Ganal [2], E. Akhunov [3], S. Abugalieva [1] (1.Institute of Plant Biology and Biotechnology, Kazakhstan, 2.TraitGenetics Gmbh, 06466 Gatersleben, Germany, 3.Kansas State University, Manhattan, KZ, USA)

P005 TOMATOMICS: An Integrated Database for Omics Information in Tomato

☆Ozaki, S. [1], M. Takazawa [1], M. Kanno [1], K. Morimoto [1], S. Asano [1], M. Saito [1], M. Kobayashi [1], H. Ohyanagi [1], K. Aoki [2], K. Yano [1] (1.School of Agriculture, Meiji University, 2.Graduate School of Life and Environmental Sciences, Osaka Prefecture University)

P006 Research applications of PODC (Plant Omics Data Center) for discovering new environmental response genes on the basis of transcriptome information and PubMed

○Asano, S. [1], T. Takano [1], S. Terashima [1], M. Kanno [1], M. Saito [1], K. Morimoto [1], H. Kanegae [1], T. Kudo [1], S. Ozaki [1], Y. Sasaki [1], K. Yokoyama [1], M. Kobayashi [1], K. Aya [2], K. Suwabe [3], G. Suzuki [4], M. Watanabe [5], M. Matsuoka [2], H. Ohyanagi [1,6], K. Yano [1] (1.Sch. of Agri., Meiji Univ., 2.Bioscience and Biotechnology Center, Nagoya Univ., 3.Grad. Sch. of Bioresources, Mie Univ., 4.Div. of Natural Science, Osaka Kyoiku Univ., 5.Grad. Sch. of Life Science, Tohoku Univ., 6.Mitsubishi Space Software Co., Ltd.)

P007 Characteristics extraction of leaf morphology by image processing using core collection in rice

○Sugita-Konishi, S. [1], C. Nishihara [1], Y. Senzaki [1], A. Matsushima [1], T. Higaki [2], N. Kutsuna [2] (1.Faculty of Agriculture, Kagawa University, 2.Graduate School of Frontier Sciences, The University of Tokyo)

P008 Characteristics extraction of leaf morphology in rice by image processing using multiple angle shooting

☆Kawada, R. [1], T. Okamoto [1], N. Kutsuna [2], S. Sugita-Konishi [1] (1.Faculty of Agriculture, Kagawa University, 2.Graduate School of Frontier Sciences, The University of Tokyo)

P009 The construction of pedigree haplotype viewer using Web interface

○Yonemaru, J. [1], S. Fukuoka [1], Y. Takeuchi [2], T. Yamamoto [1] (1.NIAS, 2.NARO-NICS)

P010 New software 'Light-Interception Simulator' for interactively conducting the simulation experiment on light-interception efficiency of virtual paddy field

○Oka, M. (Miyagi Univ. Educ.)

P011 Efficient improvement of genomic selection accuracy using active learning

☆Tanaka, R., H. Iwata, A. Onogi (Grad. Ach. Agric. Life Sci., Univ.Tokyo)

P012 Imputation of multi-trait multi-environment trial data using tensor princinpal 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.Univ. Abomey-Calavi, 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

P013 Breeding of an early maturing soybean cultivar “Fukuhayate” for western Japan with high tofu processing suitability

○Oki, N. [1], M. Takahashi [1], M. Takahashi [1], Y. Kono [1], K. Komatasu [2], Y. Nakazawa [1], M. Hajika [3] (1.NARO, KARC, 2.NARO, HARC, 3.NICS)

P014 Field evaluation of a new salt tolerant rice line “Kanto-shi 265” for whole crop silage

○Takeuchi, Y. [1], N. Kobayashi [1], Y. Arai-Sanoh [1], Y. Takemoto-Kuno [1], M. Kondo [1], T. Endo [2], K. Abe [3], M. Monma [4], M. Kuroki [1], A. Goto [1], H. Hirabayashi [1], M. Yamaguchi [1], T. Ishii [1] (1.NARO Natl. Inst. Crop Sci., 2.Miyagi Pref.Furukawa Agr.Exp.Stn, 3.Ishinomaki Agr. Extension Center, 4.Kitakami River Coast Land Improvement District)

P015 Estimation of genetic parameters and prediction of breeding values for fruit-quality traits in NIFTS citrus breeding program

○Imai, A. [1,6], N. Hiehata [1,2], R. Matsumoto [1], T. Takahara [1], T. Kuniga [1,3], T. Yoshioka [1], K. Nonaka [1], N. Mitani [1], H. Fukamachi [1], M. Yamamoto [1,4], T. Hayashi [5,6] (1.NIFTS,NARO, 2.Nagasaki Agriculture and Forestry Technical Development Center, 3.WARC,NARO, 4.Faculty of Agriculture, Kagoshima University, 5.NARC, NARO, 6.Grad. Life Env. Sch., Univ. Tsukuba)

P016 Yield improvement potential by altering allele combination among flowering related loci in soybean

☆Sayama, T. [1], A. Kaga [1], S. Watanabe [1,2], M. Hajika [3], T. Yamada [3], K. Takahashi [3], A. Hishinuma [3], M. Ishimoto [1] (1.NIAS, 2.Fac. Agric., Saga U., 3.NICS)

P017 The responsible gene mapping of two novel cleistogamous rice mutants

○Ohmori, S. [1], H. Yoshida [2] (1.Hokuriku Research Center, NARC, 2.NICS)

P018 Breeding of 'Hitachimochi 36', which has lower rice cake hardening speed

○Okamoto, K. [1], K. Kawamata [1], Y. Fukazawa [1], S. Higuchi [1], T. Manabe [2] (1.Plant Biotech. Inst. IBARAKI Agri. Cent., 2.IBARAKI Kennan Agri. & For. Management Office)

