16 March (8:30-11:30) Oral Presentation Program

	Chair: Hiroki Takagi (Ishikawa Pref. Univ.)		Chair: Kotaro Miura (Fukui Pref. Univ.)		Chair: Yusuke Hosokawa (HRO)		Chair: Eigo Fukai (Niigata Univ.)		Chair: Kenta Shirasawa (Kazusa DNA)		
8:30	101	Development of "Pedigree Tracer (PEDIT)", a Web-Database system to support crop breeding in Hokkaido Research Organization (HRO) ☆Adegawa, S.1, K. Horikawa2, Y. Tanaka1, T. Suzuki3 (1.Central Agr. Exp. Stn., HRO, 2.Kamikawa Agr. Exp. Stn., HRO, 3.Agr. Res. Dept., HRO)	201	Development of multi-wavelength image analysis method for objective evaluation of seed quality of soybean ○Yamada, T.1, Y. Nanjo1, J. Sun2, E. Aoki1, K. Hirata1, S. Kato1, R. Yamazaki1, J. Yonemaru2, H. Nakamura1, G. Ishikawa1, A. Kaga1 (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)	301	Development of a predicting model for heading time and yield of a rice progeny population based on genomic information, meteorological and spatial effect. ○Goto, A.1,2, S. Taniguchi2, T. Hayashi2, S. Yabe1, K. Matsushita1, H. Kajiya-Kanegae2, M. Yano2, J. Yonemaru2 (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)	401	Resistance to the herbicide metribuzin conferred to Arabidopsis thaliana by targeted base editing of the chloroplast genome ☆Nakazato, I.1, W. Yamori1, H. Matsumura2, M. Okuno3, N. Tsutsumi1, S. Arimura1 (1.Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo, 2.Col. of Life Sci., Ritsumeikan Univ., 3.Sch. of Med., Kurume Univ.)	501	Variations in the novel fertility restorer gene, Rfs, of Ogura cytoplsmic male sterility in radish. ○Yamagishi, H.1, A. Fukunaga2, M. Takenaka3, T. Terachi2 (1.Professor Emeritus of Kyoto Sangyo Univ., 2.Fac. Life Sci., Kyoto Sangyo Univ., 3.Grad. Sch. Sci., Kyoto Univ.)	8:30
8:45	102	Improvement of Plant GARDEN, a portal site for plant genome information (FY2023, Q4 ver): Development of tools to use evolutionary information. ☆Ichihara, H.1, M. Yamada1, Y. Toda1, A. Nakaya2, S. Yamashita1, T. Shimizu1, S. Shirasawa1, M. Kohara1, H. Hirakawa1, Y. Nakamura1,3, T. Tanabata1, S. Tabata1, S. Isobe1 (1.Kazusa DNA Res. Inst., 2.Grad. Sch. Front. Sci., Univ. Tokyo, 3.Nat. Inst. Genet.)	202	Estimation of amylose content of white rice flour by near-infrared spectroscopy ○Araki, E.1, T. Umemoto1, K. Hori2 (1.Inst. Food Res., NARO, 2.Inst. Crop. Sci., NARO)	302	Estimating growth curves from fragmented time series measurements: application to citrus growth assesment ☆Kimura, S.1, M. Minamikawa2, K. Nonaka3, T. Shimizu3, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.IAAR, Chiba Univ, 3.NIFTS, NARO)	402	Rice lipid-related gene family, OsGELP, differentiated latitude-adapted haplotypes ☆LUBBA, K.1, K. YAMAMORI2, Y. KISHIMA1 (1.Grad. Sch. Agriculture, Univ. Hokkaido, 2.Grad. Sch. Agriculture, Univ. Kyoto)	502	Identification of a Temperature-Sensitive Male Sterility Factor ○Kawagishi-Kobayashi, M.1, A. Nishizawa-Yokoi1, M. Endo1,4, T. Nunome2, H. Kato1,5, Y. Tozawa3 (1.Inst. Agrobiol. Sci., NARO, 2.Inst. Vegetable Floriculture Sci., NARO, 3.Grad. Sch. Sci. Eng., Saitama Univ., 4.present address: Takii co, 5.present address: Tokyo Univ. Agriculture)	8:45
