

23 September (9:00-11:30) Oral Presentation Program

Chair: Tsuyoshi Tanaka (NAAC, NARO)		Chair: Ken Naito (Res. Cntr. Genet. Resour., NARO)		Chair: Katsuhiko Shiono (Grad. Sch. Biosci. Biotech., Fukui Pref. Univ.)		Chair: Tetsuya Yamada (Grad. Sch. Agr., Univ. Hokkaido)		Chair: Shun Sakuma (Facul. Agri., Univ. Tottori)		Chair: Takanori Yoshikawa (Grad. Sch. Agri. Kyoto Univ.)			
9:00	101	☆Hosaka, A.1,2, R. Sanetomo3, K. Hosaka3 (1.Nihon BioData Corporation, 2.KIBR., Univ. Yokohama-City, 3.Potato Germplasm Enhancement Laboratory, Obihiro University of Agriculture and Veterinary)	201	○Yamaguchi, N.1, H. Igarashi2, C. Souma1, A. Kaga3 (1.Central Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO, 3.Inst. Crop. Sci., NARO)	301	☆Day Shar, S.1, D. Nguyen2, S. Zheng2, D. Fujita2 (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ.)	401	☆Muto, N., T. Matsumoto (Tokyo University of Agriculture, Graduate School of Agriculture)	501	☆Morita, M., K. Sato (IPSR, Okayama Univ.)	601	○Umehara, M.1,2, K. Sakai1, 彦. Yamamoto1, M. Shindo2, K. Shimomura2 (1.Dept. Appl. Biosci., Fac. Life Sci., Toyo Univ., 2.Grad. Sch. Life Sci., Toyo Univ.)	9:00
		A de novo genome assembly of Solanum verrucosum Schlechtendal, a diploid A-genome species of potato relatives		Progress in recurrent selection of soybean in Hokkaido, northern Japan		Development and characterization of pyramiding lines for brown planthopper resistance genes on the genetic background of japonica rice variety, Sagabiyori		CRISPR/Cas9-Mediated Genome Editing of RsGL1a and RsGL1b in Radish (Raphanus sativus L.)		Genome-wide association study on irregular inflorescence in Barley		Effects of strigolactones on varietal differences of leaf increanation in rice	
9:15	102	○Tomita, M., Y. Taketani, H. Mori (Res. Inst. Green Sci. Technol., Shizuoka Univ.)	202	☆Edet, O., T. Ishii (Arid Land Research Center, Tottori University)	302	☆Baba, K.1, Y. Yamagata2, H. Yasui2, S. Zheng3, D. Fujita3 (1.Grad. Sch. Fac. Agr., Saga Univ., 2.Grad. Sch. Fac. Agr., Kyusyu Univ., 3.Fac. Agr., Saga Univ.)	402	○Sakai, H.1, T. Itoh2, R. Onuki3, M. Endo4, M. Tsuda5, S. Yasumoto6, Y. Tabei7 (1.NAAC, NARO, 2.National Taiwan Univ., 3.Saitama Pref. Canc. Cent., 4.NIAS, NARO, 5.T-PIRC, Univ. Tsukuba, 6.Grad. Sch. Eng., Osaka Univ., 7.Fac. Food Nutr. Sci., Toyo Univ.)	502	☆Balla, M.1, Y. Gorafi1,2, N. Kamal1,2, M. Abdalla3, I. Tahir3, H. Tsujimoto2 (1.United Grad. Sch., Tottori Univ., 2.Arid Land Research Center, Tottori Univ., 3.Agricultural Research Corporation, Sudan)	602	○Saisho, D., K. Kishiro, N. Yamaji, A. Tani (IPSR, Okayama Univ.)	9:15
		Isogenic varieties integrated with genes for robust, tiller and yield in Koshihikari.		Cowpea speed breeding using regulated growth chamber conditions and seeds of oven-dried immature pods potentially accommodates eight generations per year		Estimation and characterization of brown planthopper resistance gene from Oryza glaberrima		Development of the k-mer based analytical method for foreign DNA detection in genome-edited organisms		Interspecific variation and genome wild association analysis for heat stress tolerance adaptation in wild emmer wheat		Impacts of growing environment on barley cultivation under double cropping system	
9:30	103	☆Sogo, N.1, M. Okuma1, O. IMO1, T. Nagai1, T. Seiko2, C. Muto2, K. Naito2, Y. Monden1, M. Sugiyama3, G. Shigita4, K. Tanaka5, H. Nishida1, Y. Kawazu3, N. Tomooka2, K. Kato1 (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Genetic Resources Center, NARO, 3.Inst. Vegetable & Floriculture Sci., NARO, 4.TUM, 5.Fac. Agr. Life Sci., Hirosaki U.)	203	☆Lin, Y.1, Y. Hsu1, L. Hsu2,3, H. Khazaei1, J. Yen1, C. Lin1, K. Hoshikawa1,4, R. Schafleitner1, P. Hanson1 (1.World Vegetable Center, Headquarters, 2.Tainan District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan, Taiwan, 3.Taoyuan District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan, Taiwan, 4.Japan International Research Center for Agricultural Sciences, Biological Resources and Post-harvest Division)	303	☆Kamal, M.1,3, D. Nguyen2, S. Zheng2, D. Fujita2 (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ., 3.Agrotech. Disc., Khulna Univ.)	403	○Shimada, H.1, A. Takeuchi1, K. Asano2, T. Noda2, H. Kusano1, M. Ohnuma1, H. Teramura1, T. Asahi1, Y. Okubo1, Y. Akatsu1, K. Ito1, K. Hamada1, A. Hokura3 (1.Dept. Biol. Sci. Technol., Tokyo Univ. Sci., 2.Dev. North. Field Crop Res., Hokkaido Agric. Res. Center, NARO, 3.Dept. Appl. Chem., Tokyo Denki Univ.)	503	Nagata, T.1, M. Numamoto2, T. Masumura1, A. Nagano3,4, Y. Yasui5, ○T. Ohsako1 (1.Grad. Sch. Life Env. Sci., Kyoto Pref. Univ., 2.Fac. Agr., Setsunan Univ., 3.Fac. Agr., Ryokoku Univ., 4.Inst. Adv. Biosci., Keio Univ., 5.Grad. Sch. Agr., Kyoto Univ.)	603	○Tsuda, K. (National Institute of Genetics)	9:30
		Molecular Phylogenetics of melon based on diversity analysis of chloroplast genome		Genetic architecture of heat tolerance in Solanum lycopersicum: identifying QTL of reproductive traits under heat stress using a MAGIC population		Characterization of near-isogenic lines and pyramided lines for brown planthopper resistance genes on the genetic background of indica rice variety 'IR64'		Creation of genome-edited potato mutants with novel starch properties		Variation of prolamin and prolamin gene family among green foxtail (Setaria viridis) accessions in Japan		Development of a heatshock-inducible clonal analysis system and its application to observe internode initiation in rice.	
