20 March (9:00-11:30) Oral Presentation Program

	Chair: Yuki Monden (Okayama Univ.)		Chair: Hiroshi Hisano (Okayama Univ.)		Chair: Mai Minamikawa (Chiba Univ.)		Chair: Etsuko Araki (NARO)		Chair: Nobuhiro Suzuki (Sophia Univ.)		
9:00	101	Heading gene analysis for breeding early-heading rice lines in Saitama prefecture ☆Nakamura, Y., H. Koyama (Saitama Agricultural Technology Research Center)	201	Prototype of Generative AI to Plant Breeding Data. ○Kajiya-Kanegae, H.1,2, J. Yonemaru1 (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)	301	Estimation of tolerance to heat-induced quality decline of rice during ripening in a uniform temperature ☆Nakaoka, F.1,2, A. Kobayashi1, G. Chaya1, S. Watanabe1, Y. Morozumi1, H. Nakagawa3, M. Yamasaki3 (1.Fuku Agriculture Experimental Station, 2.Niigata University, 3.Reserch Center for Agricultural Information Technology, NARO)	401	Analysis of starch structure in different organs of rice with loss of starch synthase (SS) IIb function generated using CRISPR-Cas9 genome editing. ○Miura, S.1,2, H. Odajima1, S. Hirata3, N. Crofts4, R. Morita3, N. Fujita1,2 (1.Faclt. Biores., Akita Pref. Univ., 2.Starch Tecnologies Co., LTD, 3.The University of Tokyo, 4.National Institute of Technology, Akita College)	501	Genetic analysis of resistance to green rice leafhopper in the backcross progenies with the genetic background of African cultivated rice, Oryza glaberrima ☆Hironaka, R.1, T. Thein1, Y. Yamagata2, H. Yasui2 (1.Grad. Sch. Bioresour. Environ. Sci., Kyushu Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ.)	9:00
9:15	102	Comparative analysis of SNPs detected by three genome-wide genotyping technologies, ddRAD-Seq, GRAS-Di, and MIG-Seq ○Shirasawa, K.1, K. Mishima2, T. Iki2, T. Hirao3 (1.Kazusa DNA Res. Inst., 2.FFPRI FTBC TRBO, 3.FFPRI FTBC)	202	The Activation of Transposons Under Environmental Stress and Their Potential Applications in Breeding ○Ito, H. (Grad. Sch. Sci., Univ. Hokkaido)	302	Constructing prediction models for wheat yield by employing chronological transcriptome data and mining of yield-predictive genetic components ☆Kojima, H.1, S. Yoshioka1, S. Kimura2, S. Kinoshita2, K. Kuroki3, H. Iwata2, S. Nasuda1 (1.Grad. Sch. Agric., Kyoto Univ., 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.Grad. Sch. Sci., Univ. Tokyo)	402	Isoflavone content in seeds of soybean introduced with Soybean dwarf virus resistance gene Rsdv1 ☆Takahashi, H.1, H. Maeda2, N. Yamaguchi3 (1.Kamikawa Agr. Exp. Sta., HRO, 2.Hirosaki University, 3.Central Agr. Exp. Sta., HRO)	502	Functional analysis of quantitative blast resistance gene Pid3-I1 in rice ☆Abe, K., T. Ishihara, T. Inukai (Grad. Sch. Agric., Univ. Hokkaido)	9:15
9:30	103	A novel Fusarium head blight resistance allele derived from Japanese landrace at 2DL located QTL is more valuable than that derived from Sumai 3 ○Ohnishi, S.1, K. Horikawa2, K. Morita1, N. Yamaguchi2, C. Souma2, Y. Sato1, T. Sonoda1 (1.HRO Kitami AES, 2.HRO Central AES)	203		303	Genomic prediction of stalk lodging resistance and the associated intermediate phenotypes in maize ○Morota, G.1, C. Machado e Silva2, B. Kunduru3, C. McMahan3, D. Robertson4, R. Sekhon3 (1.Grad. Sch. Agr. Life Sci. Univ. Tokyo, 2.Federal University of Viçosa, 3.Clemson University, 4.University of Idaho)	403	Screening and evaluation of high protein content lines from a soybean mutant population. ○Ashikaga, N.1, H. Igarashi1, S. Kobayashi2, H. Takahashi3, K. Sato4, Y. Hosokawa2, N. Yamaguchi2 (1.Tokachi Agri. Exp. Stn., HRO, 2.Central Agri. Exp. Stn., HRO, 3.Kamikawa Agri. Exp. Stn., HRO, 4.Kitami Agri. Exp. Stn., HRO)	503	Fine Mapping and Identification of a Locus Conferring Resistance to Cucumber Mosaic Virus in Spinach ☆Wu, Y.1, H. Hirakawa2, C. Masuta3, Y. Onodera3 (1.Grad. Sch. Agr., Hokkaido Univ., 2.Res. Fac. Agr., Kyushu Univ., 3.Res. Fac. Agr., Hokkaido Univ.)	9:30
			Chair: Ayumi Agata (Nagoya Univ.)				Chair: Etsuo Shimosaka (NARO)				