9:00	103	A mutation database for 2,000 tobacco EMS lines by whole genome sequencing ○UDAGAWA, H., T. TAKEUCHI, Y. TAKAKURA (JAPAN TOBACCO INC. Leaf Tobacco Research Center)	203	Cloning of MP3 gene from a rice cultivar "Koshihikari" that forms an ideal plant architecuture and improves grain yield under climate change ○Takai, T.1, Y. Taniguchi2, M. Takahashi2, H. Nagasaki6, E. Yamamoto5, S. Hirose2, N. Hara2, H. Akashi3, J. Ito3, Y. Arai (Sanoh)2, K. Hori2, S. Fukuoka2, H. Sakai2, T. Tokida2, Y. Usui2, H. Nakamura7, K. Kawamura1, H. Asai1, T. Ishizaki1, K. Maruyama1, K. Mochida4, N. Kobayashi1,2, M. Kondo2,8, H. Tsuji3,8, Y. Tsujimoto1, T. Hasegawa2, Y. Uga2 (1.JIRCAS, 2.NARO, 3.Yokohama City Univ., 4.RIKEN, 5.Meiji Univ., 6.Kazusa DNA Research Institute, 7.Taiyo Keiki Co. Ltd., 8.Nagoya Univ.)	303	Genomic prediction of fruit shape using elliptic Fourier descriptors in pepper ☆Kumanomido, Y.1, K. Matsushima2, M. D'Andrea3, V. Palombo3, K. Nemoto2, F. Kondo3,4,5 (1.Grad. Sch. Sci. Tech., Univ. Shinshu, 2.Inst. Agric. Acad. Assay. Fac., Univ. Shinshu, 3.Fac. Agric., Univ. Molise, 4.Grad. Sch. Med. Sci. Tech., Univ.Shinshu, 5.JSPS Research Followship for Young Scientists)	403	Genetic progress for anther and stigma morphology under different nitrogen fertilization regimes of cultivars released during past 109 years in Japan ○Shimono, H.1,2, R. Sato1, A. Abe3, H. Nishio4,5, H. Kudoh5 (1.Fac.Agric., Iwate Univ., 2.Agri.Innov.Center, Iwate Univ., 3.Iwate Biotech. Res. Center, 4.Data Sci. AI Innov.n Res.Prom. Cent., Shiga Univ., 5.Cent. Ecol. Res., Kyoto Univ.)	503	Protein analysis of temperature-sensitive male sterility factor ☆Tozawa, Y.1, Y. Takani1, T. Tezuka1, H. Suda1, K. Atsuzawa2, A. Nishizawa-Yokoi3, Y. Kaneko4, M. Toyota1, M. Kawagishi-Kobayashi3 (1.Grad.Sch.Sci.&Eng., Saitama Univ., 2.Comprehensive Anal. Centr. for Science, 3.Inst. Agrobiol. Sci., NARO, 4.Fac. Liberal Arts)	9:00
9:15	104	Development of a novel alignment-free approach for investigating past hybridizations ☆Minoji, K.1, T. Sakai1, A. Ohta1, Y. Sugihara2, A. Kudoh1, R. Terauchi1,3 (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.IBRC)	204	Characteristics of paddy rice lines introduced with the DENSE AND ERECT PANICLE 1 (DEP1) gene in Hokkaido. ○Kinoshita, M.1, K. Douman2, K. Horikawa1, Y. Yamashita2, S. Adegawa2, C. Souma2 (1.Kamikawa Agr. Exp. Stn., HRO, 2.Central Agr. Exp. Stn., HRO)	304	Development of a sweet potato spoilage risk detection system trained from 3D data ○Taguchi, K.1, K. Kodama2, M. Nishinaka1, H. Inoue3, W. Guo2, Y. Nishiba3 (1.NARO CARC, 2.Univ. Tokyo, 3.NARO KARC)	404	Field trials of barley core collections in stressed soils with different pH ○Hisano, H., H. Shirato (IPSR, Okayama University)	504	The gene responsible for cytoplasmic male sterility in Oryza glaberrima with the cytoplasm of Taichung 65 is orf288 ☆Igarashi, K.1, Y. Iwai1, A. Takatsuka1, T. Kazama2, S. Arimura3, K. Toriyama1 (1.Grad.Sch. Agri. Sci., Tohoku Univ., 2.Fac. Agri. Sci., Kyusyu Univ., 3.Grad.Sch. Agri. Life Sci., Univ. Tokyo)	9:15
9:30											9:30

