

10 September (9:00-11:45) Oral Presentation Program

10 September (9:00-11:45) Oral Presentation Program								
Chair: Hiroshi Hisano (Okayama Univ.)		Chair: Hideki Takanashi (Univ. Tokyo)		Chair: Takeshi Kuroha (NARO)		Chair: Lanzhuang Chen (Minami Kyushu Univ.)		
9:00	101 Reference-based chromosome-scale assembly of Japanese barley (<i>Hordeum vulgare</i> ssp. <i>vulgare</i>) cultivar "Hayakiso 2" ○Tanaka, T. I., Y. Horaguchi2, T. Todoroki2, D. Saito3, T. Abiko4, H. Kai2 (1.NAAC, NARO, 2.Fukuoka Agriculture and Forestry Research Center, 3.Okayama University, 4.Kyushu University)	201 Regulation of chromatin accessibility in the shoot apical meristem of rice by florigen activation complex ☆Funayama, E. I., A. Hosaka3, H. Akashi2, K. Yamaguchi2, A. Yoshida2, H. Kida2, H. Yoshida2, J. Ito2, T. Kawakatsu4, H. Tsuji2,5 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Kihara Inst. Biol. Res., Yokohama City Univ., 3.Nihon BioData Co., 4.RIKEN BRC, 5.Biosci. Biotechnol. Center, Nagoya Univ.)	301 A mutant allele in qSOR1, rice gravitropism QTL, confers deeper rooting, resulting in enhanced drought resistance ○Uga, Y. I., Y. Kitomii1, R. Kuroda1, R. Nakata1, M. Iba1,2, F. Soma1, S. Teramoto1, K. Sugimoto1, T. Kawai1 (1.Inst. Crop Sci., NARO, 2.Tokyo Univ. Agri.)	401 Development of multimodal generative AI agents harnessing breeders' insights ○Yamada, T. I., A. Kaga2, J. Yonemaru1 (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)	501 Identification of the rice resistance locus Pi-eT05 consisting of four NLR genes ○Shimizu, M. I., S. Asuke2, A. Abe1, H. Takata2, H. Adachi3, T. Fujiwara3, T. Sakai4, Y. Tosa2, R. Terauchi1,4 (1.IBRC, 2.Grad. Sch. Agric. Sci., Kobe Univ, 3.Fac. Adv. Life Sci., Hokkaido Univ, 4.Grad. Sch. Agric., Kyoto Univ.)	601 Development of maize transformation system using leaf primordia ○Kojima, T. I., K. Tanaka1, Y. Mano2, T. Furuta3, M. Ashikari4, H. Tsuji4, A. Agata1, H. Takahashi1, M. Nakazono1 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Inst. Lifest. Grassl. Sci., NARO, 3.IPSR, Okayama Univ., 4.Biosci. Biotechnol. Center, Nagoya Univ.)	701 Developmental stage-specific genotype-by-environment interactions for grain quality in Etsun rice lines. ○Kobayashi, A. I., E. Yamamoto2, H. Yoshida3, S. Watanabe1, Y. Machida1, G. Chaya1, F. Nakaoka1, M. Matsuoka3 (1.Fukui Agr. Exp. Stn., 2.Meiji Univ., 3.Fukushima Univ.)	9:00
9:15	102 De novo genome assembly of wild emmer wheat using nanopore sequencing ☆Nishimura, K. I., K. Ushijima1, Y. Yasui2, N. Takanob1, R. Nakano2, Y. Monden1, K. Kato1, H. Nishida1 (1.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ., 2.Grad. Sch. Agr., Kyoto Univ.)	202 Development of PHYTOMap for rice shoot apical meristem II ☆Iwama, K. I., Y. Morishita1, H. Tsuji2,3 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Biosci. Biotechnol. Center, Nagoya Univ., 3.Kihara Inst. Biol. Res., Yokohama City Univ.)	302 Estimation of Genetic Regions Associated with Waterlogging-Inducible Soil-Surface Root in the Wild Rice <i>Oryza glumaepatula</i> ☆Tamaru, S. I., T. Miyashita1, K. Katayama1, T. Kimoto1, H. Tokuo1, Y. Uga3, K. Shiono1 (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.JSPS Research Fellow, 3.Inst. Crop Sci., NARO)	402 Breeding support system enhancing use of breeding data Tanaka, R. I., T. Yamada2, E. Yamamoto1, ○H. Kajiyama-Kanegae1,2 (1.Institute of Crop Science, NARO, 2.Research Center for Agricultural Information Technology, NARO)	502 Mapping of a wheat blast resistance gene possessed by the Japanese wheat accession R3 ☆Sota, K. I., S. Asuke2, Y. Tosa2, H. Handa1 (1.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ.)	602 Variation on crossabilities of bread wheat with Triticeae species ☆Ryu, A., S. Sakuma (Fac. Agr. Tottori U.)	702 Population structure analysis of Indochinese rice landraces preserved as seed specimens collected over 60 years ago ○Numaguchi, K. I., L. Sathya1, O. Chhoun2, Y. Higashikubo3, H. Saito4, Y. Sato5, R. Gutaker6 (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodia Agr. Res. Dev. Inst., 3.Fucl. Agr., Kobe Univ., 4.Trop. Agr. Res. Front, JIRCAS, 5.Natl. Inst. Genet., 6.Royl. Bot. Gard., Kew)	9:15
