

Title of Papers Presented at the 129th Meeting of The JAPANESE SOCIETY Oral presentations

Oral Presentations

101 QTL Mapping of Antixenosis Resistance to Common Cutworm (*Spodoptera litura* Fabricius) in Wild Soybean (*Glycine soja*)

☆Oki, N.¹, A. Kaga², T. Shimizu², Y. Shu², H. Yano³, M. Takahashi¹, Y. Kono¹, M. Takahashi⁴ (1.NARO, KARC, 2.NIAS, 3.NARO, WARC, 4.NARO, NICS)

102 Studies on soybean QTLs associated with tolerance to seed cracking by low temperature. I. Comparative analyses between NILs

Yamaguchi, N.¹, K. Yamashita², M. Hiraoka², F. Taguchi-Shiobara³, M. Ishimoto³, M. Kawasaki², ○M. Senda² (1.Tokachi Agr. Exp. Sta., HRO, 2.Fac. Agric. Life Sci., Univ. Hirosaki, 3.NIAS)

103 Analysis of the mechanism of the salt stress-induced internalization of the plasma membrane aquaporin in *Arabidopsis thaliana*

☆Ueda, M., M. Fujimoto, N. Tsutsumi (Grad. Sch. Agric. Life Sci., Univ. Tokyo)

104 Overexpressing of *BSR2* confers resistance to bacterial and fungal diseases in tomato

☆Maeda, S.¹, N. Yokotani², K. Oda², S. Seo¹, H. Hirochika¹, M. Mori¹ (1.National Institute of Agrobiological Sciences, 2.RIBS Okayama)

105 Analysis of wild emmer-derived leaf rust resistance gene in common wheat accession "RW-12"

○Kobayashi, F., T. Tanaka, H. Kanamori, Y. Katayose, J. Wu, T. Matsumoto, H. Handa (NIAS)

106 The cost of blast resistance genes for yield properties of rice

○Kobayashi, A., K. Tomita, M. Tanoi, T. Hayashi, Y. Machida, F. Nakaoka, T. Shimizu
(Fukui Agr. Exp. Stn.)

107 QTL analysis of the trait for iron toxicity tolerance using rice cultivar "Dadahup" and "Milyang 23"

☆Hirakawa, T.¹, H. Takahashi¹, S. Nishiuchi¹, H. Sunohara¹, J. Murase¹, K. Doi¹, Y. Inukai², M. Nakazono¹ (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.ICCAE, Nagoya Univ.)

108 Development of a method for regulating gene expression in response to disease and disease-resistant rice

○Morino, K., M. Kimizu (Agri., Res. cen., NARO)

109 QTL analysis and identification of a gene for the susceptibility to the 4-HPPD inhibitor herbicide in rice

○Murata, K.¹, H. Maeda², K. Sekino³, M. Kawata⁴, M. Ohshima⁴, H. Yoshida⁴, I. Ando⁴, A. Yamazaki³, Y. Yamada³, S. Hirose⁵, M. Kawagishi-Kobayashi⁴, Y. Taniguchi⁴, H. Kato⁵ (1.Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, 2.NARO National Agricultural Research Center, 3.SDS Biotech K.K., 4.NARO Institute of Crop Science, 5.National Institute of Agrobiological Sciences)

110 Development of marker-assisted selection system for the susceptibility to the 4-HPPD inhibitory herbicide in rice

○Maeda, H.¹, K. Murata², K. Sekino³, M. Kawata⁴, M. Ohshima⁴, H. Yoshida⁴, I. Ando⁴, A. Yamazaki³, Y. Yamada³, S. Hirose⁵, M. Kawagishi-Kobayashi⁴, Y. Taniguchi⁴, H. Kato⁵ (1.NARO Agricultural Research Center, 2.Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, 3.SDS Biotech K.K., 4.NARO Institute of Crop Science, 5.National Institute of Agrobiological Sciences)

111 Characterization of 4-HPPD inhibitory herbicide resistance gene from japonica rice

○Kawata, M.¹, S. Hirose², M. Kawagishi-Kobayashi¹, H. Yoshida¹, Y. Taniguchi¹, H. Maeda³, K. Murata⁴, H. Kato², Y. Yamada⁵, K. Sekino⁵, A. Yamazaki⁵, M. Ohshima¹ (1.NARO Institute of Crop Science, 2.National Institute of Agrobiological Sciences, 3.NARO National Agricultural Research Center, 4.Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, 5.SDS Biotech K.K.)