9:45	104	☆Su, Z.1, S. Takenaka2, M. Kakitani1, M. Nitta1, S. Nasuda1 (1.Grad. Sch. Agr., Kyoto Univ., 2.Fac. Agr., Ryukoku Univ.)	204	○Yonemaru, J.1, K. Matsushita1,2, H. Kajiya-Kanegae2, A. Onogi2,3 (1.Inst. Crop. Sci., NARO, 2.RCAIT, NARO, 3.Faculty of Agr., Ryukoku Univ.)	304	☆Seto, S.1, Y. Ban2, N. Mizuno3, K. Kato2, F. Kobayashi3, y. Hyuga1, H. Handa4 (1.Fac. Life Envi. Sci., Kyoto Pref. Univ., 2.WARC, NARO, 3.NICS, NARO, 4.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ.)	404	☆Nakazato, I., N. Tsutsumi, S. Arimura (Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo)	504	○Takada, H. (NARO Fellow)	604	○Takanashi, H., M. Shichijo, J. Yamada, M. Ishimori, H. Iwata, N. Tsutsumi (Grad. Sch. Agric. Life Sci., Univ. Tokyo)	9:45
		Evaluation of genetic diversity and population structure in the tetraploid wheat accessions ex situ conserved in NBRP-Wheat for development of a core collection		Historical data reveals characteristics in rice varieties bred at NARO		RNA-seq analysis associated with Cd low accumulation in wheat.		Trials of modifying and developing the method for target base editing of chloroplast genomes using TALECD		Amadokoro, As a New Crop (Vegetable)		Mechanisms controlling differences in the degree of development of pedicellate spikelets in sorghum germplasm	

24 September (13:30-17:15) Oral Presentation Program

Chair: Satoshi Okada (Biosci. and Biotech. Center, Nagoya Univ.)		Chair: Shoji Taniguchi (Res. Cent. Agric. Info. Tech., NARO)		Chair: Daisuke Fujita (Fac. Agr., Saga Univ.)		Chair: Hideki Takanashi (Grad. Sch. Agr. Life Sci., Univ. Tokyo)		Chair: Akira Komatsu (Inst. Agrobio. Sci., NARO)		Chair: Eigo Fukai (Niigata Univ.)	
13:30	111 ☆Oka, T.1, T. Furuta1, K. Kashihara1, Y. Kishima2, T. Yamamoto1 (1.Inst. Plant Sci. & Res., Okayama Univ., 2.Grad. Sch. Agr., Hokkaido Univ.) Genetic analysis of agronomic traits in progeny of fertile tetraploid hybrids between O. sativa and O. glaberrima	211 ☆Sano, H.1, Y. Unno2, W. Guo1, N. Miura1, K. Kusunoki2, H. Ito2, H. Iwata1 (1.Grad. Sch. Agri., Univ. Tokyo, 2.Sumitomo Forestry Co., Ltd.) Development of individual tree-based phenotyping methods for larchs using LiDAR remote sensing	311 ○Shiono, K.1, M. Ejiri1, T. Miyashita1, Y. Uga2 (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.Inst. Crop Sci., NARO) Searching for reduced-soil stress tolerance genes using Oryza glumaepatula introgression lines	411 ☆Kojima, K.1, K. Ishibashi2, K. Oikawa5, H. Katsuyama1, N. Kikuchi2, T. Kohzuma3, M. Harada5, A. Hoshikawa4, T. Kuboyama1 (1.Col. Agr., Ibaraki U., 2.QFF, 3.Col. Sci., Ibaraki U., 4.iFRC,Ibaraki U., 5.JAEA) Mutagenesis in rice by neutron irradiation on seed using J-PARC facility	511 ☆Nakaoka, F., A. Kobayashi, K. Tomita, Y. Machida, T. Hayashi, M. Tanoi, T. Shimizu, Y. Morozumi, S. Watanabe, K. Sakai, K. Watanabe, Y. Sato, N. Sato (Fukui Agri. Exp. Stn.) A new new high-yield, good-tasting rice cultivar for export "Etsunan 305".	611 ☆Nakazawa, A.1, Y. Takahara2 (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering, Nagaoka University of Technology) Changes in gene expression of carrot somatic embryogenesis by stress treatment	13:30				
13:45	112 ○Tanaka, J., N. Tanaka, Y. Taniguchi, H. Itoh (NICS/NARO) Extremely early heading QTL of rice indica variety 'Kasalath' in sBBS environment	212 ☆Nagamatsu, S.1, T. Shimoda1, A. Hayashi2, T. Tanabata3, S. Isobe3 (1.Fukuoka Agriculture and Forestry Research Center, 2.Research Center for Agricultural Robotics, NARO, 3.Kazusa DNA Research Institute) Proposal of a quantitative evaluation method for morphological variation of strawberry fruit tip and calyx	312 ☆Yamada, T.1, S. Atumi1, M. Arakawa2, S. Ota2, A. Itou2, H. Takahashi1, M. Nakazono1 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Aichi Agric. Res. Cent.) Analysis of waterlogging tolerance in the field using five wheat varieties	412 ☆Kuwada, E.1, T. Akagi1,2 (1.Grad. Sch. Environ. & Life Sci., Okayama Univ., 2.JST-PRESTO) Origins and convergent evolutions in molecular pathways of climacteric fruit ripening.	512 ○Kobayashi, A.1, M. Nishimura2,3, F. Nakaoka1, K. Tomita1, Y. Machida1, Y. Morozumi1, R. Morita2, S. Watanabe1, T. Hayashi1, T. Shimizu1, Y. Sato1, N. Sato1, K. Hori2 (1.Fukui Agri.Exp. Stn., 2.NARO, 3.Niigata Univ.) A new rice variety, 'Shinfuku 1', which contains about three times as much dietary fiber in white rice as 'Koshihikari'.	612 ☆Tezuka, T.1, K. Ta2, S. Shimizu-Sato2, M. Nosaka-T1,2, T. Hattori3, Y. Sato1,2 (1.Sch. Life Sci., Grad. Univ. Adv. Study/SOKENDAI, 2.Plant Genet., Natl. Inst. Genet., 3.Grad. Sch. Bioagr. Sci., Nagoya U.) Polarity establishment of rice embryo by auxin localization	13:45				
14:00	113 ○Araki, E.1, J. Tanaka2, K. Ebana3 (1.Inst. Food Res., NARO, 2.Inst. Crop. Sci., NARO, 3.Inst. Gen. Resources Cent., NARO) Identification of chromosome 1 region associated with variation in γ-oryzanol content using population derived from rice chromosome segment substitution line	213 ☆Mochizuki, H.1, M. Minamikawa1,2, K. Hamazaki1, M. Kuniyama3, S. Moriya3, K. Abe3, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ., 2.IAAR, Chiba Univ., 3.NIFTS, NARO) Predicting phenotypes using IBS/IBD-based genomic relationship and pedigree-based numerator relationship matrices.	313 ☆Takatori, M.1, S. Sakaguchi1, Y. Koide2, K. Fujino3, Y. Kishima2 (1.Graduate School of Agriculture, Hokkaido University, 2.Research Faculty of Agriculture, Hokkaido University, 3.National Agriculture and Food Research Organization, NARO) Control of heading dates by low-temperature and its relationship with photosensitive genes.	413 ☆Horiuchi, A.1, K. Masuda1,2, N. Onoue3, R. Matsuzaki3, K. Shirasawa4, Y. Kubo1, K. Ushijima1, T. Akagi1 (1.Grad. Sch. Environ. LifeSci., Okayama Univ., 2.Grad. Sch. Agri. LifeSci., Univ. Tokyo, 3.Inst. Fruit Tree and Tea Sci., NARO, 4.Kazusa DNA Res. Inst.) Variety differentiation in hexaploid persimmon, with a wide fruit shape diversity	513 ○Nishinaka, M.1, K. Taguchi1, K. Katayama2, T. Kuranouchi3 (1.Central Reg. Agri. Res. Cent., NARO, 2.Hokkaido Reg. Agri. Res. Cent., NARO, 3.Inst. Crop. Sci., NARO) Breeding of a new sweetpotato variety "Amahazuki" with sweet even immediately after harvest.	613 ☆Kuronuma, S.1, T. Yamaguchi2, K. Murata3, M. Yamamoto1, T. Yamada1, M. Kanekatsu1 (1.Grd. Sch. Agr., Tokyo U. Agr. Tec., 2.Tonami Agr. For. Prom. Cent., 3.Toyama Pref. Agr. Forest. Fish. Res. Cent.) Characterization of low-temperature germinability of the Japanese native red rice cultivar "Awa-akamai"	14:00				