P019 A new soybean cultivar 'Koganesayaka' that lacks three lipoxygenase isozymes for temperate regions

○Saruta, M. [1], Y. Takada [1], A. Okabe [1], A. Kikuchi [2] (1.WARC, 2.TARC)

P020 Breeding of a new sweetpotato cultivar "Karayutaka" with early storage root growth

○Takada, A. [1], T. Kumagai [1], T. Kuranouchi [1], Y. Nakamura [1], T. Fujita [2], M. Nakatani [3], K. Katayama [1] (1.Naro Inst. of Crop Sci., 2.Naro Inst. of Kyushu Okinawa Agric. Res. Ctr., 3.MAFF)

P021 Studies on molecular breeding of ‘Evergreen Kirinso’ (*Phedimus aizoon*)

☆Koji, T. [1], M. Fujita [1], S. Cho [2], A. Elsadig Eltayeb [2], H. Tsujimoto [2] (1.Fujita Co., Ltd., 2.ALRC, Univ. Tottori)

P022 Measures to continuously utilize genetic resources under the Nagoya Protocol to the Convention on Biological Diversity

○Yamamoto, A. (Environment Policy Division, Minister’s Secretariat, MAFF)

P023 Evaluation on diversity in *Elymus tsukushiensis*, a wild Triticeae species indigenous to Japan, based on morphological traits and molecular markers

☆Hirata, R., T. Sasanuma (Grad. Sch. Agr., Yamagata Univ.)

P024 Evaluation of genetic variation among wild rice populations in Cambodia

☆Orn, C. [1], R. Shishido [2], H. Kageyama [1], M. Akimoto [3], R. Ishikawa [1], M. Ouk [4], S. Men [4], T. Ishii [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Grad. Sch. Bioresource Sci., Nihon Univ., 3.Agric. Vete. Medi. Obihiro Univ., 4.CARDI)

P025 Modern einkorn: Back into cultivation (3) Early, free threshing Triticum monococcum with differing plant height

○Watanabe, N. (College. Agr., Ibaraki U.)

P026 Fine mapping of QTL affecting primary rachis length of panicle in rice

☆Hobo, T. [1], S. Ota [2], K. Ando [2], M. Ikeda [1], K. Doi [2], H. Kitano [1] (1.Biosci. Biotech. Ctr.,Nagoya U., 2.Grad. Sch. Bioagar. Sci.,Nagoya U.)

P027 Genetic diversity of Myanmar rice landraces from different agro-ecological zones investigated with SSR markers and agronomic traits

○U, W. [1], Y. Fukuta [3], S. Yanagihara [3], R. Ohsawa [2], P. Aung [4], K. Watanabe [2] (1.Graduate School of Life and Environmental Sciences, University of Tsukuba, 1-1-1, Tennoudai, Tsukuba, Ibaraki,305-8572,Japan., 2.Gene Research Center and Faculty of Life and Environmental Sciences, University of Tsukubas,1-1-1, Tennoudai, Tsukuba, Ibaraki, 305-8572,Japan, 3.Japan International Research Center for Agricultural Sciences (JIRCAS), 1-1, Ohwashi, Tsukuba, 305-8686, Japan,, 4.Plant Biotechnology Center, Department of Agriculture, Ministry of Agriculture and Irrigation, Yangon, Myanmar)

P028 Development of tomato mutant population and collection of fruit metabolism information

☆Hoshikawa, K. [1], M. Shikata [1], T. Ariizumi [1], N. Fukuda [1], Y. Kanayama [2], Y. Kubo [3], K. Aoki [4], H. Ezura [1] (1.Fac. Life Environ. Sci., Univ. Tsukuba, 2.Grad. Sch. Agri. Sci., Tohoku Univ, 3.Grad. Sch. Envi. Life Sci., Okayama Univ, 4.Grad. Sch. Lif. Envi. Sci., Osaka Pref. Univ)

P029 Geographical and ecological differentiation in *Aegilops geniculata* Roth

○Ohta, S., K. Imukai, S. Sakaguchi, M. Hattori, Y. Teraguchi (Dep. Biosci., Fukui Pref. Univ.)

P030 Phylogeographical Variation of the W14/15 genes in *Gentiana scabra* and *G. zollingeri*

☆Takahashi, Y. [1], T. Hikage [1,2], S. Watanabe [3], Y. Saitoh [1], K. Tsutsumi [1] (1.Cryobiofrontier Res. Center, Iwate Univ., 2.Hachimantai City Floricultural Res. and Dev. Center, 3.Iwate Prefectural Museum)

P031 A SNP of *Hwc1-1* responsible for a hybrid weakness in rice reduces interaction between HWC1 proteins

☆Okiyama, Y. [1], K. Ichitani [2], N. Watanabe [1], T. Kuboyama [1] (1.Col. Agri., Univ. Ibaraki, 2.Fac. Agri., Univ. Kagoshima)

P032 Estimation of the number of loci involved in a loss of seed shattering in an Indica-type cultivated rice, *Oryza sativa* cv. IR36

Nishimura, A., H. Than Myint, C. Inoue, Y. Oka, T. Ishii, ○R. Ishikawa (Grad. Sch. Agr. Sci., Kobe Univ.)

P033 Identification of quantitative trait loci involved in Aluminium tolerance between wild rice, *Oryza rufipogon*, and cultivated rice, *O. sativa*

☆Wada, M. [1], M. Iwata [1], S. Yoshida [1], P. Thanh [1], T. Ishii [1], J. Ma [2], R. Ishikawa [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.IPSR, Okayama Univ.)