	Chair: Tomoki Hoshino (Yamagata Univ.)		Chair: Toshiyuki Takai (JIRCAS)		Chair: Kazunori Taguchi (NARO)		Chair: Hiroshi Hisano (Okayama Univ.)		Chair: Makiko Kawagishi (NARO)		
9:30	105	Development of KASP markers for the potato virus Y resistance gene Rychc using whole-genome resequencing data.	205	Field trial test of Gn1a knockout rice line aiming enlarged sink capacity by genome-editing. II. When “IR64” is used as the original variety.	305	Image Selection of Planted seedlings from Strawberry Crossbreeding seedlings through Machine Learning	405	Analysis of the regulatory mechanism of Ghd7 expression using rice with upstream deletion by genome editing	505	Identification of hybrid sterility gene S13 detected in African wild rice, Oryza longistaminata	9:30
		○Asano, K.1,2, J. Endelman2 (1.HARC, NARO, 2.University of Wisconsin–Madison)		○Komatsu, A.1, M. Ohtake1, M. Nagata1, H. Kato2, M. Kondo3 (1.Institute of Agrobiological Sciences, NARO, 2.Institute of Crop Science, NARO, 3.Graduate School of Bioagricultural Sciences, Nagoya University)		○Yamada, H.1, T. Kawata1, S. Mochizuki1, Y. Nomura2, H. Mineno2 (1.Shizuoka Pref. Res. Inst. Agri. Forest . Station, 2.Fac. Inform., Dept. Comp. Sci., Shizuoka Univ.)		○Ogo, Y.1, H. Itoh2, K. Naito3, T. Izawa4 (1.NIVFS, 2.NICS, 3.NGRC, 4.Grad. Sch. Agr. Life Sci., Univ. Tokyo)		☆Takanishi, W., Z. Mar Myint, Y. Kishima, A. Kanazawa, Y. Koide (Graduate School of Agriculture, Hokkaido University)	
9:45	106	DNAMarkMaker: developing ARMS and CAPS marker development from resequencing data with NGS short reads	206	Genetic characterization of an Indica Group rice variety Supa in Zambia	306	Selection method of a high milling yield soft wheat by multispectral imaging analysis of cross-sections of wheat grains.	406	Transcriptional control of a floral repressor gene Ghd7 by distal cis-regulatory elements	506	SDV1 and SDV2, duplicate genes involved in the seed development in the AA genome Oryza species.	9:45
		☆Saiga, S.1, T. Segawa1, M. Takata1, R. Kumazawa1, M. Hara1, H. Yamakawa2, H. Takagi1 (1.Ishikawa Prefectural University, 2.NICS,NARO)		○Fukuta, Y.1, T. Sato2, K. Toriyama2, H. Kobayashi1, N. Nagano1, R. Mochizuki1 (1.University of the Ryukyus, 2.Tohoku University)		○Kato, K., T. Ikeda, Y. Ban, K. Kawaguchi, M. Ito (Western Region Agricultural Research Center, NARO)		☆Kawauchi, T.1, Y. Ogo2, M. Mimura3, T. Izawa3 (1.Faculty of Agriculture, Univ. Tokyo, 2.NIVFS, 3.Grad. Sch. Agr. Life Sci., Univ. Tokyo)		☆Shibata, Y.1, D. Toyomoto2, M. Uemura3, S. Taura4, T. Sato5, R. Henry6, R. Ishikawa7, K. Ichitani2,8 (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.United Grad. Sch. Agr. Sci., Kagoshima Univ., 3.Grad. Sch. Agr., Kagoshima Univ., 4.Inst. Gene Res., Kagoshima Univ., 5.Grad. Sch. Agr., Tohoku Univ., 6.QAAFI, Univ. of Queensland, 7.Fac. Agr. and Life Sci., Hirosaki Univ., 8.Fac. Agr., Kagoshima Univ.)	
10:00	107	QTL analysis for petal length using interspecific crosses among Eustoma species.	207	Detection of QTLs controlling internode elongation pattern using rice dwarf mutants d1 (No.1)	307	Breeding selection criteria for grain size of high-yielding indeterminate Soybeans in Hokkaido, Japan.	407	Understanding of molecular mechanisms on lateral root development by our1 mutation and its application to further root system improvement in rice	507	Overcoming the hybridization barrier in interspecific hybrid seeds from a cross between Oryza sativa and O. officinalis using the Osemf2a mutant.	10:00
		○Kawakatsu, K.1, A. Nagano2, N. Fukuta1, T. Kawakatsu3 (1.NIVFS, NARO, 2.Fac. Agr., Ryukoku Univ., 3.Inst Agrobiological Sci, NARO)		☆Moe, S.1, T. Ha1, V. Reyes1, K. Doi1, K. Miura2, A. Maeno3, K. Tsuda3,4, K. Nagai5, M. Ashikari5 (1.Graduate School of Bioagricultural Sciences, Nagoya University, 2.Faculty of Biotechnology, Fukui Prefectural University, 3.National Institute of Genetics, 4.Graduate University for Advanced Studies, 5.Bioscience and Biotechnology Center, Nagoya University)		☆Igarashi, H.1, A. Kaga2, N. Yamaguchi3 (1.Tokachi Agr. Exp. Stn., HRO, 2.Inst. Crop Sci., NARO, 3.Central Agr. Exp. Stn., HRO)		☆Dong, Y.1, M. Kanao1, C. Wainaina2, P. Lipio1, Y. Inukai3 (1.Grad. Sch. Bioagr., Nagoya U., 2.Dept. Hort. Food Sec., JKUAT, 3.ICREA, Nagoya U.)		☆Sakurai, F.1, K. Tonosaki1, H. Furuumi2, Y. Sato2, T. Kinoshita1 (1.KIBR, Yokohama City Univ., 2.NIG)	
				Chair: Satoshi Okada (Nagoya Univ.)							
10:15	108	Identification of the pigment and causative gene for reddish seed coat in soybean	208	Detection of QTLs controlling internode elongation pattern using rice dwarf mutants d1 (No.2)	308	Evaluating the suitability for mechanical harvesting of adzuki beans and consideration of ideal plant architecture	408	Do microspores of rice anther have the callus formation ability?	508	Phylogenetic analysis of Capsicum using SSR markers and investigation of reproductive isolation including hybrid weakness in interspecific hybridization.	10:15
		☆Suganami, M.1, S. Kojima2, H. Yoshida1, H. Takahashi1,3, N. Nihei1,3, T. Matsuda1,3, M. Watanabe4, M. Matsuoka1 (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Graduate School of Agricultural Science, Tohoku University, 3.Department of Agriculture, Fukushima University, 4.Graduate School of Life Sciences, Tohoku University)		☆Ha, T.1, S. Moe1, V. Reyes1, K. Doi1, K. Miura2, A. Maeno3, K. Tsuda3,4, K. Nagai5, M. Ashikari5 (1.Graduate School of Bioagricultural Sciences, Nagoya University, 2.Faculty of Biotechnology, Fukui Prefectural University, 3.National Institute of Genetics, 4.Graduate University for Advanced Studies, 5.Bioscience and Biotechnology Center, Nagoya University)		☆Hosokawa, Y.1, K. Yoshida1, K. Sekiguch1, H. Nagasawa1, K. Shirasawa2, N. Yamaguchi3 (1.Tokachi Agr. Exp. Stn., HRO, 2.Kazusa DNA Res. Inst., 3.Central Agr. Exp. Stn., HRO)		☆Xu, M.1, N. Kudo1, C. Nachilima1, K. Miyamoto1, J. Kim2, Y. Kishima1 (1.Grad. Sch. Agriculture., Univ. Hokkaido, 2.Grad. Sch. Agricultural and Life Sci., Univ. Tokyo)		☆Seko, S., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)	