9:30	103 Identification of early-heading genes in wild emmer wheat by repeated QTL analysis using F2 populations ☆Takano, N. I., K. Nishimura1, Y. Chang2, M. Okuma1, K. Murata2, R. Nakano2, T. Nakazaki2,3, K. Kato1, Y. Monden1, H. Nishida1 (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. of Agri., Kyoto Univ., 3.Office of Institutional Adv. and Comm., Kyoto Univ.)	203 Development of super resolution expansion microscopy for rice shoot apical meristem ☆Ishida, Y. I., Y. Morishita2, K. Iwama2, H. Tsuji3,4 (1.Sch. Agric., Nagoya Univ., 2.Grad. Sch. Bioagric. Sci., Nagoya Univ., 3.Biosci. Biotechnol. Center, Nagoya Univ., 4.Kihara Inst. Biol. Res., Yokohama City Univ.)	303 Development of Culture Conditions for Genetic Transformation in the Sweetpotato Cultivar 'J-Red' ☆Kobayashi, H. I., M. Otani2, H. Matui1, H. Tabuchi3, K. Nishimura1, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Res. Inst. Biore. Biotech., Ishikawa Pref. Univ., 3.KARC/NARO)	403 Demonstrating a breeding strategy using genomic prediction based on a NAM population ☆Sakai, T. I., R. Terauchi1,2, A. Abe2 (1.Grad. Sch. Agr., Kyoto Univ., 2.IBRC)	503 Development of DNA markers and discovery of novel alleles for tan spot of wheat resistance genes ☆Taro, S. I., G. Ishikawa2, H. Nakamura3, A. Kurono1, T. Touyama1 (1.Aichi Agr. Res. Cent., 2.NICS, NARO, 3.HARC, NARO)	603 Time-course single pollen RNA-seq analysis for elucidating a gametocidal gene in wheat ☆Yamamori, K. I., K. Murata1, H. Kakui3, T. Yoshikawa1, S. Nasuda1 (1.Grad. Sch. Agric., Kyoto Univ., 2.IPSR, Okayama Univ., 3.Grad. Sch. Agric. Life Sci., Univ. Tokyo)	703 Genetic variation of grown root angle in rice (<i>Oryza sativa</i> L.) germplasm from Zambia ☆Fujiwara, N. I., K. Ohshiro1, S. Komatsubara2, P. Mabvuto3, Y. Fukutai (1.Univ. Ryukus, 2.JICA, 3.ZARI)	9:30
Chair: Tsuyoshi Tanaka (NARO)								
9:45	104 High-Resolution Genomic Assembly of Hops (<i>Humulus</i>) to Unveil Sex Determination Factor ☆Segawa, T. I., T. Akagi2,3, R. Uchida2, H. Tanaka4, K. Shirasawa5, N. Yamagishi6, H. Yaegashi6, S. Natsume7, H. Takagi7, A. Abe7, M. Okuno4, A. Toyoda8, K. Sato9, Y. Honniden2, C. Zhang2, K. Ushijima2, J. Patzak10, L. Horáková11, V. Bačovský11, R. Hobza11, D. Charlesworth12, T. Itoh4, E. Ono1 (1.Res. Inst. SIC Ltd., 2.Okayama Univ., 3.Nihon BioData Co., Ltd., 4.Inst. Sci. Tokyo, 5.Kazusa DNA Res. Inst., 6.Univ. Iwate, 7.Iwate Bio. Res. Cen., 8.Natl. Inst. Genet., 9.Univ. Toyama, 10.Hop Res. Inst. Co. Ltd., 11.Institute of Biophysics, Czech Acad. Sci., 12.Inst. Ecol. Evol., Univ. Edinburgh)	204 Chromatin state analysis of the rice shoot apical meristem using ATAC-seq imaging ☆Morishita, Y. I., R. Takata2, A. Yoshida2, A. Higo2, A. Harada3, H. Tsuji2,4 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.Kihara Inst. Biol. Res., Yokohama City Univ., 3.Grad. Sch. Med. Sci., Kyushu Univ., 4.Biosci. Biotechnol. Center, Nagoya Univ.)	304 Establishment of a genetic transformation system in <i>Echinochloa phyllopan</i> ☆Sugahara, M. I., S. Iwakami2, K. Yasuda3, T. Gondo4 (1.Grad. Sch. Agr., Univ. Miyazaki, 2.Tokyo Univ. Of. Agr. Tech, 3.Agr. Bior. Sci., Akita Pre. Univ, 4.FSRC, Univ. Miyazaki)	404 Integrative Analysis of Drought Response Using Multi-Omics Data in a Soybean RIL Population ☆Takahashi, Y. I., K. Sakurai2, Y. Toda3, Y. Fujii4, Y. Ohmori2, Y. Yamasaki2, H. Takahashi5, H. Takanashi2, M. Tsuda6, M. Hirai4, H. Tsujimoto7, M. Nakazono5, T. Fujiwara2, A. Kaga8, H. Iwata2, G. Morota2 (1.Fac.Agr., Univ. Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Inst. Agro-Env. Sci., NARO, 4.RIKEN Center for Sustainable Resource Science, 5.Grad. Sch. Bioagri. Sci., Nagoya Univ., 6.Faculty of Food and Nutritional Sci., Toyo Univ., 7.Arid Land Res. Ctr., Tottori Univ., 8.Inst. Crop Sci., NARO)	504 GWAS-based identification of genomic regions conferring root-knot nematode resistance derived from the black oat (<i>Avena strigosa</i>) cultivar 'Terara' ○UWATOKO, N. I., K. Uesugi2, T. Mizubayashi1, G. Murata2, H. Yamakawa1, M. Katsura3 (1.Institute of Crop Science, NARO, 2.Institute for Plant Protection, NARO, 3.Kyushu Okinawa Agricultural Research Center, NARO)	604 Evaluation of the self-incompatibility inhibitor gene from cultivated potatoes ☆Yamashita, M., I. Asai, A. Yasuga, K. Suzuki, K. Hosaka, R. Sanetomo (Obihiro University of Agriculture and Veterinary Medicine)	704 Evaluation of salinity tolerance in Bangladesh rice varieties under soil and two hydroponic cultivation conditions ☆Inoue, Y. I., Y. Yamagata2, H. Yasui2 (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Fac. Agr., Kyushu Univ.)	9:45

		Chair: Junichi Itoh (Univ. Tokyo)	Chair: Shuji Matsushita (Agr. Tech. Res. Cent., HiTRI)				Chair: Hiroyasu Kitashiba (Tohoku Univ.)	Chair: Koji Numaguchi (Kobe Univ.)	