9:45	104	TE insertion and constitutive expression of VmSOS1 in salt-tolerant species Vigna marina ○Naito, K.1, Y. Noda2, F. Wang1, C. Muto1, H. Ohashi3, H. Sakai4, N. Suzui2, Y. Yin2, Y. Miyoshi2, K. Enomoto2, N. Kawachi2, J. Furukawa5 (1.Res. Cntr. Genet. Resour., NARO, 2.Takasaki Inst. Adv. Quant. Sci., QST, 3.Grad. Sch. Adv. Sci., Univ. Tokyo, 4.Res. Centr. Adv. Anal., NARO, 5.Grad. Sch. Life. Environ. Sci., Univ. Tsukuba)	204	Narrowing down the CAD, casual gene of orange lemma mutation in barley ☆Kako, R.1, M. Morita2, N. Yamaji2, H. Hisano2, K. Sato1,2 (1.Grad. Sch. Agr., Setsunan Univ., 2.IPSR, Okayama Univ.)	304	Estimation of known gene effects via analysis of historical rice field experiment data ☆Chigira, K.1, E. Yamamoto1, A. Goto1, T. Ikegaya1, N. Suzuki1, Y. Kawahara2, M. Yamasaki3, K. Sugimoto1, K. Hori1 (1.Institute of Crop Science, NARO, 2.Research Center for Advanced Analysis, NARO, 3.Faculty of Agriculture, Niigata University)	404	Genotype-by-environment interaction (GEI) and yield stability of soybean genotypes in Hokkaido ☆Igarashi, H.1, N. Yamaguchi2 (1.Tokachi Agr. Exp. Stn., HRO, 2.Central Agr. Exp. Stn., HRO)	504	Dominant genes encoding resistance to soil-borne wheat mosaic virus in barley (Hordeum vulgare L.) ○Komatsuda, T. (Shandong Academy of Agricultural Sciences (SAAS) Crop Research Institute)	9:45

		Chair: Masayoshi Teraishi (Kyoto Univ.)				Chair: Gota Morota (Univ. Tokyo)				Chair: Tsuyoshi Inukai (Hokkaidou Univ.)	
10:00	105	Whole genome resequencing analysis of 96 diverse adzuki varieties: A step toward genome breeding in adzuki	205	Characterization of an A-to-G base editor in the Arabidopsis chloroplast genome	305	Development of a predicting model for the quality of brown rice based on genomic information and the temperature during the ripening period.	405	Genotype by environment interactions for grain yield observed among adzuki bean cultivars in Hokkaido	505	Mixed infections of wheat yellow mosaic virus (WYMV) and soil-borne wheat mosaic virus (SBWMV) reduce wheat yields.	10:00
		☆Adegawa, S.1, N. Yamaguchi1, C. Souma1, K. Shirasawa2 (1.Central Agr. Exp. Stn., HRO, 2.Kazusa DNA Research Institute)		☆Nakazato, I., Y. Tamura, R. Masuda, N. Tsutsumi, S. Arimura (Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo)		☆Suzuki, N.1, S. Taniguchi2, T. Hayashi2, K. Matsushita1, H. Kanegae1,2, H. Nakagawa2, A. Goto1,2 (1.Inst. Crop Sci., NARO, 2.Res. Ctr. Agric. Info. Tech., NARO)		☆Hosokawa, Y.1, H. Nagasawa2, N. Yamaguchi1, Y. Horiuchi2 (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO)		○Kurushima, M.1, T. Todai1, T. Sonoda2, S. Ohnishi2, M. Ishikawa3, H. Ishimura4 (1.Tokachi Agricultural Experiment Station, Hokkaido Research Organization, 2.Kitami Agricultural Experiment Station, Hokkaido Research Organization, 3.Tokachi Agricultural Extension Center, Hokkaido, 4.Agricultural Technologies and Extension Division, Hokkaido)	
10:15	106	Sex determination in Dioscorea tokoro, a dioecious wild yam species	206	Base editors using CRISPR-Cas3 in rice	306	Evaluation of Segregation Prediction Accuracy for Aboveground Traits Using Soybean RILs and Subsequent Progeny Populations	406	Development of 'Kitahonami'-derived wheat lines with breaking the linkage of resistance to wheat yellow mosaic disease and high-activity polyphenol oxidase.	506	The establishment of a method for inducing clubroot disease by local heating	10:15
		☆Kudoh, A.1, S. Natsume2, Y. Sugihara3, H. Katoh1, A. Abe2, K. Oikawa2, M. Shimizu2, K. Itoh2, M. Tsujimura4, T. Terachi5, T. Sakai1, A. Ohta1, R. Terauchi1 (1.Grad. Agri., Kyoto Univ., 2.IBRC, 3.The Sainsbury Laboratory, 4.Grad. Agri., Ryukoku Univ., 5.Faculty of Life Sciences, Kyoto Sangyo Univ.)		○Saika, H.1, K. Yoshimi2 (1.Inst. Agrobiological Sci., 2.Inst. Med. Sci., Univ. Tokyo)		☆Sakurai, K.1, Y. Toda2, H. Tsujimoto3, A. Kaga4, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Inst. Agro-Env. Sci., NARO, 3.Arid Land Res. Ctr., Tottori Univ, 4.Inst. Crop Sci., NARO)		○Kiuchi, H.1, T. Sonoda1, S. Adegawa2, N. Yamaguchi2, C. Souma2, S. Ohnishi1 (1.HRO Kitami AES, 2.HRO Central AES)		☆Haraguchi, K., S. Bang, T. Koyama, T. Ohnishi (Sch. Agr., Univ. Utsunomiya)	
								Chair: Satoko Miura (Akita Pref. Univ.)			