Chair: Kyoko Kawakatsu (NARO)

10:30	109	Identification of QTLs associated with good eating quality in Dadachamame and estimation of responsible genes for these QTLs ☆Shioya, N.1, S. Yokoyama2, Y. Takagi1, A. Miyagi1,2, M. Kawai-Yamada3, E. Ogiso-Tanaka4, T. Hoshino1,2 (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ., 3.Grad. Sch. Sci. Eng., Saitama Univ., 4.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci.)
10:45	110	MSH1 is involved in Mitochondrial Genome Repair through Introduction of Double-Strand Breaks around Mismatched Base Pairs. ☆zhou, c., N. Tsutsumi, S. Arimura (Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo)
11:00	111	Does gene dosage compensation occur in Arabidopsis chromosomes? Ikoma, T.1, R. Nishijima2, M. Ikeda1,2, A. Nagalla3, T. Abe3, ○Y. Kazama1,2,3 (1.Grad. Sch. Biosci. Biotech., Fukui Pref. Univ., 2.Dep. Biosci. Biotech., Fukui Pref. Univ., 3.RIKEN Nishina Cent.)
11:15		

209	Genetic differentiation of safflower genetic resources revealed by variation analysis in chloroplast trnF region ☆Hosono, K.1, S. Kimura2, H. Suzuki2, T. Sasanuma1,2 (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ.)
210	Is NEKODE in foxtail millet caused by transposon-insertion into the YABBY gene? ○Fukunaga, K.1, N. Abe1, A. Abe2, M. Hamashita1, I. Watanabe1 (1.Faculty of Bioresource Sci., Pref. U. Hiroshima, 2.Iwate Biotech.Res.Center)

Chair: Keita Kato (NARO)

309	Genome region associated with resistance to brown stem rot in adzuki bean derived from "Akamame" ○Sato, K.1, H. Nagasawa2, S. Adegawa1, C. Souma1, T. Suzuki1,3 (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO, 3.Agr. Res. Dept., HRO)
310	Useful wheat leaf rust resistance genes in Hokkaido and evaluation of near-isogenic lines carrying the resistance gene Lr34 ☆Doman, K.1, S. Ohnishi2, H. Jinno1,2, S. Maeno1, C. Souma1, T. Sonoda2, H. Ito3, A. Nakamaru3, S. Ikenaga3, K. Hatta4,5 (1.Central AES, HRO, 2.Kitami AES, HRO, 3.TARC, NARO, 4.HARC, NARO, 5.NICS, NARO)
311	Evaluation and genetics of bacterial blight resistance of rice mutant lines induced by ion beam irradiation ☆Takahashi, R.1, K. Kato1, Y. Maeda1, Y. Shibata1, Y. Gatayama2, S. Taura3, K. Ichitani4 (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.KIAD Tokunoshima, 3.Inst. Gene Res., Kagoshima Univ., 4.Fac. Agr., Kagoshima Univ.)
312	Breeding of cracked tolerant rice and added valuable traits as giant embryo and high content of saturated fatty acid ○Ishikawa, R., L. Dinh Thi (Fac. Agri. and Life Sci.m Hirosaki Univ.)

Chair: Yuko Ogo (NARO)

409	Functional analysis of Trehalose-6-Phothphate Synthase 1 during rice embryogenesis ☆Homma, D.1, T. Tezuka3, M. Nosaka-Takahashi2,3, M. Okada1, K. Okazaki1, Y. Sato2,3, E. Fukai1 (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Plant Genet., Natl. Inst. Genet., 3.Sch, Life Sci.,Grad. Univ. Adv. Study/SOKENDAI)
410	Analysis of transcription factors and downstream genes involved in the regulation of tomato fruit set ☆Nomura, Y.1, Y. Lu2, K. Harada1, Y. Shinozaki2, H. Enomoto3, 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)
411	Producing transformants for identifying a yet-to-be discovered gene associated with southern root-knot nematode resistance in sweetpotato ☆Izumitani, M.1, M. Otani2, O. Nakayachi2, H. Tabuchi3, H. Nishida1, K. Kato1, K. Nishimura1, Y. Monden1 (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 2.Res. Inst. Biore. Bioen., Ishikawa Pref. U., 3.KARC/NARO)
412	Development of transformation method and tissue culture system toward gene editing in sweetpotato cultivar J-Red ☆Nakamura, S.1, M. Izumitani2, M. Otani3, H. Matsui2, H. Tabuchi4, K. Nishimura2, H. Nishida2, K. Kato2, Y. Monden2 (1.Fac. Agri., Okayama Univ., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 3.Res. Inst. Biore. Bioen., Ishikawa Pref. Univ., 4.KARC/NARO)

Chair: Keisuke Igarashi (Tohoku Univ.)