10:00	I05	Assembling autotetraploid genomes only by nanopore sequencing ○Naito, K. I., K. Akai2 (1.Res. Cntr. Genet. Resour., NARO, 2.Hokkaido Agr. Res. Cntr., NARO)	205 The first developmental changes in rice shoot apical meristem during the transition ☆Honda, M. I., M. Tanaka1, W. Tanaka2, H. Tsuji1,3 (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 3.Biosci. Biotechnol. Center, Nagoya Univ.)	305 Development of a highly efficient genome editing technique in melon by iPB and creation of a long shelf-life melon ripened by exogenous ethylene ○Sasaki, K. I., K. Urano1, N. Mimida2, S. Nonaka3, H. Ezura2,3, R. Imai1 (1.NIAS, NARO, 2.Sanatech Life Science Co., Ltd., 3.Fac. Life Environ. Sci., Univ. Tsukuba)	405 Selection and crossing of soybean RILs based on iomic and genomic data for improving drought tolerance across distinct controlled environments ☆Taruimoto, H. I., K. Sakurai1, S. Kinoshita1, Y. Toda2, Y. Ohmori1, M. Tsuda3, H. Tsujimoto4, A. Kaga5, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Inst. Agro-Env. Sci., NARO, 3.Faculty of Food and Nutritional Sci., Toyo Univ., 4.Arid Land Res. Ctr., Tottori Univ., 5.Inst. Crop Sci., NARO)	505 Genetic linkage analysis between the genes for seed coat color and resistance to Bean Common Mosaic Virus using DNA markers in common bean. ○Yamaguchi, N. I., H. Sato2, K. Nakagawa3, K. Tanaka4, A. Hosoi5, K. Nakahara6 (1.Central Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO, 3.Kitami Agr. Exp. Sta., HRO, 4.Tokyo Univ. of Info. Sci., 5.Genome Res. Center, Tokyo Univ. of Agri., 6.Res. fac. Agr., Hokkaido Univ.)	605 Knockout of mitochondrial gene, orf352, in Wild Abortive-cytoplasmic male sterile rice ☆Mon, H. I.,2, S. Arimura3, T. Kazama1 (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Dept. Agri. Biotech, Yezin Agri. Univ., 3.Grad. Schl. Agri. Life Sci., The Univ. of Tokyo)	705 Production of prebreeding lines from crosses between wild species <i>Aegilops umbellulata</i> Zhuk. lines encompassing genetic diversity and ph2 mutant bread wheat. ☆Son, I. I., K. Yoshida2, Y. Matsuoka1 (1.Grad. Sch. Agr. Sci., Kobe U., 2.Grad. Sch. Agr., Kyoto U.)	10:00
10:15	I06	New strategy for allele identification in autoploid sweet potato by Nanopore sequencing using allele-specific k-mer ☆Nakahara, T. I., M. Tanaka2, K. Ushijima1, K. Nishimura1, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Environ. Life Sci. Tech., Okayama U., 2.KARC/NARO)	206 Functional analysis of ASPI and TAB1 during axillary bud development in rice ☆Ohyama, A. I., T. Toriba2, M. Sato3, H. Tsuji3,4, W. Tanaka1 (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ., 3.Kihara Inst. Biol. Res., Yokohama City Univ., 4.Biosci. Biotechnol. Center, Nagoya Univ.)	306 Genome editing of the S-locus EARLY FLOWERING3 gene in 'Kitawasesoba' via iPB-RNP method. ☆Someya, R. I.,2, K. Kuchitsu3, R. Imai1,2 (1.Grad. Sch. Sci. Tech., Tokyo Univ. Sci., 2.Inst. Agrobiol. Sci., NARO, 3.Dept. Appl. Biol. Sci., Tokyo Univ. Sci.)	406 Strategic crossing using genome data to improve genetic potential in soybean RIL population ☆Sakurai, K. I., Y. Toda2, M. Inamori1, K. Hamazaki3, H. Tsujimoto4, A. Kaga5, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Inst. Agro-Env. Sci., NARO, 3.Adv. Int. Proj., RIKEN, 4.Arid Land Res. Ctr., Tottori Univ., 5.Inst. Crop Sci., NARO)	506 Identification of Candidate Regions for Tolerance in the Turnip Mosaic Virus Tolerance Mustard Cultivar 'BIAN QING' ☆Hoshino, H. I., R. Kuwahara2, O. Kim2, K. Komatsu3, S. Yoshida3, K. Irie4, K. Wakui3 (1.Grad. Sch. Agric., Tokyo Univ. of Agri., 2.Dept. of Agri., Tokyo Univ. of Agri., 3.Dept. of Biores. Dev., Tokyo Univ. of Agri., 4.Dept. of Int. Agri. Dev., Tokyo Univ. of Agri.)	606 Production of neo-tetraploid and -diploid hybrids between <i>Oryza sativa</i> and <i>O. rufipogon</i> /longistaminata exhibiting high salt tolerance by in vitro fertilization ☆Wongla, W. I., S. Ono1, Y. Sato2, T. Okamoto1 (1.Dept. Biol., TMU, 2.Plant Gen., NIG)	706 Rice and wheat hybrid mitochondrial genome changes rice – wheat root system architecture ○Ubi, B. I.,2, R. Sugiura3, K. Ikpa-agodo3, N. Onda4, A. Sato4, T. Maryenti4,5, T. Okamoto4, T. Ishii1,6,7 (1.IPDRE, Tottori Univ., 2.Dept. of Biotech., Ebonyi State Univ., Nigeria, 3.Grad. Sch. Sustainability Sci., Tottori Univ., 4.Grad. Sch. Sci., Tokyo Metro. Univ., 5.Bio. Fac. of Math. and Nat. Sci., Univ., Indonesia, 6.ALRC, Tottori Univ., 7.Ch. Eng. Res., Tottori Univ.)	10:15
	Chair: Ken Naito (NARO)								