10:30	107	Whole-genome sequencing of sesame plants	207	Exploration of rice genes targeted by MEL1, a germ cell-specific Argonaute protein	307	Application of Random Forest in a Bayesian Optimization Framework: To propose optimal rice genotype and environment combinations	407	Variation in rice bran lipid content in high-yielding rice varieties and genetic resource lines	507	Response to low-fertilizer in the panicle architectures of cultivated rice	10:30
		Tanaka, H.1, E. Ono2, T. Segawa2, J. Murata3, H. Takagi4, Y. Uegaki5, H. Toyonaga3, A. Shiraishi3, M. Takagi6, A. Toyoda7, K. Sato8, T. Wakasugi8, M. Horikawa3, M. Kawase9, T. Itoh1, ○M. Yamamoto8 (1.School of Life Science and Technology, Institute of Science Tokyo, 2.Res. Inst. Suntory Global Innovation Center Ltd. (SIC), 3.Suntory Fdn. Life Sci. (SUNBOR), 4.Fac. Biores. Env. Sci., Ishikawa Pref. Univ., 5.Grad. Sch. Sci. Eng., Univ. Toyama, 6.Suntory System and Technology Ltd. (SST), 7.National Institute of Genetics, 8.Fac. Sci. Acad. Assem., Univ. Toyama, 9.Dep. Agr., Tokyo Univ. Agr.)		○Nonomura, K.1,2, H. Liu3, M. Mimura4, W. Wu3, R. Hiratsuka5, K. Tanaka6, M. Ohtani7, T. Demura8, S. Liu3, T. Sasaki9 (1.Plant Cytogen., Natl. Inst. Genet., 2.Genet. Program, SOKENDAI, 3.Zhejiang A&F Univ., 4.Grad. Sch. Agr. Life Sci, Univ. Tokyo, 5.Jikei Univ. Sch. Med., 6.Dept. Informatics, Tokyo univ. Info. Sci., 7.Grad. Sch. Front. Sci., Univ. Tokyo, 8.Div. Bio. Sci., Nara Inst. Sci. Tech., 9.NODAI Res. Inst., Tokyo Univ. Agr.)		☆Mochizuki, H.1, K. Hamazaki2, C. Sato3, A. Abe4, C. Kim5,6, H. Shimono5, H. Iwata1 (1.Grad. Sch. Agr. Life Sci., Univ., 2.Adv. Int. Proj., RIKEN, 3.Ifu-Rinrin, 4.Iwate Biotechnology Research Center, 5.Iwate University, 6.Sky Ocean Technology Co., Ltd. Sky Ocean Technology Co., Ltd.)		○Araki, E.1, T. Miyazawa2, T. Miyazawa2, R. Sogame2, Y. Ito3, K. Ebana4, K. Toriyama3 (1.Inst. Food Res., NARO, 2.New Indust. Creat. Hatchery Cent., Tohoku Univ., 3.Grad. Sch. of Agri. Sci., Tohoku Univ., 4.Inst. Gen. Resources Cent., NARO)		☆Ito, H.1, T. Mori1, K. Hasegawa1, M. Amano1, H. Yoshida2, S. Nishiuchi1, J. Murase1, M. Matsuoka2, H. Takahashi1, M. Nakazono1 (1.Grad. Sch. Bioagric. Sci., Nagoya Univ., 2.IFeS, Fukushima Univ.)	

	Chair: Masayuki P. Yamamoto (Univ. Toyama)		Chair: Hiroaki Saika (NARO)		Chair: Kiyosumi Hori (NARO)					Chair: Yoshiyuki Yamagata (Kyushu Univ.)		