112 Effectiveness of 4-HPPD inhibitory herbicide resistance gene from japonica rice

☆Yamazaki, A. ¹, K. Sekino ¹, Y. Yamada ¹, H. Maeda ², K. Murata ³, H. Kato ⁴, H. Yoshida ⁵, M. Kawagishi-Kobayashi ⁵, S. Hirose ⁵, Y. Taniguchi ⁵, M. Kawata ⁵, M. Ohshima ⁵, Y. Tozawa ⁶ (1.SDS Biotech K.K., 2.NARO National Agricultural Research Center, 3.Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, 4.National Institute of Agrobiological Sciences, 5.NARO Institute of Crop Science, 6.Saitama University, Graduate School of Science and Engineering)

113 Development and QTL verification of chromosomal segment substitution lines derived from Yamadanishiki with Koshihikari genetic background

☆Okada, S., T. Sakamoto, M. Suehiro, M. Yamasaki (Food Resources Education and Research Ctr., Grad. Agric. Sci., Kobe U)

114 The 'Koshihikari' allele of qGTH3 contributes to increase of the yield in rice

☆Yamaguchi, T. ¹, R. Mizobuchi ², S. Fukuoka ², F. Taguchi-Shiobara ², N. Kitazawa ², Y. Iyama ¹, K. Fujita ³, T. Ebitani ¹ (1.Toyama Pref. Agr. For. Fis. Res. Cent., 2.NIAS, 3.Niikawa Agr. For. Prom. Cent.)

115 Complex haplotype structure causes synthetic spurious signals in GWAS

☆Yano, K. ¹, H. Takeuchi ¹, E. Yamamoto ², K. Hirano ¹, H. Kitano ¹, M. Matsuoka ¹ (1.Bioscience and Biotechnology Ctr, Nagoya U., 2.NIVTS)

116 Analysis of rice cultivars by graphical genotyping of genome wide SNPs

○Miyao, A. ¹, M. Nakagome ¹, K. Doi ¹, H. Yamashita ², K. Kogou ², S. Niwata ², H. Yasue ³ (1.Genome Resource, NIAS, 2.KURABO INDUSTRIES LTD., 3.Tsukuba GeneTech. Lab. Inc.)

117 Development of a bioinformatics tool for identification of SSR markers with high-throughput sequencing data

☆Kobayashi, M., K. Yano (Sch. of Agri., Meiji Univ.)

201 Evaluation of characteristics related to phosphorus uptake ability in spelt wheat: genetic variation of root hair length and arbuscular mycorrhizal colonization

○Onishi, K. ¹, A. Kadota ¹, N. Okano ¹, K. Ishida ¹, A. Kinoshita ¹, T. Kawahara ², H. Miura ¹, Y. Hashimoto ¹, M. Tani ¹ (1.Obihiro. Univ. Agric. & Vet. Med., 2.Grad. Sch. Agri., Kyoto Univ.)

202 Open pollination fertility of photoperiod-sensitive cytoplasmic male sterility (PCMS) wheat lines

○Murai, K.¹, M. Kurushima², Y. Yoshimura³, H. Oota⁴, N. Ishikawa⁵ (1.Dep. Biosci., Fukui Pref. U., 2.Kitami Agri. Exp. Stn., HRO, 3.Chuo Agri. Exp. Stn., HRO, 4.HOKUREN, Agr. Res. Inst., 5.NARO/WARC)

203 Search for wild tetraploid wheat populations with non-dormant individuals at a high frequency

○Ohta, S.¹, N. Mori², H. Ozkan³ (1.Dep. Biosci., Fukui Pref. Univ., 2.Lab. Crop Evol., Grad. Sch. Agric. Sci., Kobe Univ., 3.Fac. Agric., Cukurova Univ., Turkey)

204 Exploration and collection of Triticeae genetic resources on Tibetan plateau in Qinghai Province, China

○Sasanuma, T.¹, H. Tanaka², K. Sato³, M. Zhu⁴, C. Long⁴ (1.Fac. Agr., Yamagata Univ., 2.Fac. Agr., Tottori Univ., 3.IPSR, Okayama Univ., 4.Chinese Academy of Sciences)

205 Agronomic characteristics of wheat lines developed in CIMMYT and their application in breeding for high yield

☆Ashikaga, N., M. Kurushima, H. Jinno (Kitami Agri. Exp. Stn., HRO.)