P034 Fluorescence in situ hybridization on chromosome of Camellia species and interspecific hybrid using rDNA probes

○Furukawa, K. [1], S. Iida [1], K. Teramae [1], S. Ogawa [1], N. Ohmido [2] (1.National Institute of Technology, NUMAZU college, 2.Kobe University, Graduate school of human development and environment)

P035 Evaluation on growth traits of safflower genetic resources in Yamagata

☆Aoyagi, S. [1], C. Tang [2], Y. Lang [2], T. Miwa [2], T. Sasanuma [1] (1.Fac. Agr., Yamagata Univ., 2.AJINOMOTO CO., INC.)

P036 Analysis of genetic diversity for the seed accumulation of cesium in the soybean germplasm

☆Takagi, K. [1], A. Kaga [2], M. Ishimoto [2], M. Hajika [3], T. Matsunaga [1] (1.NARO/ARC, 2.NIAS, 3.NICS)

P037 Genetic analysis on fruit color variation in *Capsicum baccatum* 2

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

P038 2. The differences in the flowering trait and the number of runner between homozygous and heterozygous genotypes at the everbearing locus in strawberry

○Honjo, M. [1], S. Yui [1], M. Morishita [2], M. Hamano [1], H. Yamazaki [1] (1.NARO/TARC, 2.NARO/KARC)

P039 Agronomic characteristics of early heading mutant of Kernel Basmati of rice

Gichuhi, E. [1], ○M. Maekawa [1], H. Murage [2], N. Ahmed [3], E. Fushimi [4], H. Saito [4], Y. Okumoto [4] (1.Inst. Plant Sci. Res., Okayama U., 2.Dept. Hort., Jomo Kenyatta U. Agr. Tech, 3.CABB, U. Agr., 4.Grad. Sch. of Agric. Kyoto U.)

P040 Construction of a high density mutant library of Japanese soybean cultivar Enrei and development of mutant retrieval method using next generation sequencing

☆Tsuda, M. [1], A. Kaga [1], T. Anai [2], S. Watanabe [1,2], M. Nishimura [1,3], N. Yamada [4], T. Sayama [1], K. Takagi [1,5], T. Shimizu [1], K. Machita [1], S. Mori [1], H. Sasaki [1], H. Kanamori [1], Y. Katayose [1], M. Ishimoto [1] (1.NIAS, 2.Saga University, 3.Niigata University, 4.Nagano vegetable and ornamental crops exp.stn., 5.NARC/ARC)

P041 Induction of Lolium temulentum mutants by sodium azide

○Takamizo, T. (NARO Institute of Livestock and Grassland Science)

P042 Development of pipeline for whole-genome mutation analysis in *Arabidopsis thaliana*

☆Ishii, K. [1], T. Hirano [2], Y. Kazama [1], M. Hamada [3], Y. Ono [4], T. Abe [1] (1.RIKEN Nishina Cent., 2.Fac. Agric., Univ. Miyazaki, 3.Waseda Univ., 4.IMSBIO Co., Ltd.)

P043 A convenient method to construct a plant TALEN system for genome engineering

Kusano, H., M. Kihira, H. Onodera, H. Aoki, ○H. Shimada (Depatment of Biological Science and Technology, Tokyo University of Science)

P044 Plant hormone ethylene suppresses fruit set in tomato (Solanum lycopersicum)

Shinozaki, Y. [1], M. Kojima [2], H. Sakakibara [2], Y. Okabe [1], H. Ezura [1], ○T. Ariizumi [1] (1.Grad. Sch. Life Env. Sci., Univ. Tsukuba, 2.CSRS Riken)

P045 Production of interspecific hybrids between cultivated gentians and wild species of gentians

☆Takamura, Y. [1], C. Asano [1], T. Hikage [2], S. Yokoi [1], Y. Takahata [1] (1.Fac. Agri., Univ. Iwate, 2.Hachimantai City Floricultural R & D Center)

P046 Characterization of *O. glaberrima* CSSLs showing annual growth habit

☆Ozaki, Y. [1], K. Ishihara [2], X. Zhu [1], M. Fujioka [1], H. Sunohara [1], T. Takashi [3], H. Kitano [4], K. Doi [1] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Fac. Agr., Nagoya U., 3.STAY GREEN Co., Ltd., 4.Biosci. Biotec. Ctr., Nagoya U.)

P047 Accumulation of insoluble proteins in hybrid tobacco cells and seedlings (*Nicotiana suaveolens* × *N. tabacum*) showing temperature-sensitive lethality

☆Ueno, N. [1], H. Ishikawa [1], M. Kashiwagi [1], W. Marubashi [2], M. Kanekatsu [1], T. Yamada [1] (1.Grad. Sch. Agr., Tokyo U. Agr. Tech., 2.Sch. Agr. Meiji U.)

P048 Backcrossing between intergeneric hybrids (*Carica papaya* × *Vasconcellea cundinamarcensis*) and *C. papaya*

○Tarora, K. [1], Y. Yabiku [1], C. Miyazato [1], T. Takamine [2], K. Yasuda [1], S. Kawano [1], H. Ueno [3], H. Matsumura [4], N. Urasaki [1] (1.Okinawa Pref. Agric. Res. Ctr., 2.Okinawa Pref. Inst. Health Env., 3.Dep. Biosci. Tex. Tech., Shinshu Univ., 4.Gene Res. Ctr., Shinshu Univ.)