10:45	108	Two QTLs that act additively to accelerate the flowering of Koshihikari and their interactions with meteorological environments.	208	Functional analysis of a KNOTTED1-like gene, a candidate for a gene regulating flowering in pearl millet	308	Potential assessment of genomics-assisted breeding using fruit morphological features of citrus	408	Trait analysis of the AGPase gene OsAGPL1 mutation in Non-Flowering Rice	508	Disruption of lipid-related gene alters pollen fertility, lipid accumulation, and cold tolerance in rice	10:45
		○Yonemaru, J.1, K. Wada1, S. Watanabe2 (1.NARO-RCAIT, 2.Fukui Pref. Government)		☆Kambara, K.1, S. Gupta2, T. Takano1, D. Tsugama1 (1.Grad. Sch. Agr., Univ. Tokyo, 2.ICRISAT)		☆Hironaga, K.1, T. Seino2, K. Nonaka3, T. Shimizu3,4, M. Minamikawa5 (1.Fac. Hort., Chiba Univ., 2.Grad. Sch. Hort., Chiba Univ., 3.NIFTS, NARO, 4.Kazusa DNA Res. Inst., 5.IAAR, Chiba Univ.)		☆Miyazaki, K., M. Suzuki, N. Nishide, S. Hashimoto, R. Morita, N. Aoki, T. Izawa (Grad. Sch. Agr. Life Sci., Univ. Tokyo)		☆Lubba, K.1, K. YAMAMORI2, Y. KISHIMA1 (1.Hokkaido University Graduate School of Agriculture, 2.Kyoto University Graduate School of Agriculture)	
11:00	109	Candidate genes for ratio of nodule bacteria species on soybean root	209	A CMF gene specific for sweetpotato and its wild relative are involved in storage roots formation in sweetpotato	309	Prediction of wheat milling yield based on the combination of multispectral image analysis, near-infrared spectrometry and morphometrics of grains	409	A new medium early maturing potato variety “Shinsei” suitable for long-term storage with good chipping quality	509	Effects of interaction between red rice genes Rd and Rc common to weedy rice on seed freezing tolerance	11:00
		○Teraishi, M.1, K. Sakaguchi1, T. Tsuchimoto1, T. Yoshikawa1,2 (1.Grad. Sch. Agri., Kyoto Univ., 2.Natl. Inst. Genet.)		☆Suematsu, K.1, R. Morita2, M. Otani3, R. Suzuki2, M. Tanaka1 (1.Kyushu Okinawa Agr. Res. Cent., NARO, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Fac. Biores. Env. Sci., Ishikawa Pref. Univ.)		☆Yoshioka, M., T. Ikeda, Y. Ban, M. Ito, K. Kawaguchi, T. Sugita, K. Kato (Western Region Agricultural Research Center, NARO)		○Shimosaka, E.1, S. Tamiya1,2, K. Asano1,3, S. Tsuda1, M. Nishinaka1,4, M. Mori1,5, A. Kobayashi1,6, N. Mukojima1,7, K. Akai1, S. Okamoto1,8, A. Takada1,9 (1.Hokkaido Agri. Res. Cent., NARO, 2.Tohoku Agri. Res. Cent., NARO, 3.AFFRC, MAFF, 4.Central Region Agri. Res. Cent., NARO, 5.Calbee Potato, Inc, 6.Kyushu Okinawa Agri. Res. Cent., NARO, 7.Nagasaki Agri. For. Dev, 8.Cent. for Seeds and Seedlings, NARO, 9.Headquarters, NARO)		☆Takama, R.1,2, J. Tanaka2,3 (1.Inst. Plant Protection, NARO, 2.Univ. Tsukuba, Grad. Sch. Sci. Tech., 3.Headquaters, NARO)	
11:15	110	Potato blight resistance QTNs revealed by GWAS using a historical phenotype dataset from the HRO breeding program	210	Prediction of targets for the Rf-like PPR gene cluster in the fertility-restored line RT98C derived from wild rice Oryza rufipogon W1109.	310	Identification and application of non-shattering genes in the mutant lines induced from an Indica Group variety, Nan-jing11	410	Approach to melon breeding from Miyazaki - Development of high-sugar and high-flavor F1 melon strains -	510	Elucidating salt-tolerant mechanisms in Vigna luteola by grafting and identifying salt tolerant gene candidates via root transcriptome	11:15
		○Sato, K.1, Y. Ishikawa1, T. Wazaki1, H. Shinada1, K. Shirasawa2, N. Yamaguchi3 (1.Kitami Agri. Exp. Stn., HRO., 2.Kazusa DNA Res. Inst., 3.Chuo Agri. Exp. Stn., HRO.)		☆Igarashi, K., A. Kobayashi, K. Toriyama (Grad.Sch. Agri. Sci., Tohoku Univ.)		Nagano, N.1, ○Y. Fukuta1,2 (1.Univ. Ryukyu, Fac. Agr., 2.JIRCAS)		○Chen, L.1,2, K. Hahismoto1, A. Yamaguchi1, R. Watanabe1, R. Watanabe1, A. Hironaka1 (1.Fac. Envir. Hort. Sci., Minami Kyushu Univ., 2.Grad. Sch. Hort. & Food Sci., Minami Kyushu Univ.)		☆Iki, Y.1, F. Wang2, K. Ito1, T. Wakatake3, K. Tanoi4, K. Naito2 (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO, 3.Grad. Sch. Sci. and Technol, NAIST, 4.Grad. Sch. Agri. and Life. sci., Univ. Tokyo)	

21 March (13:00-15:45) Oral Presentation Program

	Chair: Tomoki Hoshino (Yamagata Univ.)		Chair: Mao Suganami (Fukushima Univ.)		Chair: Kazama Tomohiko (Kyushu Univ.)		Chair: Ryo Matsushima (Okayama Univ.)		Chair: Ken Naito (NARO)		