10:30	I07	Comparative genomic analysis of Koshihikari-related varieties based on the telomere-to-telomere sequence of Koshihikari genome ○Yoshida, H. I., H. Takahashi1,2, T. Akagi3, D. Saisho4,7, M. Suganami1, G. Tamaiya5,6,7, E. Yamamoto8, A. Kobayashi9, M. Matsuoka1 (1.IFeS, Fukushima Univ., 2.Fac. Food Agric. Sci., Fukushima Univ., 3.Nihon BioData Corp., 4.JPSR, Okayama Univ., 5.Grad. Sch. Med., Tohoku Univ., 6.ToMMo, Tohoku Univ., 7.AIP Center, RIKEN, 8.Grad. Sch. Agri., Meiji Univ., 9.Fukui Agri. Exp. Stn.)	207 Functional analysis of strigolactone-related genes in rice shoot formation ☆Aimori, S. I., A. Ohyama1, T. Toriba2, W. Tanaka1 (1.Grad. Sch. Integr. Sci. Life, Hiroshima Univ., 2.Miyagi Univ.)	307 Biochemical and molecular biological characterization of bas1 mutant in soybean seed ☆Asa, H. I., H. Morita2, H. Seki2, K. Matsumoto3, R. Shigeta3, K. Fujii3, T. Yamamoto3, Y. Masuda3, T. Yamada1 (1.Grad. Sch. Agric., Hokkaido Univ., 2.Grad. Sch. Eng., Univ. of Osaka, 3.Kanematsu Corp.)	407 Single-step genomic best linear unbiased predictions in sugarcane ○Morota, G. I., M. Goncalves2, L. Peternelli2 (1.Grad. Sch. Agr. Life Sci. Univ. Tokyo, 2.Federal Univ. of Vicosa)	507 Selection and evaluation of herbicide-tolerant azuki bean lines derived from callus of 'Benidainagon' ☆Adegawa, S. I., N. Yamaguchi1, C. Souma1, H. Nagasawa2, M. Oonami1,2, T. Maruta1,3, K. Shirasawa4 (1.Central AES, HRO, 2.Tokachi AES, HRO, 3.Donan AES, HRO, 4.Kazusa DNA Research Institute)	607 Mode of inheritance for the fertility restoration found in near isogenic lines of the F1 pollen sterility gene S21 from <i>Oryza rufipogon</i> and <i>O. meridionalis</i> ☆HARA, K. I., R. KUBOTA1, H. YASUI2, Y. YAMAGATA2 (1.Grad. Sch. Bioresour. Bioenviron. Sci., Kyushu Univ., 2.Fac. Agr., Kyushu Univ.)	707 Analysis of genetic diversity and population structure of Himalayan wheat landraces ☆Li, Y. I., Z. Meng1, M. Nitta1, A. Ohta1, K. Nemoto2, S. Gorafil3, S. Nasuda1 (1.Grad. Sch. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Shinshu Univ.)	10:30
	Chair: Tetsuya Yamada (NARO)					Chair: Yusaku Uga (NARO)		Chair: Naohiro Uwatoko (NARO)	
10:45	I08	A Paradigm Shift in Genetics Driven by Complete Genomes: Mutation Biases in Genic and Non-genic Regions Akagi, T. I., ○D. Saisho2,7, H. Yoshida3, H. Takahashi3,4, Y. Ikeda2, T. Matsuda3,4, G. Tamaiya5,6,7, A. Kobayashi8, M. Matsuoka3 (1.Nihon BioData Corp., 2.IPSR, Okayama Univ., 3.IFeS, Fukushima Univ., 4.Fac. Food Agric. Sci., Fukushima Univ., 5.Grad. Sch. Med., Tohoku Univ., 6.ToMMo, Tohoku Univ., 7.AIP Center, RIKEN, 8.Grad. Sch. Agri. Expt. Stn.)	208 Expression analysis of tillering-related genes in ectopic meristems of adaxial bipolar leaf mutants ☆Chiba, K. I., M. Kikuchi1, K. Yashima3, T. Yamazaki3, R. Okamoto3, M. Watanabe3, H. Sunohara2, N. Nagasawa3, N. Satoh-Nagasawa3 (1.Grad. Sch. Biores. Sci., Akita Pref. Univ., 2.Fac. Sci., Univ. Kumamoto, 3.Fac. Biores. Sci., Akita Pref.)	308 Generation and characterization of lipoxygenase-deficient soybean mutants by site-directed mutagenesis ☆Tamamoto, Y. I., K. Okada1, Y. Haga2, Y. Takata1, K. Matsumoto3, R. Shigeta3, K. Fujii3, T. Yamamoto3, Y. Masuda3, H. Matsura1, T. Yamada1 (1.Grad. Sch. Agric., Hokkaido Univ., 2.Fac. Agric., Hokkaido Univ., 3.Kanematsu Corp.)	408 Validation of genomic selection efficiency in Perilla via crossing experiments ☆Kinoshita, S. I., K. Sakurai1, T. Tsusaka2, M. Sakurai2,3, K. Shirasawa4, S. Isobe1,4 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.TSUMURA & CO., 3.LAO TSUMURA CO.,LTD, 4.Kazusa DNA Res. Inst.)	508 Imaging of the dynamics of root growth and radial oxygen loss during the seedling stage of rice using a planar oxygen optode ○Shiono, K. I., S. Tamaru1,2, N. Fujiwara1, H. Shiba1,2 (1.Grad. Sch. Biosci. Biotech., Fukui Pred. Univ., 2.JSPS Research Fellow)	608 Allelic divergence of hybrid sterility gene S13 found between African wild rice <i>O. longistaminata</i> and Asian cultivated rice <i>O. sativa</i> ☆Shiozaki, K., M. Zin Mar, W. Takanishi, Y. Kishima, Y. Koide (Grad. Sch. Agriculture, Hokkaido Univ.)	708 Breeding of the Japanese two-row hulless waxy barley variety 'Fukei 1103' for Hokkaido. ○Kihara, M., R. Kanatani, T. Hoki (Crop Research Laboratories, SAPPORO BREWERIES LTD.)	10:45

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Chair: Shun Sakuma (Tottori Univ.)		Chair: Kazumitsu Onishi (Obihiro Univ.)	Chair: Jun Ito (Yokohama City Univ.)	Chair: Gota Morota (Univ. Tokyo)	Chair: Asako Kobayashi (Fukui Agri. Exp. Stn.)	Chair: Yu Takahashi (NARO)	Chair: Tomohiko Kazama (Kyushu Univ.)	