P049 Effects on freezing tolerance in *Lolium perenne* of introgression of partial genomic regions around candidate genes from *Festuca pratensis*

○Tamura, K. [1], K. Tase [1], Y. Sanada [1], A. Kubota [2], Y. Akiyama [2] (1.NARO/HARC, 2.NARO/TARC)

P050 Production of an alloplasmic Brassica oleracea line carrying Diplotaxis erucoides cytoplasm

☆Fujita, Y., S. Shim, S. Bang, Y. Kaneko (Fac. Agric., Utsunomiya. U)

P051 Analysis of gene expression during hybrid weakness caused by *HWA1* and *HWA2* genes in rice by real-time RT-PCR

Shiragaki, K. [1], K. Ichitani [2], T. Kuboyama [3], M. Yanase [4], T. Morikawa [4], ☆T. Tezuka [4] (1.Sch. Life Envi. Sci., Osaka Pref. U., 2.Fac. Agr., Kagoshima U., 3.Col. Agr., Ibaraki. U., 4.Grad. Sch. Life Envi. Sci., Osaka Pref. U.)

P052 Fine mapping of Hch1 inducing hybrid chlorosis in crosses between tetraploid wheat and Aegilops tauschii

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

P053 Fine mapping of Net2 inducing type II necrosis in crosses between tetraploid wheat and Aegilops tauschii

☆Sakaguchi, K., R. Nishijima, M. Iehisa, S. Takumi (Grad. Sch. Agr. Sci., Kobe Univ.)

P054 Over-expression of the gene induced by salt stress in barley

☆Hisano, H., M. Yamane, N. Yamaji, K. Sato (IPSR, Okayama U.)

P055 The functional analysis of apomixis specific genes: The spatiotemporal expression of ASG-1 gene in the transformants of Arabidopsis

○Chen, L. [1], Y. Nishimura [1], K. Yoshida [2], T. Tetsumura [3], T. Sugita [4], D. Kurihara [5], T. Higashiyama [5] (1.Fac. Environ & Horti. Sci., Minami Kyushu U., 2.Fac. Agri., U. Tokyo, 3.Fac. Agri., U. Miyazaki, 4.Miyazaki Pref. Agri. Experi. Stan., 5.Fac. Sci., Nagaya U.)

P056 The functional analysis of apomixis specific genes: The approach to making the transformants of ASG-1 using the matured guinea grass seeds

○Nishimura, Y. [1], K. Yoshida [2], T. Sugita [3], L. Chen [1] (1.Fac. Environ. & Horti. Sci., Minami Kyushu U., 2.Fac. Agri., U. Tokyo, 3.Miyazaki Pref. Agri. Experi. Stan.)

P057 Development of gene transfer system of grass biomass plant, *Sorghum bicolor*

☆Izawa-Sato, K., S. Nonaka, K. Tokue, H. Ezura (Fac. Life Environ. Sci., Gene Research Center, Univ. Tsukuba)

P058 Effect of over-expression of *Msh1* on organellar genome in *Brassica napus*

☆Mita, K., J. Imamura (Department of Bioresource Science Faculty of Agriculture Tamagawa University)

P059 Generation of transgenic rice plants by RdDM-mediated epigenome editing

○Wakasa, Y. [1], T. Harada [2], F. Takaiwa [1] (1.NIAS, 2.Fac. Agric. Life Sci., Hirosaki U.)

P060 Development of the multi-desease resistant transgenic rice. III Evaluation of field resistance for leaf blast (2014)

○Yamazaki, M., N. Hayashi, S. Goto, F. Shimoda, H. Takatsuji (Natl. Inst. of Agrobiol. Sci.)

P061 Improvement of *BSR1*-expressing disease resistant rice using constitutive and pathogen-inducible promoters 2. *Burkholderia glumae* resistance

☆Maeda, S., S. Goto, F. Sasakura-Shimoda, H. Takatsuji, M. Mori (National Institute of Agrobiological Sciences)

P062 Pedigree analysis using SSR markers associated with SBWMV resistant QTL in Japanese wheat

○Fujita, Y. [1], M. Chono [1], H. Kojima [1], T. Takayama [1], M. Fujita [1], C. Otobe [1], M. Seki [2], H. Matsunaka [3], S. Oda [1] (1.NARO/NICS, 2.NARO/ARC, 3.NARO/KARC)

P063 Development of DNA markers linked to the gene for the bean common mosaic virus (BCMV) resistance in azuki bean (Vigna angularis)

☆Nishizaki, M. [1], A. Konishi [2], N. Furutani [2], Y. Shizukawa [2,3], H. Sassa [1] (1.Grad. Sch. Hort., Chiba U., 2.Kyoto Pref. Inst. Agri. Biotech., 3.Kyoto Pref. Inst. Agri. Kyoto. Exten. Center)

P064 Utilization of near-isogenic lines for brown planthopper and green rice leafhopper resistance genes in rice

Fujita, D. [1], M. Matsumura [2], T. Mai [1], A. Yoshimura [1], ○H. Yasui [1] (1.Faculty of Agriculture, Graduate School, Kyushu University, 2.NARO Kyushu Okinawa Agricultural Research Center)

P065 Correlation analysis of heat stress tolerance and adaptation traits in hexaploid wheat

☆Elbashir, A. [1,2], I. Tahir [2], M. Abdeldaim [2], M. Reynolds [3] (1.Arid Land Res. Center, Tottori U., 2.Agric. Res. Corp., Sudan, 3.CIMMYT)

P066 Functional analysis of bZIP18, a Group I bZIP transcription factor of *Arabidopsis thaliana*

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

P067 Diversity of cadmium tolerance at seedling stage plants in the genus *Oryza*

☆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.)

P068 Detection of QTLs for rice chalkiness under high temperature and low solar radiation during ripening period at two different regions

○Kataoka, T. [1], K. Tamura [1], A. Kobayashi [2], S. Morita [1], J. Yonemaru [3], Y. Tamura [1], M. Sakai [1], H. Sato [1] (1.NARO/KARC, 2.Fukui Agr. Exp. Stn., 3.Nat. Inst. Agr. Sci.)