13:00	111	QTL mapping of agronomic traits in true seed- and tuber-derived diploid potatoes	211	Development of genomic information on wild soybean mini-core collection and its application to gene identification using GWAS	311	Development of transformation protocols in Brassicaceae and points to be resolved	411	Estimating fruit traits QTLs in two Japanese melon landraces of Makuwa and Conomon and their origin	511	Decoding Plant Stress Communication: VOC-Induced HsfA2 Expression and Heat Stress Tolerance in Arabidopsis thaliana	13:00
		☆Kawamata, M., R. Sanetomo, K. Hosaka (Obihiro University of Agriculture and Veterinary Medicine)		○Li, F.1, R. Yano2, R. Nakata1, K. Kanako1, M. Hashiguchi3, R. Akashi4, H. Tanaka4, K. Takagi1, S. Hiraga1, M. Ishimoto1 (1.Inst. Crop. Sci., NARO, 2.Res. Cent. Adv. Anal.,NARO, 3.Fac. Reg. Innov., Miyazaki Univ., 4.Fac. Agric., Miyazaki Univ.)		○Koizuka, N. (Coll. Agr., Tamagawa Univ.)		○Tanaka, K.1, K. Nakajima1, G. Shigita2,3, M. Okuma4, R. Ishikawa1, H. Nishida4, K. Kato4 (1.Fac. Agr. Life Sci., Hirosaki Univ., 2.Tech. U. Munich, 3.Life Environ. Sci., Univ. Tsukuba, 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)		☆Barbaruah, B.1, F. Shuo1, H. Ito2 (1.Grad. Sch. Life Sci., Hokkaido Univ., 2.Fac. Sci., Hokkaido Univ)	
13:15	112	The effect of CDF1 alleles on the phenotype of the progeny from a very early-maturing potato cultivar	212	Collecting genome sequences, phenotypes and pedigree information in 104 Sake brewing rice cultivars.	312	Reconstitution of the stigma-side dominance relationship in Brassica self-incompatibility using transgenic Arabidopsis thaliana	412	Phylogenetic analysis based on the chloroplast genome in sweetpotato	512	Investigation on Drought Stress Effect on Four Japanese Chili Pepper Varieties	13:15
		☆Eguchi, K., R. Sanetomo (Obihiro University of Agriculture and Veterinary Medicine)		○Hori, K.1, K. Ebana2, S. Matthew1, N. Tanaka1, K. Ishimaru1, H. Hirabayashi1, Y. Kawahara3, H. Kajiya-Kanegae1,4, T. Okunishi5, K. Sugimoto1 (1.Inst. Crop Sci., NARO, 2.Res. Cent. Genet. Resources, NARO, 3.Res. Cent. Adv. Anal., NARO, 4.Res. Cent. Agric. Info. Tech., NARO, 5.Inst. Food Res., NARO)		☆Chen, J., h. kitashiba, m. yamamoto (Grad. Sch. Agric. Sci., Tohoku Univ)		☆Kurihara, M., M. Nishinaka, K. Taguchi (NARO·CARC)		☆Airlangga, R.1, H. Ito2 (1.Grad. Sch. Life Sci., Hokkaido Univ., 2.Fac. Sci., Hokkaido Univ.)	
13:30	113	Detection of QTLs associated with anthocyanin content and composition in sweetpotato storage roots	213	Genetic diversity and genome-wide association analysis of grain quality and starch traits in sake rice cultivars	313	Identification of mutations repressing the unstable self-incompatibility of Arabidopsis thaliana transformant expressing AlSRKb(S367L) under high temperature	413	Towards the utilization of genetic resources in the original countries by using local rice varieties collected more than half-century ago	513	Response of tomato plants to salt stress, waterlogging and their combination	13:30
		○Tanaka, M., K. Suematsu, R. Kurata, T. Sakaigaichi (Kyushu Okinawa Agr. Res. Cent., NARO)		○Shenton, M.1, K. Ishimaru1, H. Hirabayashi1, N. Tanaka1, K. Ebana3, K. Sugimoto2, K. Hori1 (1.Institute of Crop Science, NARO, 2.Institute of Crop Science, NARO, 3.Research Center of Genetic Resources, NARO)		☆Yokosawa, S., H. kitashiba, M. Yamamoto (Grad. Sch. Agri., Tohoku Univ.)		○Ishii, T.1, S. Lim1, C. Orn2, R. Ishikawa1, H. Saito3, Y. Sato4 (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodian Agr. Res. Dev. Inst., 3.Trop. Agr. Res. Front, JIRCAS, 4.Natl. Inst. Genet.)		☆ANEE, T.1, N. Suzuki2 (1.Graduate School of Green Science and Engineering, Sophia University, 2.Faculty of Science and Technology, Sophia University)	
13:45	114	Identification and validation of QTLs controlling southern root-knot nematode (SP6-2) resistance utilized by bulked-segregant analysis	214	Construction of genomic prediction models for 100-seed weight in natto soybean	314	Recognition specificity analysis of Brassica and Raphanus S genes showing highly homology using Arabidopsis thaliana transformants.	414	Genetic variation of heading date in rice germplasm from Zambia	514	RbohD, an ROS-producing gene, regulates memory of short-term heat stress and responses to flooding with physical flow in Arabidopsis thaliana	13:45