14:15	114 ☆Sakuta, M., S. Sugiyama, Y. Tsujimura, T. Htun, C. Inoue, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.) Evaluation of novel loci involved in non-seed-shattering behaviour of indica rice cultivar, 'IR36'	214 ○Tanaka, R.1, S. Yabe1, T. Kawakatsu2, N. Tanaka1, M. Shenton1, Y. Uga1 (1.Institute of Crop Science, NARO, 2.The Institute of Agrobiological Sciences, NARO) Prediction of phenotypic values of the world rice core collection based on genome and transcriptome	314 ☆Kawata, T., H. Yasui, Y. Yamagata (Fac. Agr., Grad. Sch., Univ. Kyushu) Identification of a QTL, qSG11 causing pollen and spikelet sterility in an interspecific cross between Oryza sativa L. and O. glumaepatula Steud.	414 ☆Igarashi, T.1, Y. Takahara2 (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering) Analysis of Phalaenopsis blue flower color gene	514 ○Taguchi, K.1, M. Nishinaka1, K. Katayama2, K. Ishiguro2, T. Kuranouchi3 (1.Central Reg. Agri. Res. Cent., NARO, 2.Hokkaido Reg. Agri. Res. Cent., NARO, 3.Inst. Crop. Sci., NARO) High-yielding and high-quality cultivar "Yukikomachi", approaching northern limit of Sweet potato	614 ○Kai, H.1, T. Tanaka2, Y. Haraguchi1, T. Todoroki1, T. Abiko3, D. Saisho4 (1.Fukuoka Agric. Forest. Res. Cent., 2.NAAC, NARO, 3.Kyushu Univ., 4.IPSR, Okayama Univ.) Genetic analysis of breaking seed dormancy by machine-threshing in barley	14:15				

Chair: Sachiko Isobe (Kazusa DNA Res. Inst.)		Chair: Guo Wei (Grad. Sch. Agr. Life Sci., Univ. Tokyo)		Chair: Kazuyoshi Kitazaki (Grad. Sch. Agr., Univ. Hokkaido)		Chair: Shin-ichi Arimura (Grad. Sch. Agr. Life Sci., Univ. Tokyo)		Chair: Ryosuke Mega (Grad. Sch. Sci. Tech. Innov., Yamaguchi Univ.)		Chair: Tomoyuki Furuta (Inst. Plant Sci. Res., Okayama Univ.)			
14:30	115	☆Chen, T., K. Nishimura, K. Motoki, K. Nagasaka, R. Nakano, T. Nakazaki (Grad. Sch. Agr., Kyoto Univ)	215	○Iwata, H.1, 悠 戸田1, ム. フジ2, Y. Ohmori1, Y. Yamasaki3, H. Takahashi4, H. Takanashi1, M. Tsuda5, H. Kanegae1, M. Hirai2, Y. Ichihashi6, H. Tsujimoto3, A. Kaga7, M. Nakazono4, T. Fujiwara1 (1.Graduate School of Agricultural and Life Sciences., Univ. Tokyo, 2.Center for Sustainable Resource Science, RIKEN, 3.Arid Land Research Center, Tottori Univ., 4.Graduate School of Bioagricultural Sciences, Nagoya Univ., 5.Faculty of Life Environmental Sciences, Univ. Tsukuba, 6.BioResource Research Center, RIKEN, 7.Institute of Crop Science, NARO)	315	○Kojima, Y.1, K. Murata1, G. Mimuro1, Y. Muraoka2 (1.Toyama Agr. Fores. Fish. Res. Cent., 2.Toyama Agr. Fores. Prom. Cent., Tonami)	415	☆Suzuki, H.1, K. Ezura2, Y. Okabe2, R. Yano2,3, K. Shirasawa4, H. Ezura2, T. Ariizumi2 (1.Graduate School of Life and Environmental Sciences, University of Tsukuba, 2.Faculty of Life and Environmental Sciences, University of Tsukuba, 3.NARO, 4.Kazusa DNA Research Institute)	515	☆Tarutani, H.1, T. Maryenti2, T. Okamoto2, M. Takasawa4, H. Tsujimoto1,3, T. Ishii1,3 (1.Grad. Sch. Sus., Univ. Tottori, 2.Grad. Sch. Sci., Univ. Tokyo Metro, 3.Arid Land Research Center., Univ. Tottori, 4.Facul. Sci., Univ. Tokyo Metro)	615	☆Takata, R., J. Ito, H. Tsuji (KIBR., Yokohama City Univ.)	14:30
		Characterization of the QTL on chromosome 7AL improving both of two yield components grain number and grain weight in tetraploid wheat (<i>Triticum turgidum</i> L.)		Using multi-omics data as an intermediate phenotype to improve the accuracy of genomic prediction		Construction of foundation seeds producing system in Toyama Prefectural Agricultural Research Institute		Chromosome structural changes during fruit set in tomato		Analysis of the diversity of rice - wheat hybrid plants		Imaging of microtubules in the shoot apical meristem of rice	
14:45	116	☆Nishimura, K.1, H. Kokaji1, K. Motoki1, A. Yamazaki2, K. Nagasaka1, R. Takisawa3, Y. Yasui1, T. Kawai4, K. Ushijima4, M. Yamasaki5, H. Saito6, R. Nakano1, T. Nakazaki1 (1.Grad. Sch. Agr., Kyoto Univ., 2.Fac. Agr., Kindai Univ., 3.Fac. Agr., Ryukoku Univ., 4.Grad. Sch. Environ. Life Sci., Okayama Univ., 5.Grad. Sch. Sci. and Tech., Niigata Univ., 6.JIRCAS)	216	☆Ishiguro, Y.1, H. Yamashita2,5, T. Uchida1, J. Kawaki3, H. Katai3, A. Nagano4, A. Morita2,5, T. Ikka2,5,6 (1.Grad. Agr., Univ. Shizuoka, 2.Fac. Agr., Univ. Shizuoka, 3.Shizuoka Tea Res. Cent., 4.Fac. Agr., Univ. Ryukoku, 5.Shizuoka Univ. Res. Inst. Tea Sci., 6.Shizuoka Univ. Res. Inst. Green Sci. Tech.)	316	☆Inada, Y.1, A. Takatuka1, H. Ichida2, K. Toriyama1 (1.Grad. Sch. Agri., Univ. Tohoku, 2.RIKEN Nishina center)	416	☆Li, J.1, T. Ishii1, M. Yoshioka1, H. Yoshioka1, H. Takahashi1, T. Yamauchi2, M. Nakazono1 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Biosci. Biotech. Ctr., Nagoya Univ.)	516	○Tada, Y., S. Amakawa (Tokyo Univ. of Technol., Sch. of Biosci. Biotechnol.)	616	☆Mizuno, N.1, H. Matsunaka2, M. Yanaka3, G. Ishikawa1, F. Kobayashi1, K. Nakamura3 (1.NICS, NARO, 2.HARC, NARO, 3.KARC, NARO)	14:45
		Development of "degenerate oligonucleotide primer MIG-seq", an improved method of MIG-seq, and its application to crop genetic analysis		Genomic prediction for quality-related metabolites in tea accessions		Mapping of a novel fertility restorer gene from an indica cultivar Samba Mahsuri for CW-type cytoplasmic male sterility in rice		Molecular Mechanisms of Inducible Aerenchyma Formation by ROS and Ca ²⁺ Signaling in rice		Analysis of genetic diversity and traits of a native soybean variety 'Hayama Tanokuro'		Identification of a novel QTL that has contributed to the early heading of Japanese wheat varieties	
15:00	117	☆Kurihara, M.1, H. Tabuchi2, K. Shirasawa3, S. Isobe3, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Env. & Life Sci., Okayama Univ., 2.KARC/NARO, 3.Kazusa DNA Res. Inst.)	217	☆Hamazaki, K., H. Iwata (Grad. Sch. Agr. Life Sci., Univ. Tokyo)	317	○ozaki, y.1, Y. Takahara2 (1.Grad. Sch. Department of Bioengineering, Nagoka University of Technology, 2.Department of Materials Science and Engineering)	417	☆Yuhazu, M., R. Hara, A. Kanazawa (Res. Fac., Hokkaido Univ.)	517	☆Hoshikawa, K.1,2, Y. Lin2, R. Schafleitner2, K. Shirasawa3, S. Isobe3, D. Nguyen4,5, Y. Yoshioka6 (1.JIRCAS, 2.World Veg, 3.Kazusa DNA Res. Inst., 4.VAAS, 5.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 6.Fac. Life & Environ. Sci., Univ. Tsukuba)	617	Tanaka, M.1, H. Akashi1, ○H. Tsuji1,2 (1.KIBR, Yokohama City Univ., 2.Bioscience and Biotechnology Center, Nagoya Univ.)	15:00