509	Genetic mapping of the HLA1 locus, a gene causing hybrid lethality, in Nicotiana interspecific hybrids by bulked segregant RNA-Seq ☆Nagai, S., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)	10:30
510	Cell biotechnology utilizing developmental and reproductive regulators. ○Igawa, T.1,2,3, Y. Sato1, B. Pratama1, S. Koyama1, A. Yoshimura1 (1.Grad. Sch. Hort., Chiba Univ., 2.Plant Mol. Sci. Cent., Chiba Univ., 3.Res. Cent. Space Agr. Hort., Chiba Univ.)	10:45
511	Involvement of plasma membrane H+-ATPase in female papilla cells in the control of pollen hydration in Brassicaceae. ☆Hayashi, M.1, K. Fukushima1, H. Masuko-Suzuki1, T. Kinoshita2,3, S. Inoue2, S. Takayama4, Y. Takada1, M. Watanabe1 (1.Grad. Sch. Life Sci., Tohoku Univ., 2.Grad. Sch. Sci., Nagoya Univ., 3.ITbM, Nagoya Univ., 4.Grad. Sch. Agric. Life Sci., Univ. Tokyo)	11:00
512	Modification of W14 medium for wheat anther culture and validation of its applicability to wheat breeding in Hokkaido. ○Maruta, T.1, K. Satou2, K. Tomita2, C. Souma2, M. Okuyama3, T. Suzuki4 (1.Donan AES , HRO, 2.Central AES, HRO, 3.Tokachi AES, HRO, 4.Agri. Res. Dept, HRO)	11:15
		11:30