		☆Tsuchiya, S.1, M. Kurihara2, H. Tabuchi3, 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.)		○Yamaguchi, N.1, K. Shirasawa2, H. Igarashi3, T. Yamada4 (1.Central Agr. Exp. Sta., HRO, 2.Kazusa DNA Res. Inst., 3.Tokachi Agr. Exp. Sta., HRO, 4.Res. fac. Agr., Hokkaido Univ.)		☆Suzuki, T.1, M. Ogura1, T. Makino2, H. Kitashiba1, M. Yamamoto1 (1.Grad. Sch. Agrisci., Univ. Tohoku, 2.Grad. Sch. Sci., Univ. Tohoku)		○Oshiro, K.1, T. Sato2, K. Triyama3, S. Komatsubara4, R. Mulenga5, M. Chitambi5, G. Munkombwe5, M. Chinji5, E. Musabula5, N. Museta5, L. Kamguya5, J. Njobvu5, Y. Fukuta6 (1.Grad. Sch. Agr., Univ. Ryukyus, 2.Fac. Agr., 3.Grad. Sch. Agr. Sci., 4.JICA, 5.ZARI, 6.Univ. Ryukyus)		○Suzuki, N.1, M. Yunose2, K. Katano3, R. Shimizu2, C. Sumi1, M. Kaji4, S. Shigaki5, H. Suzuki6 (1.Faculty of Science and Technology, Sophia University, 2.Graduate School of Science and Technology, Sophia University, 3.College of Life Sciences, Ritsumeikan University, 4.Division of Environmental Design, Graduate School of Science and Engineering, Kanazawa University, 5.Principles of Informatics Research Division, National Institute of Informatics, 6.Faculty of Engineering, Hokkai-Gakuen University)	

	Chair: Rena Sanetomo (Obihiro Univ.)		Chair: Hiroaki Sakai (NARO)		Chair: Shun Sakuma (Tottori Univ.)		Chair: Katsunori Tanaka (Hirosaki Univ.)		Chair: Takanori Yoshikawa (NIG)		
14:00	115	Genetic analysis of heterosis in culm length of sorghum F1 hybrid 'Kazetachi'	215	Development of NARO Open Rice Collection (NRC) and seed ionome analysis	315	Which S haplotypes are used in Japanese Brassica F1 varieties?	415	Relationship between agronomic traits and QTL for hybrid weakness in RILs derived a cross between Milyang 23 and Akihikari	515	Analysis of rice lateral root formation mechanism by WOX gene cluster.	14:00
		☆Iri, Y.1, S. Okada2, S. Hashimoto3, S. Nakamura (Araki)2, K. Shinohara (Omae)2, S. Kasuga4, T. Sazuka2 (1.Grad. Sch. Bioagri., Univ. Nagoya, 2.Biosci. and Biotech. Center, Univ. Nagoya, 3.Grad. Sch. Agric. Life. Sci., Univ. Tokyo, 4.AFC, Fac. of Agri., Univ. Shinshu)		○Tanaka, N.1, Y. Kawahara2, K. Ebana3, M. Shenton1 (1.NARO, NICS, 2.Research Center for Advanced Analysis, NARO, 3.Research Center of Genetic Resources, NARO)		☆Kato, R., J. Ji, X. Zhu, M. Yamashita, S. Miyashita, M. Yamamoto, H. Kitashiba (Grad. Sch. Agri. Sci., Tohoku Univ.)		☆Kobayashi, H.1, Y. Fukuta1,2 (1.Faculty of Agriculture of University of the Ryukyus, 2.JIRCAS)		☆Kushida, S.1, Y. Dong1, P. LIPIO1, M. Inari-Ikeda2, Y. Inukai3 (1.Grad. Sch. Bioagr., Nagoya U., 2.Sch. Hel. Nut., U. Tokaigakuen., 3.ICREA, Nagoya U.)	
14:15	116	Yield prediction based on QTLs for yield components using yield dissection models in tomato	216	Genetic control of seed iron and zinc concentration in Rwandan common bean population revealed by the Genome Wide Association Study (GWAS)	316	Development of the digital PCR analysis method for estimation of selfing seed contamination rate in strawberry F1 seed production	416	Origin of crop varieties by cultivar-wild species hybridizations: a case study of yams (Dioscorea spp.) in Japan	516	Growth analysis of all cells of the rice leaf primordium by live imaging	14:15
		☆Tsutsumi-Morita, Y.1,2,3, E. Heuvelink2, S. Khaleghi2, D. Bustos-Korts3,4, L. Marcelis2, K. Vermeer5, H. van Stappen-van Dijk5, F. Millenaar5, G. Van Voorn3, M. Boer3, F. Van Eeuwijk3 (1.CCCA, NIES, 2.Horticulture and Product Physiology, Wageningen University & Research, 3.Biometris, Wageningen University & Research, 4.Universidad Austral de Chile, 5.BASF’s vegetable seeds business (Nunhems))		☆Mukamuhirwa, F.1,2, K. Shirasawa3, K. Naito4, E. Rurangwa2, V. Ndayizeye2, A. Nyombayire2, J. Muhire2, M. Govindaraj5, N. Ohtake1, K. Okazaki1, M. Okada1, E. Fukai1 (1.Grad.Sch.Sci.Tec., Niigata Univ., 2.Crop In.Tec.Trans, Rwanda Agri. Anim.Res.Dev. Board, 3.Kazusa DNA Res.Inst., 4.Research Cen.Gen.Res., Nat.Agri.Fo.Res.Org. (NARO), 5.Alliance of Bio.Int.and Int.Cen.Trop.Agri. (CIAT))		○Ishimori, M.1, S. Kataoka2, T. Sueyoshi3, S. Nagamatsu3, M. Tanaka3, M. Ogura2, Y. Noguchi2, Y. Higuchi1, S. Isobe1 (1.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 2.NIVFS, NARO, 3.Fukuoka Agr. Forest Res. Cent.)		☆Minoji, K.1, A. Ohta1, T. Sakai1, Y. Sugihara2, A. Kudoh1, R. Terauchi1,3 (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.IBRC)		☆Taguchi, M.1, Y. Tokuyama2, R. Kelly-Bellow3, R. Smith3, Y. Kishima2, Y. Koide2 (1.Sch. Agr., Hokkaido Univ., 2.Grad. Sch. Agr., Hokkaido Univ., 3.Department of Computational and System Biology, JIC)	