P069 Studies on the mechanism of drought tolerance via acetic acid

☆Ogawa, D. [1,4], J. Kim [2,4], M. Kusano [2,3], M. Muramatsu [1], M. Miyao [1], M. Seki [2,4], Y. Habu [1,4] (1.NIAS, 2.CSRS, RIKEN, 3.Facult Life Environ Sci, Univ Tsukuba, 4.CREST, JST)

P070 Mapping of QTLs controlling cool temperature tolerance on chromosome 3 in rice and breeding of near isogenic lines

○Kon, C. [1], T. Ono [2], S. Kanda [1], T. Endo [3], S. Moriyama [1], M. Suto [1] (1.AITC Agric. Res. Inst., 2.Aomori Prefecture Seihoku District Administration Office, 3.Miyagi Prefectural Furukawa Agricultural Experiment Station)

P071 QTLs for tolerance to iron toxicity detected in upland NERICA 7

☆Tomita, A. [1,2], J. Pariasca Tanaka [1], M. Wissuwa [1], M. Obara [1], S. Yanagihara [1], Y. Fukuta [1] (1.JIRCAS, 2.University of Tsukuba)

P072 Characterization of the Arabidopsis Calcium/hydrogen antiporter (ChaC) proteins in response to salt and drought stresses

○Eltayeb, A., K. Tanaka, H. Tsujimoto (Arid Land Res. Cen., Tottori Univ.)

P073 Galactinol accumulation under abiotic stress conditions in wheat

○Shimosaka, E. (NARO Hokkaido Agricultural Research Center)

P074 Effect of different *ant* genes on pre-harvest sprouting in barley

○Yoshioka, T. [1], K. Suzuki [2], A. Takahashi [1] (1.NARO/WARC, 2.Niihama Natl. Coll. Tech.)

P075 Genetic analysis of low cadmium accumulation traits in heaploid wheat

○Kiribuchi-Otobe, C. [1,2], Y. Fang [2], M. Fujita [1], T. Takayama [1], H. Kojima [1], Y. Fujita [1] (1.NARO Inst. Crop Sci., 2.Grad. Sch. Life Envir. Sci., U. Tsukuba)

P076 Relationship between the overwintering ability and germination pattern of F9 RIL from "Fuyugoshi" (a domestic rice strain) X "Hoshinoyume" cross in Hokkaido

○Ushiki, J., S. Matsuba, K. Okazaki, S. Hayashi (Hokkaido Agr. Exp. Stn.)

P077 Image analysis of cooked rice appearance

○Kobayashi, A. [1], T. Tanabata [2], N. Sagara [3], K. Tomita [1], Y. Kogi [1], M. Tanoi [1] (1.Fukui. Agr. Exp. Stn., 2.RIKEN CSRS, 3.Kazusa DNA Res. Inst.)

P078 Characteristics of Koshihikari isogenic line introduced lack of the starch branching enzyme I function derived from "Hiderishirazu-D"

☆Kawamata, K. [1], Y. Fukazawa [1], S. Higuchi [1], T. Manabe [2], K. Okamoto [1] (1.Plant Biotech. Inst., IBARAKI Agri. Cent., 2.IBARAKI Kennan Agri. & For. Management Office)

P079 Cultivar difference in water absorption and gelatinization process in early stage of rice cooking

☆Kogi, Y. [1], K. Suzuki [2], A. Kobayashi [1], K. Tomita [1] (1.Fukui Agr.Exp.Stn, 2.NARO NICS)

P080 Relationship between wheat grain protein content and SPAD values in the segregating population derived from a cross between Setokirara × Yumetikara

☆Yanaka, M., W. Funatsuki, K. Takata (NARO/WARC)

P081 The blending properties of extra-strong wheat varieties, Yumechikara and Minorinochikara, in bread-making

○Ito, M. [1], T. Ikeda [2], K. Nagasawa [1], Z. Nishio [3], Y. Terasawa [1], K. Hatta [1], T. Tabiki [1] (1.NARO Hokkaido Agricultural Research Center, 2.NARO Western Region Agricultural Research Center, 3.Ministry of Agriculture, Forestry and Fisheries)

P082 Agronomic characteristics of wheat lines with a transrocation chromosome of Leymus racemosus or Gpc-B1

○Takata, K. [1], M. Kishii [2], M. Yanaka [1] (1.NARO, WeNARC, 2.CIMMYT)

P083 Quality characteristics of wheat breeding lines with very small amylograph breakdown

○Takayama, T., C. Kiribuchi-Otobe, M. Fujita, Y. Fujita, H. Kojima (NARO Inst of Crop Sience)

P084 Impact of variant *Wx* alleles on starch properties in wheat— *Wx-A1i*+ *Wx-D1f*, *Wx-A1c*+ *Wx-D1f* and *Wx-A1d*—

○Yamamori, M. (NARO Inst. Crop Sci.)

P085 Functional analysis of transcription factors controlling wheat seed storage protein using transformants

☆Kouyama, H., S. Sakuma, Y. Ogihara, K. Kawaura (KIBR, Yokohama City Univ.)