206 Breeding of early-mature durum wheat for domestic use

☆Tanno, K.¹, R. Baba¹, T. Kawahara² (1.Facl. Agr., Yamaguchi University, 2.Grad. Sch. Agr., Kyoto University)

207 Research of improving fusarium head blight resistance in durum wheat line 'Chugoku D166'

☆Kato, K.¹, W. Funatsuki¹, M. Yanaka¹, H. Okusu², K. Takata¹ (1.WARC, NARO, 2.Central Laboratory, NIPPON FLOUR MILLS CO., LTD.)

208 Evaluation of *Aegilops tauschii* genetic resources focusing on bread-making property

☆Akaike, R.¹, A. Kakizaki², T. Sasanuma^{1,2} (1.Grad. Sch. Agr., Univ. Yamagata, 2.Fac. Agr., Univ. Yamagata)

209 Development of low-calorie rice cultivars. 3.Characteristics of BC3F3 generation

○Kawamoto, T.¹, S. Shibata¹, K. Kato¹, R. Takahashi¹, M. Takahara², N. Crofts², N. Fujita² (1.Akita Prefectural Agricultural Experiment station, 2.Akita Prefectural University)

210 Characteristics of a Sake-brewing rice variety "Hanasayaka" which is different from general rice in endosperm protein composition

○Kanda, S., K. Maeda, T. Uemura, Y. Wakamoto, M. Suto (Aomori Pref Indust.Tech. Res. Cent. Agric. Res. Inst)

211 Induction of resistant to bacterial wilt caused by *Ralstonia solanacearum* into the potato breeding line derived from *Solanum acaule*

☆Habe, I.¹, K. Ohbayashi², Y. Sakamoto¹, K. Mori¹ (1.Nagasaki prefectural Agriculture & forestry technical development center, 2.Nagasaki prefectural ken'ou development bureau)

212 Selection for tuber greening in a segregating population of the greening tolerance line "Hokkai 107"

☆Ozaki, H.^{1,2}, S. Tamiya², M. Mori^{1,2}, H. Miura¹ (1.Obihiro U. Agr. & Vet. Med., 2.NARO Hokkaido Agr. Res. Cent.)

213 Diversity of melon fruit and seed cultivated in Eastern and Western Cambodia

☆Tanaka, K.¹, D. Thanh Thuy², Y. Hiroshi², M. Hiroshi³, M. Kenichi⁴, S. Layheng⁵, S. Theavy⁵, S. Sophany⁵, T. Norihiko⁶, K. Kenji² (1.Fac. Humanit., Hirosaki U., 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.NARO/ NIVTS, 4.Grad. Sch. Agric., Shinshu U., 5.CARDI, 6.NIAS)

214 Conservational study on wasabi as cultural plant resources in Ashu, the venue for wasabi festival, Nantan City, Kyoto Prefecture

☆Yamaguchi, H., K. Yamane (Fac. Appl. Biol. Sci., Gifu U.)

215 Genetic studies on Bambuseae species in Japan. XXXIX. Plant geographical distribution of the species, particularly of the genus *Sasa*

○Muramatsu, M. (Univ. Okayama, Prof. emeritus)

216 Evolution of N. section Tomentosae and origin of N. tabacum inferred from the presence or absence of Gemini-virus derived sequence and sequencing of NFL gene

○Kadotani, N.¹, M. Ito² (1.NRI, Tokyo U. Agric., 2.Grad. Sch. Art. Sci., U.Tokyo)

217 Genetic variation for root distribution at young seedling stage of rice (*Oryza sativa* L.)

☆Tomita, A.^{1,2}, T. Sato³, Y. Uga⁴, M. Obara², Y. Fukuta² (1.Grad. Sch. Life and Envi. Sci., Univ. Tsukuba, 2.JIRCAS, 3.Grad. Sch. Life. Sci., Univ. Tohoku, 4.NIAS)

218 Evaluation for heading behavior of *Hd1*, *Hd16* and *Hd18* controlling heading date of rice in Miyagi and Yamagata prefecture

○Saeki, K.¹, T. Endo¹, Y. Nakagomi¹, Y. Abe², R. Mizobuchi³, T. Mizubayashi³, S. Fukuoka³ (1.Miyagi Prefectural Furukawa Agricultural Experiment Station, 2.Rice Breeding and Crop Science Experiment Station of Yamagata Integrated Agricultural Research Center, 3.NIAS)

219 Dispersion of genes for adaptability

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

301 Genome-wide survey of polymorphisms in a wheat relative *Aegilops umbellulata* revealed by RNA-seq analysis

☆Okada, M.¹, K. Yoshida², R. Nishijima¹, K. Sato³, S. Takumi¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Org. Adv. Sci. Tech., Kobe Univ., 3.IPSR, Okayama Univ.)