17 March (13:15-16:00) Oral Presentation Program

	Chair: Takanori Yoshikawa (NIG)		Chair: Mao Suganami (Fukushima Univ.)		Chair: Asako Kobayashi (Fukui Agri. Exp. Stn.)		Chair: Katsuhiro Shiono (Fukui Pref. Univ.)		Chair: Satoshi Watanabe (Saga Univ.)	
13:15	I13	Identification of novel QTLs for heading date and lodging resistance using a population derived from a cross between temperate japonica rice in Japan ☆Chigira, K.1, M. Yamasaki2, S. Adachi1, T. Ookawa1 (1.Graduate School of Agriculture, Tokyo University of Agriculture and Technology, 2.Graduate School of Science and Technology, Niigata University)	213	A loss-of-function mutation in the ortholog of soybean maturity gene E3 detected in early maturing cultivars of common beans ○Yamaguchi, N.1, K. Tanaka2, A. Hosoi3, K. Nakagawa4, H. Sato4 (1.Central Agr. Exp. Sta., HRO, 2.Tokyo Univ. of Info. Sci., 3.Genome Research Center, Tokyo Univ. of Agri., 4.Tokachi Agr. Exp. Sta., HRO)	313	"Maitebo", a new otebo bean variety with resistance to lodging and less leaf retention at maturity ○Nakagawa, K.1, Y. Horiuchi1, H. Sato1, H. Nagasawa1, M. Okuyama1, H. Sato2, S. Hagihara1, N. Yamaguchi2, Y. Saito3 (1.Tokachi Agri. Exp.Sta., HRO, 2.Central Agri. Exp.Sta., HRO, 3.Kamikawa Agri. Exp.Sta., HRO)	413	A frame-shift mutation of InCO presumed to be necessary for Japanese morning glory to spread over temperate Asia Katsuyama, H.1,5, K. Ezura1,6, A. Hoshino2,3, E. NItasaka4, ○T. Kuboyama1 (1.Col. Agr. , Ibaraki U., 2.National Inst. Basic Biol., 3.SOKENDAI, 4.Grad. Sch. Sci., Kyushu U., 5.Fac. Life Environ. Sci., U. Tsukuba, 6.Pref. Gov., Ibaraki Pref.)	513	Effect of loci related to below-ground tuber pigmentation in the turnip cv. 'Akamaru' on the phenotype of progeny crossed with non-pigmented below-ground turnip ☆Segawa, T.1, K. Miyaki1, K. Tonosaki2, R. Kumazawa1, M. Hara1, S. Saiga1, M. Takata1, H. Takagi1 (1.Ishikawa Prefectural University, 2.Yokohama City University)	13:15
13:30	I14	QTL analysis for aphid resistance in sorghum ☆Inui, R., M. Ishimori, H. Tanaka, A. Makino, J. Yamada, N. Tsutsumi, H. Takanashi (The University of Tokyo / Graduate School of Agricultural and Life Sciences)	214	Genome-wide association study of resistance to Phytophthora stem rot of Adzuki bean, using phenotyping data obtained by breeding programs ☆Horikawa, K.1, M. kayamori1, K. Shirasawa2, N. Yamaguchi3, C. Souma3, K. Sato3, M. Nagahama1, R. Ogura4, O. Fujine5, K. Todai6, n. Murata6, H. Nagasawa6, Y. Horiuchi6 (1.Kamikawa Agri. Exp. Stn., HRO, 2.Kazusa DNA Res. Inst., 3.Central Agri. Exp. Stn., HRO, 4.Kitami Agri. Exp. Sta., HRO, 5.Ornamental plant & Veg. Res. Ctr., HRO, 6.Tokachi Agri. Exp. Sta., HRO)	314	Breeding of a new sweetpotato cultivar for table use, “Benihinata”, with strong resistance to sweetpotato foot rot, and selecting of its virus-free lines ○Kawata, Y.1, T. Sakaigaichi1, K. Suematsu1, Y. Kai1, T. Sakai1, Y. Takahata1, M. Enomoto2, A. Kobayashi1 (1.KARC, NARO, 2.Kaneko Seeds Co., Ltd.)	414	Developmental analysis of rice shoot apical meristem by microtubule imaging and depolymerization ☆Takata, R.1, M. Tanaka1, H. Takeuchi2, D. Maruyama1, J. Ito1, H. Tsuji1,3 (1.KIBR, Yokohama City Univ., 2.ITbM, Nagoya Univ., 3.BBC, Nagoya Univ.)	514	Functional characterization of Stach Synthase in Cassava tuberous root ☆Utsumi, Y.1, C. Utsumi1, M. Tanaka1,2, T. Tsuchihashi3, H. Fujihara3, M. Seki1,2,4 (1.RIEKN CSRS, 2.RIKEN CPR, 3.Matsutani Chemical Industry Co., Ltd., 4.KIBR, Univ. Yokohama City)	13:30
13:45	I15	Mapping of genes controlling prostrate trait of barley using high-density linkage map ☆Nishimura, K.1, M. Okuma2, N. Fukushima2, Y. Monden1, H. Nishida1, K. Kato1 (1.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ., 2.Grad. Sch. Environ. Life Sci., Okayama Univ.)	215	Application of Genome-Wide Association studies and Genomic selection to potato breeding. ○Shinada, H.1, N. Yamaguchi2, K. Shirasawa3 (1.Kitami Agr. Exp. Sta., HRO, 2.Central Agr. Exp. Sta., HRO, 3.Kazusa DNA Res. Inst.)	315	Identification of sweetpotato cultivar 'Benihinata' using DNA markers based on cultivar-specific InDels ○TANAKA, M., Y. Kawata, A. Kobayashi (Kyushu Okinawa Agr. Res. Cent., NARO)	415	Epigenetic modification analysis using single-cell resolution 3D immunostaining for rice shoot apical meristem ☆Morishita, Y.1, R. Takata2, A. Yoshida2, A. Higo2, H. Tsuji3 (1.Sch Agri, Nagoya Univ., 2.KIBR, Yokohama City Univ., 3.BBC, Nagoya Univ.)	515	Natural variation in rice mitogen-activated protein kinase 4 contributes to improve photosynthesis rate in the field. ☆Ueda, T.1, S. Adachi2, K. Sugimoto1, Y. Taniguchi1, T. Hirasawa2, T. Yamamoto1,3, J. Tanaka1,4 (1.NARO, 2.Tokyo University of Agriculture and Technology, 3.Okayama University, 4.University of Tsukuba)	13:45
14:00			216	Design and validation of genomic prediction models for fruit traits to improve the efficiency of the sweet cherry breeding program ☆Shimada, N.1, K. Shirasawa2, N. Yamaguchi1, M. Sato1, M. Yoshida1 (1.Central Agr. Exp. Sta., HRO, 2.Kazusa DNA Res. Inst.)	316	Genome analyses of Japanese Azuki beans ○Ota, T.1, H. Nasu2 (1.RCIES, SOKENDAI, 2.Ctr. Fund. Edu., Okayama Univ. Sci.)	416	Cell biological analysis of stem cell activity and cell death during abortion of the barley inflorescence ☆Matsumoto, H.1, J. Ito1, Y. Nomura1, M. Wakazaki2, M. Sato2, N. Takeda-Kamiya2, D. Saisho3, K. Toyooka2, H. Tsuji1,4 (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Bioscience and Biotechnology Center, Nagoya Univ.)	516	Genetic interactions of starch-related mutations differ between endosperm and pollen ○Matsushima, R.1, H. Hisano1, M. Rose2, ジ. キム1,3, F. Brendan2, N. Oitome4, S. David2, N. Fujita4, K. Sato1 (1.Institute of Plant Science and Resources, Okayama University, 2.John Innes Centre, 3.RIKEN Center for Sustainable Resource Science, 4.Faculty of Bioresource Sciences, Akita Prefectural University)	14:00
14:15										14:15

Chair: Ken Naito (NARO)