P086 Change of the β-glucan content by the cultivation condition in barley cultivar 'Beau Fiber'

○Yanagisawa, T. [1], A. Takahashi [2], T. Yoshioka [2], T. Tonooka [3], M. Taira [1], E. Aoki [1] (1.NARO Institute of Crop Science, 2.NARO/WARC, 3.NARO/KARC)

P087 Development of markers closely linked to *fra* locus in barley

○Saito, M. [1], M. Taira [2], E. Aoki [2], T. Yanagisawa [2], G. Ishikawa [1], T. Nakamura [1] (1.NARO/TARC, 2.NICS)

P088 Effect of the *Wx1-1* allele for low-amylose-content and temperature sensitivity during ripening, on the NIL of the rice cultivar ‘Akidawara’

☆Ogawa, S. [1], J. Tanaka [2], Y. Suzuki [2], T. Ishii [2] (1.National Institute of Technology, Numazu College, 2.NARO Institute of Crop Science)

P089 QTL analysis on the grain number of rice panicle using the indica type multi-grain cultivar, VT-101, and the japonica type cultivar, Koshihikari

☆Ota, S. [1], T. Hobo [2], T. Touyama [1], T. Kunishima [1], A. Agata [3], M. Doi [3], D. Tran [4], D. Tran [5], H. Le [5], H. Kitano [2] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.Fac. Agr., Nagoya U., 4.Grad. Sch. IDEC, Hiroshima U., 5.Dep. Mol. Biol. Agric. Genet. Inst., Ha Noi, Vietnam)

P090 Mapping of the genes affecting the number of primary branches of 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.)

P091 Yeild peformance of the abundant tillering rice strain under sparse planting condition

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

P092 Diversity of rice straw for biorefinery utilization

☆Goda, T. [1], H. Teramura [2], M. Suehiro [1], R. Takayama [3], D. Saisho [4], H. Yamamoto [5], K. Kanamaru [6], H. Kawaguchi [2], C. Ogino [2], A. Kondo [2], M. Yamasaki [1] (1.Food Res. Edu. and Res. Cent., Grad. Sch. of Agri. Sci., Kobe Univ., 2.Grad. Sch. of Eng., Kobe Univ., 3.RMSB.inc, 4.Ins. of Plant Sci. and Res., Okayama Univ., 5.FCR&Bio CO.,LTD, 6.Grad. Sch. of Agri. Sci., Kobe Univ.)

P093 Duplicated Co/Hd1 regions specific to species of the genus Miscanthus

○Nagano, H. [1], E. Sacks [2], T. Yamada [1] (1.Field Science Center for Northern Biosphere, Hokkaido University, 2.Department of Crop Science, University of Illinois, USA)

P094 Characterization of introgression lines with an Indica-type rice IR64 genetic background based on nitrogen uptake at seedling stage

☆Uddin, M. [1], M. Obara [2], Y. Seiji [1,2,3], Y. Fukuta [1,2,3,4] (1.Grad Sch of Life & Environ Scie, University of Tsukuba, 2.BRPHD, Japan Intl Res Center for Agril Sci (JIRCAS), 3.BRPHD, Japan Intl Res Center for Agril Sci (JIRCAS), 4.TARF, Japan Intl Res Center for Agril Sci (JIRCAS))

P095 Agronomic characteristics of LIA-1, a recombinant inbred line carrying chromosome segments from Oryza longistaminata under non-fertilized conditions

☆Gichuhi, E. [1], M. Maekawa [2] (1.Graduate school of Environmental and Life Sciences, Okayama university, 2.Institute of Plant Science and Resources (IPSR), Okayama University)

P096 Expression of genes controlling compound leat development in Trifolium reopens L. leaflet number mutants

☆Ohashi, H., K. Segawa, K. Tsutsumi, Y. Saitoh (Cryobiofrontier Research Center, Faculty of Agriculture, Iwate University)

P098 The diversity of juvenile to adult phase change in soybean

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

P099 Morphological and molecular characterization of rice mutant showing continuous vegetative growth

○Satoh-Nagasawa, N. [1], N. Nagasawa [1], Y. Nagato [2] (1.Fac. Biores. Sci., Akita Pref. U., 2.Grad. Sch. Agric. Life Sci., U. Tokyo)

P100 Simulation analysis about the starch grain development of rice endosperm

☆Matsushima, R., M. Maekawa, W. Sakamoto (Institute of Plant Science and Resources, Okayama University)

P101 Identification of spike compactness genes using wheat mutants

☆Uchiyama, H., S. Sakuma, K. Kawaura, Y. Ogihara (KIBR, Yokohama City Univ.)

P102 In vivo imaging of auxin signaling in rice shoot apical meristem

☆Imai, Y. [1], Y. Sato [2], T. Higashiyama [2,3,4], K. Shimamoto [1], H. Tsuji [1] (1.Lab. Plant Mol. Genet., Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol., 2.WPI-ITbM, Nagoya Univ., 3.Grad. Sch. Sci., Nagoya Univ., 4.ERATO, JST.)

P103 Proteome analysis of rice shoot apical meristem

☆Yamada, M. [1], M. Fujiwara [2], Y. Nomura [3], H. Nakagami [3], K. Hanada [4], Y. Fukao [2], K. Shimamoto [1], H. Tsuji [1] (1.Lab. Plant Mol. Genet., Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol., 2.Plant Grobal Education Project, Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol., 3.Plant proteome res. unit, RIKEN CSRS, 4.Front. Res. Acad. Young Research., Kyushu Inst. Technol.)

P104 Polymorphism of floral repressor FLC in radish cultivars expressing different flowering time

☆Mochida, M., Y. Kikumoto, A. Ishii, A. Tateishi, K. Nomura (Coll. Bioresource Sci., Niohn Univ.)

P105 Identification of Polycomb complex genes in wheat

☆Umekita, K. [1], N. Mizuno [2], S. Nasuda [2], K. Kawaura [3], Y. Ogihara [3], K. Murai [1] (1.Dep. Biosci., Fukui Pref. Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.Kihara Inst. Biol. Res., Yokohama City Univ.)