9:30	112 Identification of QTL for photosynthesis and yield in bread wheat chromosome 6A and elucidation of the surrounding genes ☆Hino, K. I., T. Ishii2, K. Nishimura3, Y. Matsuoka4, H. Tsujimoto2, R. Megal (1.Grad. Sch. Sci. Tech. Innov., Univ. Yamaguchi, 2.ALRC., Univ. Tottori, 3.Grad. Sch. Sci. Environ. Life Sci., Univ. Okayama, 4.Grad. Sch. Agric., Univ. Kobe)	212 Study on floral meristem identity genes and morphological modification in German Chamomile ○Kurogi, K. I., Y. Takahara2 (1.Grad. Sch. Materials Science and Bioengineering, Nagaoka University of Technology, 2.Materials Science and Bioengineering, Nagaoka University of Technology)	312 Impact of loss-of-function of DNA maintenance methyltransferase on the phenotype of the C24 accession of /Arabidopsis thaliana/ ☆Kawamoto, Y. I., M. Yamashita1, T. Murakami1, K. Matsuo1, S. Shiraki1, M. Shimizu2, R. Fujimoto1 (1.Grad. Sch. Agri. Sci., Kobe Univ, 2.Iwate Biotechnology Res. Center)	412 Accumulation of starch characteristic data in the 'Breeding Information Infrastructure' being developed by NARO. ○Araki, E. I., E. Kimura1, T. Umemoto1, K. Horii2, T. Ikegaya2, N. Suzuki2, K. Matsushita2, A. Goto2, M. Kuroki2 (1.Inst. Food Res., NARO, 2.Inst. Crop Sci., NARO)	512 Search for genes involved in varietal differences in the accumulation of protein aggregates under high-temperature stress in rice seedlings ☆Inushima, A., T. Yamada (Grad. Sch. Agr., Tokyo Univ. Agr. Tech.)	612 Selection of high-sucrose soybean lines derived from EMS mutagenesis and crossbreeding for improvement of tofu taste ☆Takahashi, H. I., H. Igarashi2, S. Kobayashi3, N. Yamaguchi3 (1.Kamikawa Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO, 3.Central Agr. Exp. Sta., HRO)	712 Development of Tomato Mutant Resources and Public Release of Exome Sequencing Database ☆Kuya, N. I., K. Sugimoto1,2, S. Kawamoto3, N. Fukuda1, H. Ezura1,4 (1.Tsukuba-Plant Innovation Research Center, Univ. Tsukuba, 2.Research Center for Advanced Analysis, NARO, 3.Department of Informatics, National Institute of Genetics, 4.Sanatech Life Science Co., Ltd.)	9:30
9:45	113 Effectiveness of Targeted Sequencing in QTL Mapping of Mutant Barley Lines: Insights from Heading Time Analysis ☆Takeda, S., M. Okuma, A. Mandozai, K. Nishimura, K. Ushijima, Y. Monden, K. Kata, H. Nishida (Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)	213 Identification of the headings-related gene TaBBX-A19 through the genetic analysis of a wheat early heading mutant ☆Komura, S. I., F. Kobayashi2, Y. Oono2, H. Handa3, M. Kishi-Kaboshi4, F. Abe5, Y. Inoue1, K. Yoshida1 (1.Grad. Sch. Agr., Kyoto U., 2.NICS, 3.Grad. Sch. Life Env. Sci., Kyoto Pref. U., 4.Kazusa DNA Res. Inst., 5.NIAS)	313 Secondary siRNA production of CHS-A cosuppression in petunia originates from multiple mRNA cleavage sites ☆Oguri, K., M. Yuhazu, M. Dwiyanti, A. Kanazawa (Res. Fac. Agr., Hokkaido Univ.)	413 Estimation for milling performance of wheat grains using image analysis ☆Tani, M. I., T. Yamada2, G. Ishikawa3, S. Nishiuchi1 (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.RCAIT, NARO, 3.NICS, NARO)	513 Estimating the impacts of 21st-century warming trends on the percentage of first-grade rice and the effectiveness of heat-tolerant cultivars in Japan ○HASEGAWA, T., H. WAKATSUKI (National Agriculture and Food Research Organization (NARO))	613 Effects of high temperatures on sucrose content of soybean seeds in Hokkaido. ☆Igarashi, H. I., H. Takahashi2, Y. Hosokawa3, M. Kawahara4, S. Koyano3, K. Nakamichi3, S. Kobayashi3, N. Yamaguchi3 (1.Tokachi Agr. Exp. Sta., HRO, 2.Kamikawa Agr. Exp. Sta., HRO, 3.Central Agr. Exp. Sta., HRO, 4.Tokachi Foundation)	713 Development of restorer of fertility lines and elucidation of fertility restoration mechanisms toward efficient F1 seed production in tomato ☆Kuwabara, K. I., R. Nakajima2, A. Van Bosstraeten3, K. Ezura4,5, K. Toriyama1, T. Arizumi5, K. Shirasawa6 (1.Grad. Sch. Agric. Sci., Tohoku Univ., 2.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 3.Grad. Sch. Sci. and Tech., Univ. Tsukuba, 4.JIRCAS, 5.Fac. Life Env. Sci., Univ. Tsukuba, 6.Kazusa DNA Res. Inst.)	9:45