14:15	I17	Comparative genomic context analysis for the somaclonal evolution of Satsuma mandarin (Citrus unshiu) ☆Matsuda, T.1, K. Masuda1, I. Henry2, L. Comai2, T. Akagi1 (1.Graduate School of Environmental, Life, Natural Science and Technology, Okayama University, 2.Department of Plant Biology and Genome Center, University of California Davis)
14:30	I18	Evolutionary dynamics of giant sex chromosomes in the genus Silene ○Akagi, T.1, N. Fujita1, K. Masuda1, K. Shirasawa2, K. Nagaki3, A. Horiuchi1, E. Kuwada1, R. Kunou1, K. Nakamura3, Y. Ikeda3, K. Ushijima1, D. Charlesworth4 (1.Grad. Sch. Environ. Life Nat. Sci., Okayama Univ., 2.Kazusa DNA Res. Inst., 3.Inst. Plant Sci. Res., Okayama Univ., 4.Inst. Ecol. Evol., Univ. Edinburgh)
14:45	I19	"Tokoro": A rhizomatous crop cultivated in Tohoku-machi, Aomori Prefecture ☆Natsume, S.1, Y. Sugihara2, A. Kudoh3, K. Oikawa1, M. Shimizu1, Y. Ishikawa3, M. Nishihara1, A. Abe1, H. Innan4, R. Terauchi1,3 (1.Iwate Biotechnology Research Center, 2.The Sainsbury Laboratory, University of East Anglia, 3.Crop Evolution Laboratory, Kyoto University, 4.Research Center for Integrative Evolutionary Science, The Graduate University for Advanced Studies)

Chair: Tomoyuki Furuta (Okayama Univ.)

15:00	I20	Genome analysis of allotetraploid wasabi (Eutrema japonicum) ○Tanaka, H.1, N. Masahiro1, A. Toyoda2, K. Yamane3, T. Itoh1 (1.Tokyo Inst. Tech. LST., 2.Nat. Inst. of Gen. Comp. Genome., 3.Gifu U. App. Bio. Sci.)
15:15	I21	Population structure analysis of Oryza rufipogon using large-scale sequencing ○Yoshikawa, T., Y. Sato (Nat. Inst. Genet.)
15:30	I22	Population Geonmics on the Origin of Azuki Bean ○Naito, K.1, C. Chih-Cheng2, C. Muto1, C. Lee2 (1.Res. Cntr. Genet. Resour., NARO, 2.Inst. Ecol. Evol. Biol., Natl. Taiwan Univ)
15:45	I23	Painting the genome. Watanabe, S.1, H. Yoshida2, ○A. Kobayashi1, N. Saka3, M. Suganami2, M. Matsuoka2 (1.Fukui Agri. Exp. Stn., 2.Fukushima Univ., 3.Nagoya Univ.)
16:00		

Chair: Naoya Yamaguchi (HRO)

217	Mutant alleles in the SSII gene that causes low-temperature gelatinization properties of starch in sweetpotato revealed by WGS using Nanopore long reads ☆Nakahara, T.1, I. Kataoka1, K. Shimo1, K. Tada2, M. Tanaka3, A. Kobayashi3, M. Izumitani4, K. Naito5, K. Nishimura4, H. Nishida4, K. Kato4, Y. Monden4 (1.Fac. Agri., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.KARC/NARO, 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 5.NGRC/NARO)
218	Identification of genetic region related to the anthocyanin accumulation in sweetpotato storage roots and sequence analysis of the candidate gene ☆Horita, N.1, Y. Okada2, H. Kanzaki1, M. Kurihara3, K. Nishimura1, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Sci., Okayama Univ.)
219	QTL analysis of shoot morphology traits in RIL population of green foxtail and coastal green foxtail Hira, D.1, K. Fukunaga2, ○T. Ohsako3 (1.Fac. Life Env. Sci., Kyoto Pref. Univ., 2.Fac. Bioresource Sci., Pref. Univ. Hiroshima, 3.Grad. Sch. Life Env. Sci., Kyoto Pref. Univ.)

Chair: Kentaro Horikawa (HRO)

220	Genetic study on the search for the gene responsible for the amaranth shattering trait ☆Fujihara, R.1, F. Kondo2,3, T. Mikoshiba4, K. Matushima5, K. Nemoto5 (1.Fac. Agric., Univ. Shinshu, 2.Grad. Sch. Med. Sci. Tech, 3.JSPS Research Fellowship for Young Scientists, 4.Grad. Sch. Sci. Tech., Shinshu U, 5.Inst. Agric. Acad. Assy. Fac., Shinshu U)
221	Search for strawberry powdery mildew race1 resistance loci using genome wide association studies. Ebihara, Y., ☆N. Inubushi (CAFRC)
222	Genome-wide association study for flowering time using small spray-type chrysanthemum varieties. ○Inazaki, F.1, K. Shirasawa2, S. Kurihara1,3, T. Gounai1 (1.Plant Biotech. Inst., Ibaraki Agri. Cent., 2.Kazusa DNA Res. Inst., 3.Hitachiomiya Dist. Agri. Dev. Ext. Cent.)
223	Production and indentation of an interspecific hybrid between Artemisia princeps and A. vulgaris ☆Xu, T., S. Yokoi, T. Tezuka (Grad. Sch. Agr., Osaka Metro. Univ.)