P106 Localization analysis of OsSub53 protein during early phases of rice seed development

☆Tokairin, A., K. Tsutsumi, Y. Saitoh (Cryobiofrontier Research Center, Univ. Iwate)

P107 ESOFB2, an endosperm-specific F-box protein from *Oryza sativa* interacts with Orysa;KRP4 in the nucleus

☆Sugiyama, T., M. Sasaki, N. Fujiwara, M. Mizutani, K. Tsutsumi, Y. Saitoh (Cryobiofrontier Research Center, Faculty of Agriculture, Iwate University)

P108 Attempts to identify the candidate gene for tomato parthenocarpic gene by SNP analyses

☆Takei, H. [1], Y. Shinozaki [1], H. Ezura [2], T. Ariizumi [1] (1.Ariizumi Laboratory. The University of Tsukuba., 2.Ezura Laboratory. The University of Tsukuba Gene research center)

P109 Association of *BrSPA4* with an extremely late bolting of Leafy Green Parental Line No.2, which requires long days instead of vernalization for bolting

☆Kitamoto, N. [1], S. Yui [2], K. Nishikawa [3], Y. Takahata [1], S. Yokoi [1] (1.Faculty of Agri., Univ. Iwate, 2.NARO, 3.Sakata Seed Co., Ltd.)

P110 Identification of spinach sex-linked genes based on transcriptome data

☆Takahata, S. [1], H. Hirakawa [2], Y. Suzuki [3], Y. Onodera [4] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Kazusa DNA Research Institute, 3.Grad. Sch. Frontier Sciences, The Univ. of Tokyo, 4.Res. Fac. Agr., Hokkaido Univ.)

P111 Fine mapping of *qGLT11-1* locus improving low temperature germinability of rice

☆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.)

P112 Leaf margin phenotype-specific RAD markers for pineapple (*Ananas comosus*)

○Urasaki, N. [1], S. Goeku [1], R. Kaneshima [1], T. Takamine [2], K. Tarora [1], M. Takeuchi [3], C. Moromizato [3], K. Yonamine [3], F. Hosaka [4], K. Nashima [4], S. Terakami [4], H. Matsumura [5], T. Yamamoto [4], M. Shoda [3] (1.Okinawa Pref. Agric. Res. Ctr., 2.Okinawa Pref. Inst. Health Env., 3.Okinawa Pref. Agric. Res. Ctr., Nago, 4.NIFTS, NARO, 5.Gene Res. Ctr., Shinshu Univ.)

P113 Establishment of whole genome analysis technology in the single plant cell

☆Iwabuchi, H. [1], N. Takagi [2], H. Yamazaki [3], H. Matsumura [4] (1.Grad. Sch. Sci. Tech.,Univ. Shinshu, 2.KANTO CHEMICAL CO.,INC. Technology & Development Division, 3.KANTO CHEMICAL CO.,INC. Isehara Research Laboratory, 4.Gene Res.Ctr., Univ. Shinshu)

P114 Genome-wide association analysis for the target gene integrated in the genome of rice cultivar Koshihikari

○Tomita, M. [1], K. Ishii [2], Y. Katou [1], H. Doura [1], Y. Uenishi [1], J. Ohtsuki [1] (1.Res. Inst. of Green Sci. & Tech., Shizuoka Univ., 2.Tokyo Univ. of Agr. & Tech.)

P115 Evolutionary study identifies nonautonomous DNA viruses in the genomes of rice and relatives

☆Chen, S., H. Zheng, T. Takeuchi, Y. Kishima (Laboratory of Plant Breeding, Research Faculty of Agriculture, Hokkaido University)

P116 QTL analysis for salt tolerance at the germination stage in barley

☆Ito, H. [1], D. Saisho [1], M. Honjo [2], M. Yasugi [2], A. Nagano [2,3], K. Takahagi [4,5], K. Mochida [4], K. Sato [1] (1.IPSR, Okayama Univ., 2.Center for Ecological Research, Kyoto Univ., 3.JST PRESTO, 4.CSRS, RIKEN, 5.International College of Arts and Sciences, YCU)

P117 QTL Analysis of Days to Heading and Agronomic Traits in Rice Recombinant Inbred Lines of Koshihikari/Hiyokumochi

☆Maeda, M. [1], S. Okada [1], T. Goda [1], M. Sasaki [1], M. Suehiro [1], W. Yokoyama [1], R. Takayama [2], D. Saisho [3], H. Yamamoto [4], K. Hori [5], A. Garcia [6], K. Doi [7], M. Yamasaki [1] (1.Food Resources Education and Research Ctr., Grad. Sch. Agric. Sci., Kobe U, 2.RMSB.inc, 3.FCR&BIO Co., Ltd., 4.IPSR, Okayama U, 5.National Institute of Agrobiological Sciences, 6.United States Department of Agriculture-Agricultural Research Service, 7.Grad. Sch. Bioagr. Sci., Nagoya U.)

P118 QTL analysis for seed dormancy in rice respond to seed development environment 3

☆Imanishi, N., K. Hino, T. Kanzaka, Y. Sato, M. Shimamura, E. Fukuda, R. Shishido (Coll. Bioresource Sci., Nihon U.)

P119 Analysis of rice Chromosome Segment Substitution Lines (CSSLs) toward determination of Quantitative Trait Locus (QTL)

○Matsubara, K., L. Wang, K. Tsujiuchi, K. She, T. Imamura, H. Kusano, H. Shimada (Dept. of Biol. Sci & Technol., Tokyo Univ. of Sci)

P120 Estimation of a quantitative trait locus for cesium absorption using chromosome segment substitution lines in rice

○Akitoshi, G., M. Kondo (NARO Inst. CROP Sci.)