10:00	114 Identification of a candidate miRNA for sex determination in the staple crop white Guinea yam (Dioscorea rotundata) ☆Kudoh, A. I., Y. Sugihara2, K. Iseki3, R. Matsumoto4, K. Minaji1, K. Onai1, A. Abe5, S. Natsume5, T. Sakai1, K. Oikawa5, M. Shimizu5, K. Itoh5, H. Adachi6, K. Honda1, S. Yamamoto3, P. Adebolaj4, A. Asfaw4, R. Terauchi1 (1.Grad. Agri., Kyoto Univ., 2.The Sainsbury Laboratory, 3.JIRCUS, 4.IITA, 5.IBRC, 6.Adv. Life Sci., Hokkaido Univ.)	214 Estimation of rice cultivating condition based on results of QTL analyses for heading date in Zambia ☆Yonamine, K. I., H. Kobayashi1, S. Komatsubara2, R. Mulenga3, G. Munkombwe3, P. Mabuto3, M. Chinji3, E. Musabla3, N. Museta3, L. Kamguya3, J. Njobvu3, Y. Fukutai1 (1.Univ. Ryukyu, 2.JICA, 3.ZARI)	314 The petunia vein clearing virus genome encodes a suppressor against cosuppression ☆Kitagawa, T. I., H. Sobue1, K. Oguri1, M. Yuhazu1, T. Fukuhara2, A. Kanazawa1 (1.Res. Fac. Agr., Hokkaido Univ., 2.Dept. Appl. Biol. Sci., Tokyo Univ. Agr. Tech.)	414 Trials to isolate the mutants from the plastid genome random-mutagenized populations ☆Kosaka, N. I., Y. Harada1, I. Nakazato1, M. Okuno2, T. Itoh3, N. Tsutsumi1, S. Arimura1 (1.Grad. Sch. Agri. and Life Sci., Univ. Tokyo, 2.Sch. Med., Univ. Kurume, 3.Sch. Life Sci. and Tech., Inst. Science Tokyo)	514 An approach to classifying heat tolerance ranks in rice cultivars using a model for estimating chalky grain percentage and field trials ○Wakatsuki, H. I., Y. Suzuki2, M. Hirayama2, H. Ishikawa2, T. Nakano2, T. Hasegawa1 (1.Institute for Agro-Environmental Sciences, NARO, 2.Plant Biotechnology Institute, Ibaraki Agricultural Center)	614 Variation in carotenoid composition among yellow-fleshed potato varieties ☆Ishizu, Y. I., A. Endo1, H. Sasaki2, T. Igarashi2, T. Yamada1 (1.Res. Fac. Agr., Hokkaido Univ., 2.Calbee Potato, Inc.)	714 Breeding of a new potato cultivar, "Kiyominori" for strach production with slightly strong resistance to Globodera pallida ○Akai, K. I., H. Nakajima1, I. Sakata1, S. Okamoto1,2, S. Tamiya1,3, K. Katayama1, E. Shimosaka1, K. Asano1 (1.Hokkaido Agricultural Research Center, NARO, 2.Center for Seeds and Seedlings, NARO, 3.Tohoku Agricultural Research Center, NARO)	10:00
10:15	115 Considerations on Crossing and Selection Strategies in Citrus Breeding Informed by Progeny Segregation Forecasts Based on Genomic Prediction Models ☆Kimura, S. I., M. Minamikawa2, K. Nonaka3, T. Shimizu3, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ., 3.NIFTS, NARO)	215 Identification of the Genetic region Responsible for Extremely Late Bolting in the Turnip Variety 'Tokinashikokabu' ☆Yano, S. I., A. Chowdhury1, M. Hara2, M. Sakemoto2, M. Shimizu3, H. Takagi2, R. Fujimoto1, K. Tonosaki4 (1.Grad. Sch. of Agri. Sci., Kobe Univ., 2.Faculty of Bioproduction Sci., Ishikawa Prefectural Univ., 3.Iwate Biotechnology Res. Center, 4.Kihara Inst. Biol. Res., Yokohama City Univ.)	315 Study of tissue-specific expression of pATPase in Phalaenopsis orchid ☆Tashiro, R. I., Y. Takahara2 (1.Grad.Sch.Materials Science and Bioengineering.,Nagaoka University of Technology, 2.Materials Science and Bioengineering.,Nagaoka University of Technology)	415 QTL-seq GUI: A user-friendly tool for QTL-seq analysis with click-based operation. ☆Sakemoto, M. I., M. Takata1, T. Segawa1, M. Oishi1, M. Yoshizumi1, Y. Machi1, T. Shiraya2, H. Takagi1 (1.Ishikawa Prefectural University, 2.Niigata Prefectural Agricultural Research Institute)	515 Quantitative evaluation of heat tolerance of rice based on re-analysis of nationwide field experiment data collected through systematic review ○Toda, Y., H. Wakatsuki, Y. Ishigooka, T. Hasegawa (Inst. Agro-Env. Sci., NARO)	615 Analysis of Vascular Browning and Differential Gene Expression in Japanese Pear 'Rinka' During Cold Storage ○Kawahigashi, H. I., H. Hayama1, H. Sakai2, S. Hirose3, M. Tatsukii1 (1.Institute of Fruit Tree and Tea Science, NARO, 2.Research Center for Advanced Analysis, NARO, 3.Institute of Agrobiological Sciences, NARO)	715 An in-house cultivar identification method and its application to local varieties of unknown origin ☆SANETOMO, R., A. Oriyama, K. Hosaka (Obihiro University of Agriculture and Veterinary Medicine)	10:15