		Identification of QTLs controlling the resistance to multiple races of southern root-knot nematode and development of DNA markers for resistance selection		Future-oriented mating strategy via simulations optimizes breeding programs with selection indices		Examining the reproductive organ induction conditions of <i>Racomitrium japonicum</i>		Genes involved in anthocyanin biosynthesis pathway and transcriptional regulatory networks underlying anther pigmentation in petunia		Genetic diversity analysis for <i>Amaranthus tricolor</i> germplasm based on genome-wide single-nucleotide polymorphisms		Surgical manipulations of inflorescence development in barley	
15:15	118	☆Izumitani, M.1, S. Ohata1, H. Tabuchi2, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.KARC/NARO)	218	☆Sakai, T.1, R. Terauchi1,2, A. Abe2 (1.Grad. Sch. Agri., Univ. Kyoto, 2.IBRC)	Chair: Hiroyuki Kakui (Grad. Sch. Agr., Kyoto Univ.)		418	○Hisano, H., H. Munemori, K. Sato (IPSR, Okayama Univ.)	518	☆Sasaki, R., T. Masu, R. Ishikawa (Fac. Agri. And Life Sci., Hirosaki Univ.)	Chair: Nobuyuki Mizuno (NICS, NARO)		15:15
		Sequence mutations in the cis-regulatory elements of a candidate gene controlling southern root knot nematode resistance in sweetpotato		Genomic prediction using rice NAM population and its application to genomic breeding strategy	318	☆Ishihara, M.1, D. Kuniyoshi2, Y. Koide3, K. Nagaki4, Y. Kishima3 (1.Graduate School of Agriculture, Hokkaido University, 2.Tropical Agriculture Research Front, JIRCAS, 3.Research Faculty of Agriculture, Hokkaido University, 4.Institute of Plant Science and Resources, Okayama University)		Expression analysis of the genes altered by targeted mutations of grain dormancy genes in barley		Evaluation of genetic variation in <i>Shiikuwasha</i> and finding non-seasonal flowering landraces	618	☆Yoshida, M.1, S. Hirano1, S. Zheng2, D. Fujita2 (1.Grad. Sch. Fac. Agr., Saga Univ., 2.Fac. Agr., Saga Univ.)	
						Detection of meiotic abnormality in interspecific hybrids between Asian and African rice species by immunostaining method						Genetic analysis for heading date in weak photoperiod sensitivity and early heading rice variety, TNAU6484	

15:30	119	Chair: Kazusa Nishimura (Grad. Sch. Agr., Kyoto Univ.)	Chair: Hiroyoshi Iwata (Grad. Sch. Agr. Life Sci., Univ. Tokyo)	319	☆Kuwabara, K.1, T. Ariizumi2 (1.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 2.Fac. Life Env. Sci., Univ. Tsukuba)	Chair: Hiroshi Hisano (IPSR, Okayama Univ.)	Chair: Ryo Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)	619	Ueda, J.2, Y. Kazama2, T. Abe3, ○K. Murai1 (1.Dep. Sust. Agri-Culture, Fukui Pref. Univ., 2.Dep. Biotech., Fukui Pref. Univ., 3.Nishina Cent., RIKEN)	15:30				
		○Yamada, T.1, A. Onogi2, J. Yonemaru1 (1.Institute of Crop Science, NARO, 2.Faculty of Agriculture, Ryukoku University)	☆Kubota, C.1, S. Shibata2, T. Nakata2, I. Takata2, S. Nishiuchi2 (1.Sch. Agr. Sci., Nagoya Univ., 2.Grad. Sch. Bioagri. Sci., Nagoya Univ.)		☆Tanaka, H.1, A. Endo1, S. Yasumoto2, H. Sasaki3, T. Igarashi3, N. Umemoto4, T. Muranaka2, M. Mori3, T. Yamada1 (1.Grad. Sch. Agr., Univ. Hokkaido, 2.Grad. Sch. Eng., Univ. Osaka, 3.Calbee Potato, Inc., 4.CSRS, RIKEN)	○Kihara, M., T. Hoki, N. Hirota, W. Saito, Y. Tokizono, R. Kanatani, R. Makimoto, T. Zhou, N. Suda (Crop Research Laboratories, SAPPORO BREWERIES LTD.)	Prediction of seed yield using historical data of soybean breeding in Japan		Development of technology for quantification of lotus (Nelumbo nucifera) growth		Ca2+ imaging inside pollen of cytoplasmic male sterile tomato	Mutagenesis of Potato Polyphenol Oxidase and Vacuolar Invertase Genes by CRISPR-Cas9 System	Research and development of sustainable raw materials for brewing II : An inherited characteristic of novel traits in "N68-411".	late-heading1, an einkorn wheat mutant which suppresses the early-heading phenotype of early-heading mutant with a deletion of clock gene WPCL1
15:45	120	○Kajiya-Kanegae, H.1, G. Kikui1, K. Matsushita2, M. Yano1, T. Hayashi1, J. Yonemaru1,2 (1.RCAIT, NARO, 2.Inst. Crop. Sci., NARO)	☆Takata, I., N. Kobayashi, T. Nakata, S. Shibata, S. Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)	320	☆Katsura, N.1, K. Itoh1, H. Matsuhira2, Y. Kuroda2, K. Kitazaki1, T. Kubo1 (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)	☆Hosoda, A.1, I. Nakazato1, M. Okuno2, T. Ito3, H. Takanashi1, N. Tsutsumi1, S. Arimura1 (1.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 2.Sch. of Med., Kurume Univ., 3.Sch. of Life Sci. and Tech., Tokyo Institute of Tech.)	520	Watanabe, A.1, Y. Takeshima2,3, A. Kanouchi2,4, S. Takahashi2,5, K. Sasaki2,6, N. Takahashi2,7, ○Y. Ito1,2 (1.Grad Sch Agri Sci, Tohoku Univ, 2.EGGS, Tohoku Univ, 3.Akita High School, 4.Yamagata Higashi High School, 5.Hanamaki Kita High School, 6.Renaissance High School, 7.Sakata Higashi High School)	620	☆Fujioka, A., Y. Monden, H. Nishida, K. Kato (Grad. Sch. Environ. Life Sci., Okayama U.)	15:45			
		Development of knowledge-graph-based trait prediction method	Acquisition of phenotypes related to cabbage uniformity using UAV		Internal structure analysis of anthers of G-type cytoplasmic male sterility in sugar beet.	Targeted base editing in Arabidopsis nuclear genes via DNA recognition by TALE domain	Evaluation of the amount of total soluble protein in etiolated rice seedlings	Genetic study on earliness QTLs which interact with PCL1 in durum wheat						
16:00	121	○Ichihara, H.1, H. Hirakawa1, M. Yamada1, M. Kohara1, S. Yamashita1, S. Shirasawa1, Y. Toda1, Y. Nakamura1,2, T. Tanabata1, S. Tabata1, S. Isobe1 (1.Kazusa DNA Res. Inst., 2.Nat. Inst. Genet.)	☆Shibata, S., K. Doi, S. Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)	321	Chair: Masaya Yamamoto (Grad. Sch. Agr. Sci., Tohoku Univ.)		421	○Koizuka, N.1, I. Nakazato2, A. Okuzaki1, S. Arimura2 (1.Col. Agr., Tamagawa Univ., 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)	521	☆Mega, R.1, J. Kim2, T. Ishii3, H. Tanaka4, F. Abe5, M. Okamoto6 (1.Grad. Sch. Sci. Tech. Innov., Yamaguchi Univ., 2.RIKEN-CSRS, 3.ALRC, Torrori Univ., 4.Faculty of Agriculture, Tottori Univ., 5.Food Res. Inst., NARO, 6.C-Bio, Utsunomiya Univ.)	621	Chair: Ayumi Agata (National Institute of Genetics)	☆Fukushima, N.1, T. Matsuura2, Y. Monndenn1, H. Nisida1, T. Hirayama2, K. Katou1 (1.Grad. Sch. Environ. Life Sci., Univ. Okayama, 2.IPSR, Okayama Univ.)	16:00