P121 QTL analysis of white core and grain size about “Yamadanishiki”, a brewing rice cultivar (2) and the development of white core

☆Okada, S. [1], M. Suehiro [1], K. Ebana [2], K. Hori [2], M. Yamasaki [1] (1.Food Resources Education and Research Ctr., Grad. Agric. Sci., Kobe U, 2.Natl. Inst. Agrobiol. Sci)

P122 QTL analysis for sugar content of sweet sorghum

Kurami, K. [1], S. Nakamura [2], M. Yamaguchi [1], E. Ichikawa [1], K. Shinohara [2], Y. Ito [2], J. Wu [3], J. Yonemaru [3], S. Kasuga [4], M. Matsuoka [2], H. Kitano [2], ☆T. Sazuka [2] (1.Fac. of Agr., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Natl. Inst. of Agrobiol. Sci., 4.AFC, Fac. of Agri., Shinshu Univ.)

P123 QTL analysis of yield associated traits of rice by using Genotyping by Sequencing

☆Zhu, X., K. Doi (Grad. Sch. Bioagr. Sci., Nagoya U.)

P124 Development and mapping of SSR markers in foxtail millet based on genome sequence information

Takino, Y. [1], Y. Ishida [1], Y. Mukainari [2], ○K. Fukunaga [1] (1.Fac. Life and Environ. Sci., Pref. Univ. Hiroshima, 2.Grad Sch. Comprehensive Scientific Research, Pref. Univ. Hiroshima)

P125 Genetic mapping of the gene for screwed spike rachis in wheat

☆Amagai, Y. [1], P. Martinek [2], T. Kuboyama [1], N. Watanabe [1] (1.Col. Agri., Univ. Ibaraki, 2.Kroměříž, Czech Republic)

P126 Wheat PLUG markers specific for 1E chromosome with high-molecular-weight glutenin subunit genes from *Thinopyrum elongatum* associated with strong dough

○Tanaka, H. [1], M. Kurogaki [1], M. Saito [2], G. Ishikawa [2], T. Nakamura [2], H. Tsujimoto [3] (1.Fac. Agr., Tottori Univ., 2.NARO/TARC, 3.ALRC, Tottori Univ.)

P127 DNA markers linked to powdery mildew resistance gene and everbearing gene in cultivated strawberry using array based marker technology

☆Koishihara, H. [1], M. Honjo [2], H. Enoki [1], S. Yui [2], S. Nishimura [1], M. Muramatsu [1] (1.Future Project Div. TOYOTA MOTOR CORPORATION, 2.NARO/TARC)

P128 Determination of *mPing* insertion sites in Japanese major rice cultivars

☆Kishine, M., T. Okunishi (NFRI, NARO)

P130 Evaluation of gene dosage effect on X chromosomal genes of papaya

☆Ueno, H. [1], N. Urasaki [2], K. Tarora [2], H. Matsumura [3] (1.Dep. Biosci. Tex. Tech., Shinshu U., 2.Okinawa Pref. Agric. Res. Ctr., 3.Gene Res. Ctr., Shinshu U.)

P131 Comparative transcriptome analysis of rice roots in response to biofertilizer treatments

☆Higuma, S., N. Sano, H. Ono, T. Kozaki, K. Ishii, M. Kanekatsu, T. Yamada, T. Yokoyama (Fac. Agr., Tokyo U. Agr. Tec.)

P132 Selection of marker-free cells in rice

○Saika, H. [1], A. Mori [1], S. Toki [1,2] (1.Agrogenomics Res. Center, Natl. Inst. Agrobiol. Sci., 2.Kihara Inst. Biol. Res., Yokohama City Univ.)

P133 Detection system of transposition of transposable elements using SogoDB platform

Doi, K., M. Nakagome, H. Yasue, H. Hirochika, ○A. Miyao (Genome Resource., NIAS)

P134 Protein-protein interaction between *Oma1*-like gene located in *Rf1* locus and *preSatp6* associated with sugar beet CMS

☆Arakawa, T., K. Kitazaki, R. Kurino, T. Mikami, T. Kubo (Res. Fac. Agr., Univ. Hokkaido)

P135 Identification of genes involved in early embryogenesis using organogenesis defective mutants in rice

☆Akimoto, T., Y. Sato (Graduate school of bioagricultural sciences, Nagoya university)

P136 RNAseq analysis of abnormal seeds obtained from interspecific crosses of two wild diploid wheat species

☆Takamatsu, K. [1], K. Yoshida [1], K. Sato [2], S. Takumi [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.IPSR, Okayama U.)

P137 Gene duplication and reciprocal loss of *DGS1* and *DGS2* loci caused F1 pollen sterility in hybrid between *Oryza sativa* and *O. rufipogon*

Nguyen, G. [1], ○Y. Yamagata [1], Y. Shigematsu [1], M. Watanabe [1], Y. Miyazaki [1], K. Doi [1], T. Ito [2], H. Kanamori [2], J. Wu [3], T. Matsumoto [3], A. Yoshimura [1] (1.Fac. Agr., Kyushu Univ, 2.STAFF, 3.NIAS)

P138 Study for understanding the waterproof mechanism in rice seedling

☆Kurokawa, Y. [1], P. Huan [1], H. Qu [1], K. Nagai [1], Y. Toda [2], M. Shimojima [3], J. Ito [4], T. Colmer [5], O. Pedersen [6], M. Imran [5], M. Ashikari [1] (1.Nagoya U. Bioagri. Sci., 2.Nagoya U. Sci., 3.Tokyo Institute of Technology, 4.Tokyo University, 5.The University of Western Australia, 6.University of Copenhagen)

P139 Canceled

P140 Canceled

P141 Canceled

P142 Canceled