		Chair: Wakana Tanaka (Hiroshima Univ.)	Chair: Daisuke Tsugama (Univ. Tokyo)	Chair: Etsuko Araki (NARO)	Chair: Toshihiro Hasegawa (NARO)	Chair: Ryo Ishikawa (Kobe Univ.)	Chair: Kotaro Akai (NARO)		
10:30	116	Genomic Predictions and genome wide association studies of first sprouting time in tea plant. ○Aoshima, C. I., J. Kawaki1, Y. Ishiguro2, A. Nagano3,4, T. Ikka2,5,6,7, H. Yamashita2,5,6,7 (1.Tea Res. Cent., Shizuoka Pref., 2.The United Graduate School of Agricultural Science, Gifu Univ., 3.BBBC, Nagoya Univ., 4.Institute for Advanced Biosciences, Keio Univ., 5.Grad. Agr., Shizuoka Univ., 6.Res. Inst. Green Sci. Tech., Shizuoka Univ., 7.Res. Inst. Tea Sci. Tech., Shizuoka Univ.)	216 Substitution of vernalization requirement allele in the diversification of cultivated beet ☆Oishi, M., R. Hayakawa, E. Taniguchi, K. Kitazaki, T. Kubo (Grad. Sch. Agr., Hokkaido Univ)	316 Two Stabiliser loci in Antirrhinum suppress Tam3 transposition via a novel mechanism ☆Wang, S. I., T. Yoshida2, K. Nakahara1, Y. Kishimai (1.Research Faculty of Agriculture, Uni. Hokkaido, 2.Grad. Sch. Agriculture, Univ. Hokkaido)	416 A study on the development of hybrid progeny in Helleborus ☆Miyakawa, R. I., K. Koizumi2, K. Kawamura2, S. Bang1, T. Ohnishi1 (1.Grad. Reg. Cre. Sci., Univ. Utsunomiya, 2.Giardino Kawamura Co.,Ltd.)	516 Flour quality studies using candidate lines for heat stress tolerance. ○Tanaka, H. I., Y. Shikoroi, M. Tsuboi1, Y. Gorai2,3, I. Tahir3,4, H. Tsujimoto4 (1.Fac. Agr., Tottori Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.ARC, Sudan, 4.ALRC, Tottori Univ.)	616 Analysis of regulatory mechanism of gene expression associated with heterosis for low-pH tolerance during early growth in sugar beet. ☆Yamada, K. I., H. Ogawa1, Y. Hiragori1, H. Matsuhira2, K. Kitazaki1 (1.Graduate School of Agriculture, Hokkaido Univ., Kyoto Univ., 2.NARO, HARC)	716 Chloroplast pangenomics traces back to the origin of domesticated melon ☆Shigita, G. I., M. Okuma2, N. Sogo3, T. Seiko4, C. Muto4, K. Tanaka5, K. Shimomura6, M. Sugiyama6, Y. Kawazu6, H. Ezura1, K. Naito4, N. Tomooka4, K. Kato2 (1.Life Environ. Sci., U. Tsukuba, 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 3.Grad. Sch. Environ. Life Sci., Okayama U., 4.Res. Center Genet. Resour., NARO, 5.Fac. Agr. Life Sci., Hirosaki U., 6.Inst. Veget. Flora. Sci., NARO)	10:30
10:45	117	Validating genomic prediction models of the first sprouting time for genomic selection in tea plant breeding population ○Kawaki, J. I., C. Aoshima1, Y. Ishiguro2, A. Nagano3,4, T. Ikka2,5,6,7, H. Yamashita2,5,6,7 (1.Tea Res. Cent., Shizuoka Pref., 2.The United Graduate School of Agricultural Science, Gifu Univ., 3.BBBC, Nagoya Univ., 4.Institute for Advanced Biosciences, Keio Univ., 5.Grad. Agr., Shizuoka Univ., 6.Res. Inst. Green Sci. Tech., Shizuoka Univ., 7.Res. Inst. Tea Sci. Tech., Shizuoka Univ.)	217 Changes in cytokinin content and sensitivity in frill mutants of Trenia ☆Mayuzumi, T. I., K. Ishii2, M. Hatashita3, K. Takagi3, M. Kojima4, Y. Takabayashi4, H. Sakakibara4,5, T. Higashiyama6, T. Abe7, Y. Kazama1,7 (1.Fac. Biosci. Biotech., Fukui Pref. Univ., 2.NIRS, QST, 3.Wakasa-wan Ener. Cent, 4.RIKEN Center for Sustainable Resource Science, 5.Department of Applied Biosciences, Graduate School of Bioagricultural Sciences, Nagoya Univ., 6.Department of Biological Sciences, Graduate School of Science, Tokyo Univ., 7.RIKEN Nishina Center)	317 The analysis of genes related Endornavirus replication in Oryza sativa ☆Masu, T., H. Naramoto, H. Moriyama (TUAT)	417 Effects of Seed Tuber Production Methods on Sprouting Stability in Double Cropping of the Potato Cultivar 'Shimaakari' and Its Breeding Significance ○Tanaka, Y. I., M. Sato2, S. Kashiwagi1 (1.Kagoshima Pref. Inst. for Agri., 2.Kagoshima Pref. College of Agri.)	517 Identification of Heat Stress-Related Genes Using Selfed Lines of Buckwheat ☆Mochizuki, R. I.,2, K. Fujino2, H. Shimura2 (1.KARC, NARO, 2.Res. Fac. Agr., Univ. Hokkaido)	617 Pyramiding root QTLs DRO1 and qRL6.1 maintains photosynthesis and increases rice yield in paddy fields ☆Iba, M. I.,2, Y. Arai-Sanoh1, R. Tanaka1, Y. Kitomi1, S. Teramoto1, K. Irie2, Y. Uga1 (1.NICS, NARO, 2.Tokyo Univ. Agr.)	717 Is there still native mulberry variety in Japan? ○Matsumura, H. I., K. Hirauchi2, S. Yoshinobu2, R. Shimizu2, M. Suzuki2, A. Mizoguchi2 (1.Gene Res. Ctr, Shinshu Univ., 2.Grad. Sch. Sci. Tech., Shinshu Univ)	10:45