302 Recruitment of the *Aegilops tauschii* scaffolds to the specific D-genome region of synthetic wheat hexaploid based on the RNA-seq data

☆Nishijima, R.¹, K. Sakaguchi¹, K. Yoshida², N. Mizuno³, S. Nasuda³, K. Sato⁴, S. Takumi¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Org. Adv. Sci. Tech., Kobe Univ., 3.Grad. Sch. Agr., Kyoto Univ., 4.IPSR, Okayama Univ.)

303 Mutational behaviors among different length of mononucleotide repeat sequences based on intra- and interspecific phylogenetic analyses in Triticum-Aegilops

○Yamane, K.¹, T. Kawahara² (1.Fac. Appl. Biol. Sci., Gifu U., 2.Grad. Sch. Agr. Kyoto U.)

304 Nucleotide diversity on hardness gene locus Ha and variations of kernel hardness in tetraploid wheats

☆Yamaki, M. ¹, K. Tanno ², T. Kato ¹, T. Kawahara ³, K. Yamane ¹ (1.Fac. Appl. Biol. Sci., Univ. Gifu, 2.Fac. Agr., Univ. Yamaguchi, 3.Grad. Sch. Agr., Univ. Kyoto)

305 Association mapping for drought and salinity tolerance related-trait in barley

☆Elakhdar, A. ^{1,3}, M. Abdelsattar ², K. Amer ³, I. Elakhdar ³, T. Kumamaru ¹ (1.Fac., Agric., Kyushu Univ., 2.Fac., Agric., Alex., Univ., Egypt., 3.Agric., Res., Center, Egypt.)

306 Development of SNP typing system for barley breeding

○Sato, K. (IPSR, Okayama University)

307 Comparison of sequences and expression of an anthocyanin biosynthetic gene, ANS (Anthocyanidin synthase), of wheat

☆Himi, E., M. Maekawa (Institute of Plant Science and Resources, Okayama Univ.)

308 Genomic fossils in grasses reveal adaptation strategies for non-autonomous pararetrovirus species driven by convergence of noncoding regulatory sequences

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

309 The genomic region harboring sorghum fertility restorer, *Rf5* is caused by the translocation and segmental duplication of PPR motif genes

○Yonemaru, J. ¹, A. Kiyosawa ², H. Kawahigashi ¹, J. Wu ¹, H. Kanamori ¹, K. Gotoh ² (1.Natl. Inst. Agr. Sci., 2.Nagano Anim. Indust. Exp. Sta.)

310 Genome-wide association study in *Sorghum* under salt stress condition in Mexico

☆Ishimori, M. ¹, H. Kajiya-Kanegae ¹, H. Takanashi ^{1,2}, M. Fujimoto ^{1,2}, M. Minamikawa ¹, T. Koshiba ^{2,3}, M. Kobayashi ^{2,4}, K. Yano ^{2,4}, T. Tokunaga ^{2,3}, N. Tsutsumi ^{1,2}, H. Iwata ^{1,2} (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.CREST, JST, 3.Earth Note Co., Ltd., 4.Fac. Agr., Meiji Univ.)

311 QTL mapping of soybean maturity gene *E5*

☆Dissanayaka, A.¹, T. Rodriguez¹, S. Di¹, Y. Fan¹, S. Githiri², F. Rodas¹, J. Abe³, R. Takahashi^{1,2} (1.University of Tsukuba, 2.National Institute of Crop Science, 3.Hokkaido University)

312 Mapping and characterizatio of rice bacterial blight of XM14 mutant gene

☆Busungu, C.¹, K. Ichitani², J. Sakagami², T. Anai³, Y. Kawaguchi², T. Tanaka², K. Kawabe⁴, S. Taura⁴ (1.Uni. Grad. Sch. Agri. Sci., Kagoshima U, 2.Fac. Agri., Kagoshima U, 3.Fac. Agri., Saga U, 4.Div. Gene Res., Kagoshima U)

313 Comparative analysis between spinach sex chromosomes and sugar beet autosomes

☆Takahata, S.¹, K. Iwabuchi¹, H. Hirakawa², Y. Onodera³ (1.Grad. Sch. Agr., Hokkaido Univ., 2.Dept. of Technology Development, Kazusa DNA Res. Inst., 3.Res. Fac. Agr., Hokkaido Univ.)