		Improvement of Plant GARDEN, a portal site for plant genome information (2022, Q2 ver)	Mapping of rice voluntaries using UAV imagery and object detection method		Search for the genes responsible for fertility restoration of cytoplasmic male sterility derived from Oryza sativa cv. Tadukan	Genome editing for nuclear and organelle genes in Brassicaceae								
16:15	122	○Isobe, S.1, K. Horiguchi2, M. Yamada1, T. Misawa2, Y. Nakamura3, H. Ichihara1, M. Kohara1, H. Hirakawa1 (1.Kazusa DNA Res. Inst., 2.ANPLAT Co., Ltd., 3.Nat. Inst. Genet.)	Chair: Shunsaku Nishiuchi (Grad. Sch. Bioagr. Sci., Nagoya Univ.)		322	○Kakui, H.1,2, T. Tsuchimatsu3, M. Yamazaki2, K. Shimizu2,4 (1.Grad. Sch. Agr., Kyoto Univ., 2.Dept. Evo. Biol. Env. Studies, U. Zurich, 3.Grad. Sch. Sci., Univ. Tokyo, 4.Kihara Inst. Biol. Res., Yokohama City Univ.)	422	○Fukai, E.1,2,3,4,5, M. Yoshikawa2, N. Shah3, N. Sandal3, A. Miyao2, S. Ono4, H. Hirakawa5, T. Akyol3, Y. Umehara2, K. Nonomura4, J. Stougaard3, H. Hirochika2, M. Hayashi2,6, S. Sato5,7, S. Andersen3, K. Okazaki1 (1.Niigata Univ, 2.National Agriculture and Food Research Organization, 3.Aarhus University, 4.National Institute of Genetics, 5.Kazusa DNA Research Institute, 6.RIKEN, 7.Tohoku University)	522	☆Iwahori, R.1, K. Hiroki1, H. Ogawa1, M. Ohkubo1, H. Matsuhira2, K. Kitazaki1 (1.Grad. Sch. Agr., Univ. Hokkaido, 2.NARO HARC)	622	☆Nomura, Y.1, Y. Lu2, H. Enomoto3, K. Harada1, R. Yano4, M. Kojima5, Y. Takebayashi5, H. Sakakibara6, H. Ezura2,7, T. Ariizumi2,7 (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Dept. Biosci., Univ. Teikyo, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)	16:15	
		Mi-GARDEN : A platform for comparison of user's genome sequence data and reference genomes in plants	Development of a UAV-based lodging evaluation method in soybean	Complementation tests and transcriptome analysis of REDUCED POLLEN NUMBER1 in Arabidopsis thaliana										Widespread LTR retrotransposon activation in inter- and intra-species recombinant inbred populations of Lotus japonicus

16:30	Chair: Tetsuya Yamada (Inst. Crop. Sci., NARO)		223	Zhao, J.1, A. Kaga2, M. Hirafuji1, S. Ninomiya1, T. Yamada2, K. Komatsu3, K. Hirata4, A. Kikuchi4, O.G. Wei1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NICS, NARO, 3.WARC, NARO, 4.TARC, NARO)	323	☆Kojima, H.1, H. Kakui2, T. Yoshikawa2, Z. Su2, S. Nasuda2 (1.Fac. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Kyoto Univ.)	Chair: Kanako Kawaura (KIBR, Yokohama City Univ.)		Chair: Saeko Sugita-Konishi (Grad. Sch. Agri., Univ. Kagawa)		623	☆Oyama, K.1, T. Suzuki2, S. Bang1, T. Ohnishi1 (1.Sch. Agric., Utsunomiya. Univ, 2.Center for Bioscience Research and Education, Utsunomiya. University)	16:30
	123	☆Sakurai, K.1, Y. Toda1, Y. Fuji2, Y. Ohmori1, Y. Yamasaki3, H. Takahashi4, H. Takanashi1, M. Tsuda5, M. Hirai2, H. Tsujimoto3, M. Nakazono4, T. Fujiwara1, A. Kaga6, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.RIKEN Ctr. for Sustainable Sci., 3.Arid Land Res. Ctr., Tottori Univ., 4.Grad. Sch. Bioagri. Sci., Nagoya Univ., 5.T-PIRC, Univ. Tsukuba, 6.Inst. Crop Sci., NARO)		Development of infield soybean seed counting and localization method		Phenotyping of pollen-related traits and genome-wide association study in the tetraploid wheat core collection.	423	☆Nguyen, T.1,2, S. Zheng2, D. Fujita2 (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Fac. Agr., Saga Univ.)	523	☆Fujiwara, K.1, N. Miyaji2, T. Yasuda1, R. Fujimoto1 (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Iwate Biotechnol. Res. Ctr.)		Identification of the genetic region related to heterosis in Arabidopsis thaliana	
16:45	Estimating genetic correlation between traits and environments based on the analysis of high-dimensional·multi-environmental multiomics data						Substitution mapping and characterization of stable QTLs for vascular bundle number at panicle neck in rice (Oryza sativa L.)		Identification of the genetic region related to heterosis in Arabidopsis thaliana				
	124	☆Dang, T., H. Iwata (Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, Japan)	224	☆Yakou, H.1, Y. Takahara2 (1.Grad. Sch. Department of Bioengineering, Nagaoka University of Technology, 2.Department of Materials Science and Bioengineering, Nagaoka University of Technology)			424	○Ikeda, T.1, M. Seki2, T. Nagamine2, Y. Nakano2, D. Tezuka3, R. Imai3 (1.Western Reg. Agr. Res. Ctr., NARO, 2.Central Reg. Agr. Res. Ctr., NARO, 3.Inst. Agrobiol. Sci., NARO)	524	○Ishikawa, R.1, C. Castillo1,2, T. Htun1, K. Numaguchi1, K. Inoue1, Y. Oka1, M. Ogasawara1, S. Sugiyama1, N. Takama1, C. Orn1, C. Inoue1, K. Nonomura3, R. Allaby4, D. Fuller2, T. Ishii1 (1.Grad. Sch., Agr. Sci., Kobe Univ., 2.University College London, 3.National Institute of Genetics, 4.University of Warwick)			16:45
17:15	A method for clustering high-dimensional microbiome data and selecting representative microbial species			Development of a method for selecting superior strains of Racomitrium japonicum			Development of gluten-forming barley I. Gluten formation using a mutant fund in genetic resources.		Evaluation of the process of seed-shattering loss during rice domestication				
	125	☆Yoshioka, H.1, Y. Toda1, Y. Fuji2, Y. Ohmori1, Y. Ichihashi7, E. Usui7, K. Kumaishi7, T. Satou7, S. Kobori7, A. Kaga3, Y. Yamasaki4, H. Takahashi5, H. Takanashi1, M. Tsuda6, M. Ishimori1, H. Tsujimoto4, M. Nakazono5, M. Hirai2, T. Fujiwara1, H. Iwata1 (1.Grad. Sch. Agr. Life. Sci., Univ. Tokyo, 2.RIKEN Ctr. for Sustainable Sci., 3.Inst. Crop Sci., NARO, 4.Arid Land Res. Ctr., Tottori Univ., 5.Grad. Sch. Bioagri. Sci., Nagoya Univ., 6.T-PIRC, Univ. Tsukuba, 7.RIKEN BioResource Res. Ctr.)					425	☆Tezuka, D.1, T. Ikeda2, M. Seki3, T. Nagamine3, Y. Nakano3, R. Imai1 (1.Institute of Agrobiological Sciences, NARO, 2.Western Region Agricultural Research Center, NARO, 3.Central Region Agricultural Research Center, NARO)	525	○Komatsu, A.1, M. Ohtake1, A. Shimizu2, H. Kato3, F. Li2 (1.Institute of Agrobiological Sciences, NARO, 2.Institute of Crop Science, NARO, 3.Research Center of Genetic Resources, NARO)			17:15
	Modeling of plant-microbe interactions using multi-omics data						Development of gluten-forming barley II . Creation of hordein with glutenin-like structure by genome editing		Development of OsSh1 genome editing lines using Indica rice varieties and their shattering characteristics.				