14:30	117	Comparison of good eating quality QTLs using two recombinant inbred line populations derived from Enrei and Dadachamame.	217	Comparative analysis of genetic loci related to carotenoid accumulation in sweetpotato flesh using GRAS-Di and dpMIG-seq and identification of the genetic loci	317	Exploration of genes regulating grass-clump dwarf in synthetic hexaploid wheat.	417	Analysis of starch granule size diversity in t in Vigna species	517	Genetic analysis of a spontaneous mutant, dwarf and short panicle	14:30
		☆Shioya, N.1, Y. Takagi2, E. Ogiso-Tanaka3, T. Hoshino1,2 (1.Grad. Sch. Agr., Iwate Univ., 2.Grad. Sch. Agr., Yamagata Univ., 3.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci.)		☆Horita, N.1, Y. Okada2, H. Kanzaki1, M. Kurihara3, K. Nishimura1, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Env. Life. Nat. Sci. Tech., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Env. & Life Sci., Okayama Univ.)		☆Nakanishi, S.1, K. Nishimura1, M. Okada2, T. Nakazaki3,4, Y. Monden1, K. Kato1, H. Nishida1 (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad. Sch. Sci. Tech., Niigata Univ., 3.Grad. Sch. Agr., Kyoto Univ., 4.IAC, Kyoto Univ.)		○Matsushima, R.1, J. Kim1,2, T. Ishii3, J. Yamashita1 (1.Institute of Plant Science and Resources, Okayama University, 2.RIKEN Center for Sustainable Resource Science, 3.Arid Land Research Center, Tottori University International Platform for Dryland Research and Education)		Le, T.2, D. Lam1, E. Fukai3, ○R. Ishikawa1 (1.Fac. Agri. Life Sci., Hirosaki Univ., 2.Climate Change Institute, An Giang University, 3.Fac. Agri., Niigata Univ.)	
14:45	118	Verification of QTLs and prediction of candidate genes associated with grain yield-related traits in a pyramidale wheat (Triticumturgidum L.)	218	Attempts at genetic analysis of various agronomic traits in sweetpotato using image analysis	318	Functional analysis of a fertility restorer gene for Tadukan-type cytoplasmic male sterile rice	418	Growth characteristics under subtropical environmental conditions of barley genetic resources collected from Taiwan	518	Variation of thermo-sensitivity of heading date found in Hokkaido rice varieties affect heading synchrony and premature heading	14:45
		☆Chen, T.1, K. Nishimura2, K. Murata1, K. Nagasaka1, Y. Iwahashi1, T. Maki1, Y. Kinoshita1, H. Inoue1, R. Nakano1, T. Nakazaki1,3 (1.Grad. Sch. Agr., Kyoto Univ, 2.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ, 3.IAC, Kyoto Univ)		☆Tanaka, S.1, H. Tabuchi2, K. Nishimura3, H. Nishida3, K. Kato3, Y. Monden3 (1.Fac. Agri., Okayama U., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)		☆Takatsuka, A.1, Y. Iwai1, H. Mireau2,3, T. Kazama4, K. Igarashi1, K. Toriyama1 (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.IJPB, INRAe Versailles, 3.AgroParisTech, Paris-Saclay Univ., 4.Grad. Sch. Biores. Environment. Sci., Kyushu)		○Saisho, D.1, Y. Okada2, T. Suzuki2, H. Lin3, W. Chiou4 (1.IPSR, Okayama Univ., 2.Kyushu Okinawa Agricultural Research Center, NARO, 3.Taichung DARES, MOA, 4.Dept. Agronomy, National Chung Hsing University)		☆Hoque, M.1, S. Sakaguchi1, M. Takatori1, M. Kinoshita2, H. Shinada3, N. Yamaguchi4, T. Nishimura4, Y. Kishima1 (1.Grad. Sch. Agr., Hokkaido. Univ., 2.Kamikawa Agricultural Experimental Station, Hokkaido Research Organization, 3.Kitami Agricultural Experimental Station, Hokkaido Research Organization, 4.Central Agricultural Experimental Station, Hokkaido Research Organization)	

	Chair: Moeko Okada (Niigata Univ.)		Chair: Feng Li (NARO)		Chair: Motoyuki Ishimori (Univ. Tokyo)		Chair: Daisuke Saisho (Okayama Univ.)		Chair: Mitsuko Kishi-Kaboshi (Kazusa DNA)		
15:00	119	Identification of genetic loci associated with awn length in Aegilops sharonensis Eig, a wild relative of wheat	219	Loss of function haplotype of R and T were selected for improving seed appearance	319	Exploration of PPR genes that regulate the expression of orf288, a CMS-causing gene in japonica rice mitochondria	419	Development and interlaboratory validation of a cultivar-specific identification method for 'Shine Muscat' using loop-mediated isothermal amplification (LAMP)	519	Analysis of the transcription factor SIMYB21 involved in jasmonate-mediated fruit set in tomato	15:00