Chair: Kosuke Hamazaki (RIKEN)									
11:00	118	Comparative analysis of genome-wide genotyping techniques in peanut ○Shirasawa, K. I., T. Tsugane2 (1.Kazusa DNA Res. Inst., 2.Chiba Pref. Agric. Forest Res. Center)	218 Improving rice lateral root development through understanding its auxin-dependent and independent regulatory pathways ☆DONG, Y. I., S. Kushida1, M. Kanao1, C. Wainaina2, P. Lipio1, Y. Inukai3 (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Dept. Hort. Food Sec., JKUAT, 3.ICREA, Nagoya U.)	318 Identification of Candidate Genetic Loci Associated with the Frequency of Chromosomal Mutations in an Nicotiana Interspecific Hybrid ☆Nakata, K. I., K. Nishimura2, S. Nagai3,4, T. Tezuka3, T. Yamada1 (1.United Grad. Sch. Agr., Tokyo U. Agr. Tech., 2.Grad. Sch. Env. Life Nat. Sci. Tech., Okayama Univ., 3.Grad. Sch. Agr., Osaka Metro. Univ., 4.Res. Inst. Env. Agr. Fish., Osaka. Pref.)	418 Effect of combing SD1 and SPIKE genes under unfavorable environmental conditions in rice (<i>Oryza sativa</i> L.) ☆SEKIMATA, G., R. MOCHIZUKI, Y. FUKUTA (Univ. Ryukyu,)	518 Identification of salt tolerant maize-wheat (<i>ZeaWheat</i>) and pearl millet-wheat (<i>CenchrusWheat</i>) cybrid lines produced through in vitro fertilization system ☆Nowroz, F. I., N. Onda1, A. Satoh1, T. Ishii2, T. Okamoto1 (1.Dept. Biol., TMU, 2.ALRC., Univ. Tottori)	618 Genetic analysis of pre-harvest sprouting resistance by using backcross population from bread wheat X spelt wheat ☆Diaz Suarez, L., S. Kamizawa, K. Yoshikawa, K. Inoshita, K. Onishi (Obihiro U. Agric.&Vet. Med.)	718 Genetic diversity analysis of Taro (<i>Colocasia esculenta</i> Schott) with a focus on Japanese cultivars ☆Iijima, Y. I., M. Ozeki2, Y. Mitsui1 (1.Grad. Sch. Agri., Tokyo Univ. Agri., 2.NODAI Genome Res. Ctr., Tokyo Univ. Agri.)	11:00
Chair: Yoshiaki Inukai (Nagoya Univ.)									
11:15	119	Genomic breeding research on fruit traits in persimmon cultivars ☆Horiuchi, A. I.,2, N. Onoue3, R. Matsuzaki3, K. Nishimura2, K. Shirasawa4, Y. Kubo2, K. Ushijima2, T. Akagi2, M. Minamikawa5 (1.Grad. Sch. Hort., Chiba Univ., 2.Grad. Sch. Environ. Life Nat. Sci., Okayama Univ., 3.Inst. Fruit Tree and Tea Sci., NARO, 4.Kazusa DNA Res. Inst., 5.IAAR, Chiba Univ.)	219 Genetic analysis of two kinds of asymmetric divisions during stomatal development in rice ☆Miya, M. I., H. Takanashi2, Y. Satoh1, J. Itoh2 (1.Natl. Inst. Genet., 2.Grad. Sch. Agri. & Life Sci., Univ. Tokyo)	319 Investigation of Rfmulti and the corresponding the cytoplasmic male sterility gene in <i>Triticum-Aegilops</i> allotplasmic lines ○Tsujimura, M. I., Y. Oshikawa1, M. Takenaka2, T. Terachi3, S. Takenaka1 (1.Fac. Agr., Ryukoku Univ., 2.Grad. Sch. Sci., Kyoto Univ., 3.Fac. Life Sci., Kyoto Sangyo Univ.)	419 A methodology of genetic analysis for phenotypic plasticity using unstable climate of the northern-limit regions of rice cultivation ○Ito, Y. (Green Evolution Lab.)	519 Elucidating the Na ⁺ influx mechanism into the uppermost fully expanded leaf in <i>Vigna luteola</i> ☆Iki, Y. I., F. Wang2, K. Tanoi3,4, K. Naito2 (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO, 3.Grad. Sch. Agr. and Life. sci., Univ. Tokyo, 4.Fukushima Inst. Res., Educ. and Innov. (F-REI))	619 Alterations in growth patterns following polyploidization of diploid wild strawberry ☆Tomioka, H., S. Bang, T. Kurokura, T. Ohnishi (Grad. Reg. Cre. Sci., Utsunomiya U.)	719 Evaluation of adaptability and quality characteristics of sweetpotato varieties in cold region ○Ishiguro, K. I., T. Kuranouchi2, Y. Kai3, T. Harai, S. Otsuka1, M. Nishinaka4, K. Taguchi4 (1.Hokkaido Agric. Res. Cent., NARO, 2.Inst. Crop Sci., NARO, 3.Kyushu Okinawa Agric. Res. Cent., NARO, 4.Cent. Reg. Agric. Res. Cent., NARO)	11:15

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