JSB142 Poster presentations		
24 September (Odd Numbers 9:00-10:00, Even Numbers 10:00-10:00)		
P001	A simple set of plasmids for multiple genome editing and a method for high-density crop hydroponics in a plant incubator	○Kuroda, M. (Inst. Agrobiol. Sci., NARO)
P002	Efficient method of breaking dormancy of strawberry seeds without using concentrated sulfuric acid	Tanaka, J.1, ○R. Otsuka1,2, R. Yamaguchi3, Y. Taniguchi1, S. Kataoka4 (1.NICS/NARO, 2.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 3.Nagaoka Univ. of Tech., 4.NIVFS/NARO)
P003	Breeding by crossings between egg plant varieties and 「Sadowara」of Miyazaki original vegetable - A new line obtained in F5 of 'Kurowashi' x 「Sadowara」-	○Chen, L.1,2, T. Hiejima1,2, N. Emoto1, K. Yoshimura1,2, S. Yoshizaki1 (1.Fac. Environ. Hirt., Minami Kyusyu U., 2.Grad. Sch. Hort. Food Sci., Minami Kyusyu U.)
P004	Synthetic octaploid wheat production with wide hybridization between bread wheat and <i>Aegilops tauschii</i>	☆Gao, Y.1, Y. Matsuoka2, H. Tsujimoto1,3, M. Kishii4, S. Sakuma5, T. Ishii1,3 (1.Grad. Sch. Sus., Univ. Tottori, 2.Grad. Sch. Agri., Univ. Kobe, 3.Arid Land Research Center., Univ. Tottori, 4.JIRCAS, 5.Facul. Agri., Univ. Tottori)
P005	Evaluation of <i>Brassica rapa</i> accessions with resistance to three TuMV isolate groups	☆Tian, A., H. TAKAHASHI, M. YAMAMOTO, H. KITASHIBA (Grad. Sch. Aric. Sci., Univ. Tohoku)
P006	Conformation of already detected grain-size alleles from a large grain rice cultivar, BG 1, through next generation sequencing using near-isogenic lines	☆Suzuki, H.1, A. Horibata1,2 (1.Grad. Sch. of Biol.-Oriented Sci. and Tech., Kindai Univ, 2.Fac. of Biol.-Oriented Sci. and Tech., Kindai Univ.)
P007	Search for variations on the occurrence rate and on the size of white core in rice (<i>Oryza sativa</i> L.) grains by using mPing taglines	☆Hibi, T.1, H. Tanaka2, A. Horibata1,2 (1.Gra. Sch. of Biol.-Oriented Sci. and Tech., Kindai Univ., 2.Fac. of Biol.-Oriented Sci. and Tech., Kindai Univ.)
P008	Genetic evaluation of sex expression in Japanese weedy melon	☆Nashiki, A.1,2, Y. Yoshioka3 (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.JSPS Research Fellowship for Young Scientists, 3.Fac. Life Env. Sci., Univ. Tsukuba)
P009	A Novel Combination of Genes Causing Temperature-Sensitive Hybrid Weakness in Rice	☆Kutay Soe, T.1, M. Kunieda1, H. Sunohara1,2, Y. Inukai3, V. Reyes1, S. Nishiuchi1, K. Doi1 (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.Environmental Control Center Co., Ltd., 3.ICREA, Nagoya Univ.)
P010	Identification of a novel QTL controlling seed dormancy in wheat originated from <i>Aegilops tauschii</i> .	☆AHMED, M.1,2, Y. Gorafi2,3, N. Kamal2,4, I. Tahir2, H. Tsujimoto4 (1.United Graduate School of Agricultural Sciences, Tottori University, Tottori Japan, 2.Agricultural Research Corporation (ARC), P. O. Box 126, Wad-Medani, Sudan, 3.International Platform for Dryland Research and Education, Tottori University, Tottori, Japan, 4.Arid Land Research Center, Tottori University, Tottori, Japan)
P011	A role of the qSH3 mutation involved in a loss of seed shattering and its variation in wild and cultivated rice	☆Numaguchi, K., T. Htun, Y. Oka, M. Ogasawara, S. Sugiyama, N. Takama, C. Orn, C. Inoue, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)
P012	Evaluation of qCSS3, a locus involved in non-seed-shattering behaviour of japonica rice cultivar, 'Nipponbare'	☆Nagayanagi, H., Y. Tsujimura, T. Matsuda, K. Otsuka, T. Htun, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)
P013	Effect of selection of Peony (<i>Paeonia lactiflora</i> Pall.) based on medicinal ingredient paeoniflorin content	○Kawashimo, M., T. Tsusaka, M. Sakurai (Tsumura Co., Ltd.)