		☆Ye, K.1, R. Terauchi1,2, A. Ohta1 (1.Grad. Sch. Agri., Kyoto Univ., 2.Iwate Biotechnology Research Center)		☆Suganami, M.1, S. Kojima2, M. Kamakura3, M. Shiraishi3, K. Beppu3, H. Yoshida1, N. Nihei1,4, H. Takahashi1,4, S. Masumoto1,4, T. Waki5, T. Nakayama5, K. Yoshida6, T. Matsuda1,4, M. Watanabe7, M. Matsuoka1 (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Graduate School of Agricultural Science, Tohoku University, 3.Ehime Prefectural Saijo Agricultural High School, 4.Faculty of Food and Agricultural Sciences, Fukushima University, 5.Graduate School of Engineering, Tohoku University, 6.Faculty of Food and Health Sciences, Aichi Shukutoku University, 7.Graduate School of Life Sciences, Tohoku University)		○Toriyama, K.1, Y. Iwai1, K. Igarashi1, T. Kazama2 (1.Grad. Sch. Agri. Sci. Tohoku. Univ., 2.Grad Sch. Biores. Environment. Sci., Kyushu Univ.)		○Takabatake, R.1, Y. Monden2, A. Shindo2, Y. Minegishi3, F. Taniguchi4, Y. Hashimoto1, T. Takeuchi5, K. Takasaki5, S. Isobe6 (1.Institute of Food Research, National Agriculture and Food Research Organization, 2.Graduate School of Environmental, Life, Natural Science, and Technology, Okayama University, 3.Nippon Gene Co., Ltd., 4.Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization, 5.FASMAC Co., Ltd., 6.Kazusa DNA Research Institute)		☆Nomura, Y.1, Y. Lu2, Y. Shinozaki2, T. Kawakatsu3, 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.Institute of Agrobiological Sciences., NARO, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)	
15:15	120	Analysis of the genetic basis for heading date of African cultivated rice Oryza glaberrima for utilization in temperate regions	220	Exploration and validation of allele dosage estimation method for simplified selection of sweetpotato low pasting temperature lines.	320	Increased glucoraphanin content in intergeneric hybrid between Brassica oleracea var. italica and Diplotaxis tenuifolia	420	Secretory production of lysostaphin, an antimicrobial protein, from rice suspension cells	520	Identification of a novel heading time-related gene HvHY2 in barley using MutMap approach	15:15
		☆Fujii, M.1, A. Hirao1, H. Yasui2, Y. Yamagata2 (1.Grad. Sch. Bioresour. Environ. Sci, Kyushu Univ., 2.Fac. Agr., Grad. Sch., Kyushu Univ.)		☆Nakahara, T.1, M. Tanaka2, A. Kobayashi2, Y. Kawata2, K. Nishimura1, H. Nishida1, K. Kato1, Y. Monden1 (1.Grad. Sch. Environ. Life Sci. Tech., Okayama U., 2.KARC/NARO)		☆Odashima, K.1, T. Suzuki2, T. Ohnishi1, S. Bang1 (1.Grad. Sch. Agr., Utsunomiya U., 2.Center for Bioscience research and Education, Utsunomiya U.)		☆Yahara, T., G. Watarai, A. Ohtawara, S. Shimoda, H. Yoneyama, Y. Ito (Grad. Sch. Agri., Tohoku Univ.)		☆Okuma, M., K. Nishimura, Y. Monden, K. Kato, H. Nishida (Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)	
15:30	121	Exploration of quantitative trait loci for grain shape and weight in Triticum timopheevii and its ancestral species, T. araraticum	221	GenEditScan: a fast and efficient analysis tool to detect foreign DNA in the genome-edited agricultural products using high-throughput sequencing data	321	Optimizing visualization of pollen tubes in wide hybridization of wheat	421	A population of diploid interspecific hybrids between Asian and African rice reveals variations of pollen fertility associated with meiotic abnormalities	521	Diversity in the juvenile-to-adult phase transition of six common wheat cultivars with different winter-spring growth habits	15:30
		☆Hayashi, K.1, R. Terauchi1,2, A. Ohta1 (1.Grad. Sch. Agr., Kyoto Univ., 2.IBRC)		○Sakai, H.1, T. Sato2, T. Itoh3, R. Onuki4, Y. Tabei5 (1.Research Center for Advanced Analysis, NARO, 2.Mizuho Research & Technologies, Ltd., 3.National Taiwan University, 4.Saitama Cancer Center, 5.Faculty of Food and Nutritional Sciences, Toyo University)		○Sakuma, S., K. Mishina, M. Morita, S. Matsumoto (Faculty of Agriculture, Tottori University)		☆Zahidah, Q.1, M. Ishihara1, Y. Minouchi1, D. Kuniyoshi2, T. Yamamoto3, K. Nagaki3, Y. Kishima1 (1.Grad. Sch. Agr., Hokkaido Univ., 2.Tropical Agriculture Research Front, JIRCAS, 3.IPSR, Okayama Univ.)		☆Senoo, K.1, T. Yoshikawa2, S. Nasuda1 (1.Grad. Sch. Agric., Kyoto Univ., 2.Natl. Inst. Genet.)	