Chair: Shizen Ohnishi (HRO)

317	Breeding of [Sadowa] egg plant of a Miyazaki original vegetable ~ A new variety of [NANKYU SENSA No.4 GO] created by crossing between varieties and selection~ ○Chen, L., N. Emoto, T. Hiejima, S. Yoshizaki, N. Iwakiri, T. Oonishi, R. Nozaki, K. Takane, Y. Matsushita (Fac. Envir. Hort. Sci., Minami Kyushu U.)
318	Characteristics of intergeneric hybrids between marguerite and Roman chamomile, and breeding of a new variety: 'New Summer Stella'. ○Katsuoka, H.1, T. Fujii1, C. Kato1, F. Baba2, M. Taneishi1, T. Sasaki3 (1.Izu Agri. Res. Center, Shizuoka Pref. Res. Inst. Agri. Forest., 2.Kamo Agri. Forest. Office, 3.Fruit Tree Res. Center, Shizuoka Pref. Res. Inst. Agri. Forest.)
319	Hiroshige Utagawa had drown the original Someiyoshino tree 193 years ago ○Nakamura, I. (Grad. Sch. Hortic., Chiba Univ.)
320	Confectionery suitability of soft wheat lines carrying crab wheat-derived glutenin subunit genes with different combinations of SSIIa gene mutations ○Tougou, M.1, K. Hatta1, T. Okada1, H. Kojima1, M. Fujita2, M. Yamamori1, H. Matsunaka3, K. Nakamura2, T. Ikeda4 (1.Inst. Crop Sci., NARO, 2.HQ, NARO, 3.HARC, NARO, 4.WARC, NARO)

Chair: Yoshiyuki Yamagata (Kyushu Univ.)

321	Is the cytoplasm of Aegilops mutica useful for wheat breeding? ○Murai, K., Y. Watanabe, H. Tada (Dep. Sus. Agri., Fukui Pref. U.)
322	Exploration of introgressed regions between O. sativa ssp. Japonica and AA-genome species of the genus Oryza based on comparative genome analysis ○KOYANAGI, K.1, Y. Kotoku2, Y. Kishima3 (1.Faculty of Information Science and Technology, Hokkaido University, 2.Graduate School of Agriculture, Hokkaido University, 3.Research Faculty of Agriculture, Hokkaido University)
323	An early heading gene with indica genetic background widens rice cultivation area in Japan ○Dinh, T.1, Y. Ueda2, H. Saito2, R. Ishikawa1 (1.Faculty of Agriculture and Life Science, Hirosaki University, 2.JIRCAS)

Chair: Hiroyuki Tsuji (Nagoya Univ.)

417	Genetic variation in caryopsis types in the genus Triticum･Aegilops －comparisons to the genus Hordeum ○Taketa, S. (Institute of Plant Science and Resources, Okayama University)
418	Exploration of heading-time mutant genes by exome sequencing analysis in barley mutant lines ☆Takeda, S.1, M. Okuma2, C. Ibuki1, A. Mandozai3, K. Nishimura3, Y. Monden3, K. Kato3, H. Nishida3 (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)
419	Relationship of heading time-related genotype and heading-time instability in a barley RIL population ☆Okuma, M.1, K. Nishimura2, Y. Monden2, K. Kato2, H. Nishida2 (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

Chair: Takaki Yamauchi (Nagoya Univ.)

420	Identification of major loci involved in forming a constitutive barrier to radial oxygen loss in wild rice, Oryza glumaepatula ○Shiono, K.1, M. Ejiri1, R. Nishijima1, M. Baba1, H. Shiba1, Y. Yamagata2, K. Miura1 (1.Dept. Bioscience. Biotech., Fukui Pref. Univ., 2.Grad. Sch. Bioresouce Bioenviron. Sci., Kyushu Univ.)
421	Role of Jasmonic acid during secondary aerenchyma formation in soybean ☆Watanabe, K.1, Y. Baba1, A. Agata1, A. Toyoda2, Y. Sato2, M. Nakazono1, H. Takahashi1 (1.Grad.Sch.Bioagric.Sci., Univ. Nagoya, 2.National Institute of Genetics)

Chair: Ryo Matsushima (Okayama Univ.)

517	Alterations in DNA methylation during rice endosperm development ☆Uechi, M., K. Tonosaki, A. Ono, T. Kinoshita (Yokohama City University Kihara Institute for Biological Research)
518	Intraspecific comparison of ddm1 mutants in Arabidopsis thaliana Nishimura, K., K. Kunita, Y. Kamiya, ○R. Fujimoto (Grad. Sch. Agric. Sci.)
519	Exploration of CpG Methylation in Plant Mitochondrial DNA ☆ZHONG, Y.1, M. Okuno2, N. Tsutsumi1, S. Arimura1 (1.Grad. Sch. of Agri., Univ. Tokyo, 2.Kurume Univ. Sch. of Med.)

Chair: Ryo Fujimoto (Kobe Univ.)

520	Attempted excision of 641Kb Nuclear Mitochondrial DNA (NUMT) sequence in Arabidopsis thaliana chromosome 2 ☆ITO, Y., Y. Zhong, I. Nakazato, N. Tsutsumi, S. Arimura (Laboratory of Plant Molecular Genetics, Graduate School of Agricultural and Life Sciences, The University of Tokyo)
521	Development of a technology for induction of plant-organelle-genome-specific random mutagenesis by artificially-fused proteins. Evaluation of T1 plants. ☆Kosaka, N.1, 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., Tokyo Inst. Tech.)
522	Mutation in a novel soybean isoflavone O-methyltransferase (IOMT3) gene cause a accumulation of 6-hydroxydaidzein isoflavones. ○Watanabe, S.1, M. Horitani1, R. Yamada1, K. Taroura1, T. Anai2 (1.Fac. Agri., Saga Univ., 2.Fac. Agri., Kyushu Univ.)

14:15 14:30 14:45 15:00 15:15 15:30 15:45