P014	Diversity analysis between cultivars and homoeologs in wheat using pan genome information	○Tanaka, T. (NAAC, NARO)
P015	Explore of sex determination region in mulberry (<i>Morus</i> spp.) using genome resequencing data	○Matsumura, H.1, R. Shimizu2, M. Suzuki2, S. Yoshinobu2, A. Mizoguchi2, R. Atsumi2 (1.Gene Res., Shinshu Univ., 2.Grad. Sch. Sci. Tech., Shinshu Univ)
P016	Linkage map development of mulberry using F2 population from "Sekizaiso" x "Kokuso21"	☆Suzuki, M.1, A. Koyama2, M. Uemoto1, S. Kajita2, H. Matsumura1 (1.Grad. Sch. Sci. Tech., Shinshu Univ, 2.Tokyo U Agr. Tech)
P017	The ratio of introgression of C genome in BC1F1 individuals developed by backcrossing <i>Brassica rapa</i> to <i>B. napus</i>	☆Segawa, T., R. Kumazawa, T. Hanano, M. Nishikawa, S. Saiga, H. Takagi (Ishikawa Prefectural University)
P018	Developing co-dominant type DNA marker for PFRU controlling flowering habit in cultivated strawberry.	☆Saiga, S.1, M. Tada1, T. Segawa1, M. Nishikawa1, N. Makita1, M. Sakamoto2, K. Tanaka2, T. Wada2, H. Takagi1 (1.Ishikawa Prefectural University, 2.Takii Seed)
P019	Development of SNP-molecular markers from RNA sequencing in Japanese cultivated gentian	Takahashi, S.1, M. Shimizu1, T. Takase1, K. Nemoto1, A. Abe1, F. Goto1, C. Yoshida1, A. Hirabuchi1, M. Odashima2, S. Ozawa2, ○M. Nishihara1 (1.Iwate Biotechnology Research Center, 2.Iwate Agricultural Research Center)
P020	QTL analysis of femaleness in monoecious spinach	☆Yamano, K.1, A. Toyoda2, H. Hirakawa3, Y. Onodera4 (1.Grad.sch.Agr.,Hokkaido Univ, 2.Nat. Inst. Genet., 3.Kazusa DNA Res. Inst., 4.Res. Fac. Agr., Hokkaido Univ.)
P021	Comparative study on structures and expression of spinach FT homologs between early- and late- bolting lines.	☆Ishikawa, R., K. HAMADA, K. YAMANO, Y. ONODERA (Res. Fac. Agr., Hokkaido Univ.)
P022	QTL analysis of rosette size in head lettuce using UAV	☆Takamori, H.1, K. Seki2, Y. Kobayashi3, M. Okada4, K. Komatsu5, K. Tanaka6, Y. Uno7, O. Watanabe8, S. Nishiuchi9, H. Matsumura10, N. Hayashida3 (1.Grad. sch. Textile, Shinshu Univ., 2.Nagano Vegetable and Ornamental Crops Experiment Station, 3.Division of Applied Biology, Fac. Textile, Shinshu Univ., 4.Grad. Sch. Agric. and Life Sci., Tokyo Univ., 5.Fac. Agric., Tokyo Univ. Agric., 6.NODAI Genome Research Center, Tokyo Univ. Agric., 7.Fac. Agric., Kobe Univ., 8.Fac. Agric., Shinshu Univ., 9.Fac. Agric., Nagoya Univ., 10.Gene Research Center, Shinshu Univ.)
P023	Evaluation of the novel seed-shattering locus estimated on chromosome 12 using rice cultivar 'Kasalath'	☆Yamaguchi, Y., N. Shionari, N. Takama, Y. Oka, Y. Takenaka, T. Htun, C. Inoue, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)
P024	Predicting Chromosomal Contributions to Genetic Gain in Medicinal Components of Red Perilla Cross-breeding Populations	☆Kinoshita, S.1, K. Sakurai2, T. Chen2, T. Tsusaka3, M. Sakurai3, T. Kurosawa3, H. Iwata2 (1.Fac. Agr., Univ. Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.TSUMURA & CO.)
P025	Validation and genetic characterization of a seed weight quantitative trait locus, qSW17.1, in progenies of cultivated and wild soybeans	○Xu, D.1, D. Liu1,2, C. Park1, Q. Wang2 (1.Japan International Research Center for Agricultural Science, 2.College of Plant Science, Jilin University, China)
P026	GWAS analysis of parameters related to growth rate calculated from multiple environment cultivation of rice MAGIC population	○Yamamoto, T.1, T. Furuta1, K. Kashiwara1, Q. Zhang1, Y. Nonoue2, D. Ogawa2, J. Yonemaru2 (1.IPSR, Okayama Univ., 2.NICS, NARO Institute of Crop Science)

P027	GWAS analysis of elemental contents in straw and grain by using rice MAGIC population	☆ZHANG, Q.1, T. Furuta1, K. Kashihara1, D. Ogawa2, J. Yonemaru2, J. MA1, T. Yamamoto1 (1.IPSR, Okayama Univ, 2.NICS, NARO Institute of Crop Science)
P028	Genome-wide association studies for root-system breeding of sorghum.	☆Okada, S.1, Z. Hu2, Y. Inukai3, S. Nishiuchi2, T. Yamauchi1, S. Araki-Nakamura1, K. Ohmae-Shinohara1, H. Nakamura2, K. Miura4, S. Kasuga5, T. Sazuka1 (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Grad. Sch. Bioagri., Nagoya Univ., 3.ICREA, Nagoya Univ., 4.Dept. Biosci. Fukui Pref. Univ., 5.AFC, Fac. of Agri. Shinshu Univ.)
P029	Large scale resequencing of commercial melon cultivars and its application to marker-assisted breeding	○Yano, R.1, K. Shimomura2, M. Sugiyama2, Y. Kawazu2 (1.Research Center for Advanced Analysis, NARO, 2.Inst. Vegetable and Floriculture Sci., NARO)
P030	Analyzing the effect of the insertion in BrFT2 promoter region controlling non-vernalization flowering habit in Brassica rapa cv. 'CHOY SUM EX CHINA 3'	☆Nishikawa, M., T. Segawa, S. Saiga, N. Makita, T. Imamura, H. Takagi (Ishikawa Prefectural University)
P031	Genomic prediction using combined genotypic data obtained by different genotyping tools	☆Minamikawa, M.1,2, M. Kunihiisa3, S. Moriya3, K. Abe3, M. Inamori2, H. Iwata2 (1.IAAR, Chiba Univ., 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.NIFTS, NARO)
P032	Toward establishment of a novel breeding technology using molecular genetic screening and genome-editing-mediated amino acid substitutions	☆Nozaka, A., T. Kuroha, M. Kimizu, S. Chechetka, H. Yoshida (National Agriculture and Food Research Organization, NARO)
P033	CRISPR/Cas9 genome editing of TaGAD in common wheat	☆Murayama, H., Y. Kamiya, K. Kawaura (Kihara Institute for Biological Research, Yokohama City University)
P034	Identification of the gene responsible for the male sterility in eggplant by mitochondrial genome editing	☆SUSAMI, A.1, M. Tsujimura2, S. Arimura3, T. Terachi4 (1.Grad.Sch.Life Sci.,Kyoto Sangyo Univ, 2.Fac.Agr.Dept.Plant Life Sci.,Ryukoku Univ, 3.Agr Life Sci.,Tokyo Univ, 4.Fac. Life Sci., Kyoto Sangyo Univ)
P035	Genome editing to generate Ppd-H1-deficient barley and evaluation of growth characteristics in a net greenhouse.	Tezuka, D.1, H. Cho1, H. Onodera1, Q. Linghu1, T. Chijimatsu2, ○R. Imai1 (1.NIAS, NARO, 2.Sasaki Food Co.Ltd.)
P036	Morphological abnormalities observed in the floral organs of a tobacco BC3 line produced by the backcrosses between mutable and wild-type lines.	☆hanamoto, s.1, t. terachi2 (1.Grad. Sch Life Sci., Univ. Kyoto Sangyo, 2.Fac. Life Sci., Univ. Kyoto Sangyo)
P037	Analysis of rice short grain and cleistogamous mutant	○Ohmori, S., T. Mizubayashi, A. Shomura, U. Yamanouchi, S. Yamamura (Inst. Crop. Sci., NARO)
P038	Silencing mechanism by canonical and non-canonical RdDM pathway in egg cell	☆Yashiro, M., C. Kamada, A. Hasegawa, R. Kaneko, D. Susaki, N. Sugi, K. Tonosaki, D. Maruyama, T. Kinoshita (Kihara Inst. Biol. Res., Yokohama City Univ.,)
P039	Investigation of the male sterility observed in alloplasmic lines of wheat (cv. Chinese Spring) with Triticum-Aegilops cytoplasm. 1. Plasmon Type: U,M,T2,C,G	○Tsujimura, M.1, S. Takenaka1, M. Nakata1, N. Mori2, T. Terachi3 (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Agr. Sci., Kobe U., 3.Fac. Life Sci., Kyoto Sangyo Univ.)
P040	Characterization of the mitochondrial gene orf181 specific to alloplasmic male-sterile wheats	☆Shoji, Y.1, N. Oda2, M. Tsujimura3, T. Terachi2 (1.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 2.Fac. Life Sci., Kyoto Sangyo Univ., 3.Fac. Agr. Dept. Plant Life Sci., Ryukoku Univ.)
P041	Transcriptome analysis of root plasticity under high soil temperature in rice	☆Yoshida, S.1, Y. Numajiri2, K. Yoshino3, S. Teramoto2, T. Kawakatsu3, Y. Uga2 (1.Fac. of Agri., Tokyo Univ. of Agri., 2.Inst. Crop Sci., NARO, 3.Inst. Agrobiological sci., NARO)
P042	Non-destructive 3D image analysis of root system architecture in rice under drought.	☆Numajiri, Y.1, S. Yoshida2, T. Hayashi3, Y. Uga1 (1.Crop Sci., NARO, 2.Bioresource, Tokyo Nodai, 3.Agric. Info. Tech., NARO)
P043	Functional characterization of a NLR gene in the clubroot resistant locus Crr3 in Brassica rapa	Fangqi, S.1, M. Shimizu2, M. Takahashi1, K. Tonosaki3, S. Matsumoto4, N. Kubo5, ○K. Hatakeyama1 (1.Fac. Agri., Iwate Univ., 2.IBRC, 3.Kihata Inst. Biol. Res., Yokohama City Univ., 4.IVFS, NARO, 5.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ.)
P044	Nanopore sequencing of clubroot resistance (CR) cabbage genome and DNA marker development of CR-QTL region	☆Chu, T.1, M. Shimizu2, E. Fukai1, K. Hatakeyama3, K. Okazaki1 (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Iwate Biotechnology Research Center, 3.Fac. Agric., Iwate Univ.)
P045	Effect of above-ground and underground parts on the occurrence of green stem disorder in soybean.	○Ogata, D.1,2, A. Ishitsuka3, R. Matsumoto3, O. Uchikawa3, M. Miyazaki4, Y. Ishibashi1 (1.Grad. Sch. of Bior. and Bioe. Sci., Kyushu Univ., 2.Yame Agric. Ext. Cent., 3.Fukuoka Agric. Forest. Res. Cent., 4.Fukuoka Pref. Office)
P046	Evaluation of heterosis in seedlings derived from crosses between Taichung 65 and cultivars in the world rice core collection	☆Nakamura, Y.1, K. Ichitani2, S. Matthew3, N. Tanaka3, T. Kuboyama1 (1.Col. Agr.,Ibaraki U, 2.Fac. Agr.,Kagoshima U, 3.Inst.Crop.Sci, NARO)
P047	Molecular biological analysis of abscission layer formation using rice non-seed shattering mutants.	☆Tanimoto, R., S. Sugita (Konishi) (Grad. Sch. Agri., Univ. Kagawa)
P048	<i>Molecular genetic analysis for the isolation of a novel seed shattering gene in rice.</i>	○Sugita-Konishi, S., T. Inamo, R. Tanimoto, K. Nishikawa (Grad. Sch. Agri., Univ. Kagawa)
P049	Characteristics of cracking seed tolerant soybean lines in Hokuriku region	○Kono, Y.1, M. Ikegami2, K. Toda2,7, K. Fujii2, A. Kikuchi3, K. Komatsu4, N. Oki5, S. Watanabe6, K. Hirata3, Y. Tetsuya2, A. Kaga2 (1.CARC,NARO, 2.NICS,NARO, 3.TARC,NARO, 4.WARC, NARO, 5.KARC, NARO, 6.Univ. Saga, 7.Res. Cent. Genet. Resources, NARO)
P050	Genome-wide association study and genomic prediction for essential oil components in <i>Ataractylodes lancea</i>	☆Tsusaka, T.1, K. Shirasawa2, S. Isobe2 (1.Tsumura & Co., 2.Kazusa DNA Res. Inst.)
P051	Evaluation of traits in a medicinal plant, <i>Bupleurum falcatum</i> Linne	○Hiyama, H., Y. Aoki, M. Sakurai (Tsumura & Co.)
P052	A novel white-flower mutant of Japanese morning glory induced by gamma irradiation	☆Yamamura, R.1, R. Okano1, H. Katsuyama1, Y. Takahashi1, T. Mizuno2, A. Hoshino4, E. Nitasaka3, T. Kuboyama1 (1.Col. Agr., Ibaraki U., 2.Dept. Botany, NMNS, 3.Grad. Sch. Sci., Kyushu U., 4.Natl. Inst., Basic Biol.)
P053	Identification of a gene altering tocopherol synthesise pathway in soybean	☆Park, C.1, D. Liu1,2, Q. Wang2, D. Xu1 (1.Japan International Research Center for Agricultural Science, 2.College of Plant Science, Jilin University, China)
P054	Genetic analysis of lines showing reiterative branching phenotype resulted from the cross between lax2-5 and cv. Kasalath.	○Oyori, T., N. Satoh-Nagasawa, M. Tsuchida, N. Nagasawa (Biores Sci., Akita Pref. Univ.)

P055	Changes in cellular structures in the barley inflorescence meristem during abortion	☆Matsumoto, H.1, J. Ito1, S. Arai1, Y. Nomura1, M. Sugimura1, N. Sato1, M. Seki1, M. Wakazaki2, M. Sato2, N. Takeda-Kamiya2, K. Uno4,5, Y. Sato4,6, D. Saisho7, K. Toyooka2, H. Tsuji1,3 (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.Nagoya Univ., 4.Grad. Sch. of Sci., Nagoya Univ., 5.Department of NanoBiophotonics, Max Planck Institute for Multidisciplinary Sciences (MPI-NAT), 37077 Göttingen, Germany, 6.Institute of Transformative Biomolecules (WPI-ITbM), Nagoya Univ., 7.IPSR, Okayama Univ.)
P056	Genetic analysis of interactions between ADAXIAL-ABAXIAL BIPOLAR LEAF genes in rice	☆Shimizu, H., N. Nagasawa, N. Satoh-Nagasawa (Grad. Sch. Biores. Sci., Univ. Akita Pref.)
P057	Gene expression analysis of the unique inflorescence structure in barley	☆Ito, J.1, N. Sato1, Y. Nomura1, S. Arai1, K. Takahagi2, S. Okada3,4, N. Takeda-Kamiya2, K. Toyooka2, D. Saisho3, T. Hirayama3, K. Mochida2, H. Tsuji1,4 (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Bioscience and Biotechnology Center, Nagoya Univ.)
P058	Demonstration of environment-dependent genetic interactions in the control of rice flowering time	○Saito, H.1, Y. Fukuta1, A. Tomita2, E. Fushimi3, Y. Okumoto4 (1.JIRCAS, 2.Fac. Agr., Okayama Univ., 3.NARO, 4.Fac. Agr., Setsunan Univ.)
P059	Analysis of light regulation in stunting seedling growth of albino-like rice mutant	○Rikiishi, K., A. Ono, M. Maekawa, M. Sugimoto (Inst. Plant Sci. Res., Okayama U.)
P060	Analysis of level of self-incompatibility in S-tester lines of Brassica rapa	○Yamamoto, M., M. Ogura, H. Kitashiba (Graduate School of Agricultural Science, Tohoku University)