314 Genome-wide SNP genotyping in high-oleic-acid peanut breeding lines by a target amplicon sequencing strategy

○Shirasawa, K.¹, C. Kuwata², M. Watanabe², M. Fukami², H. Hirakawa¹, S. Isobe¹ (1.Kazusa DNA Res. Inst., 2.Chiba Pref. Agric. Forest Res. Center)

315 SNP typing method using CRISPR/Cas9 system

☆Maruyama, S.², H. Matsumura¹ (1.Gene Res. Ctr., Shinshu U., 2.Tex. Sci. Tech, Shinshu U.)

316 De novo while genome sequencing in a wild sweet potato, *Ipomoea tridida*

Yoon, U.¹, H. Nagasaki², M. Tanaka³, H. Hirakawa², K. Shirasawa², S. Nagano², Y. Okada³, H. Tabuchi³, Y. Takahata³, J. Hahn¹, ○S. Isobe² (1.NIAS, RDA, 2.Kazusa DNA Res. Inst., 3.KARC, NARO)

317 Development of high-density genetic maps of citrus and comparison of them with Citrus reference genome sequence

○Shimizu, T.¹, E. Kaminuma², K. Nonaka¹, T. Yoshioka¹, S. Goto¹, T. Matsumoto³, Y. Katayose³, T. Mochizuki², Y. Tanizawa², A. Toyoda², A. Fujiyama², Y. Nakamura² (1.NARO Inst. Fruit Tree Sci., 2.Nat. Inst. Genetics, 3.Nat. Inst. Agro. Sci.)

318 An experiment on the evolution of radish CMS genes using *E. coli*

○Terachi, T. ¹, T. Kishimoto ¹, K. Kinoshita ¹, K. Kojima ¹, Y. Nakayama ¹, M. Jikuya ², H. Yamagishi ¹ (1.Fac. Life Sci., Kyoto Sangyo U., 2.Grad. Sch. Life Sci., Kyoto Sangyo U.)

401 Genetic improvement of rice using rapid-cycle recurrent genomic selection (RRGS) : A simulation study

○Iwata, H. ¹, H. Kanegae ¹, T. Kataoka ², T. Ishii ³, K. Hori ⁴, J. Tanaka ³ (1.Grad. Sch. Agr. Life Sci., U. Tokyo, 2.NARO KARC, 3.NARO Institute of Crop Science, 4.NIAS)

402 Application of BLUP animal model to potato breeding 1. Construction of feasible BLUP models

○Tanaka, T. ¹, R. Fujita ¹, M. Kashima ², M. Ohnami ¹ (1.HRO Kitami Agric. Exp. Stn., 2.HRO Anim. Res. Center)

403 Application of BLUP animal model to potato breeding 2. Verification of estimated breeding value

○Fujita, R. ¹, M. Kashima ², T. Tanaka ¹, M. Ohnami ¹ (1.HRO Kitami Agric. Exp. Stn., 2.HRO Anim. Res. Center)

404 Accuracy of genomic selection models using tomato F1 varieties in their progeny populations

○Yamamoto, E., H. Matsunaga, T. Nunome, H. Yamaguchi, K. Miyatake, A. Ohyama, H. Fukuoka (NIVTS)

405 Rice introgression lines carrying high-yielding gene(s) perform better even without nitrogen fertilizer

☆Teramoto, S. ¹, H. Kitano ², T. Fujiwara ¹ (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Biosci. Biotec. Ctr., Nagoya U.)

406 Production of autopolyploid and allopolyploid by in vitro fertilization with isolated gametes

○Okamoto, T., T. Matsumura, Y. Ohnishi, E. Toda (Dept. Biol., TMU)

407 Resistance assay of rot of the seed potato by controlling of soil conditions and utilizing of image analysis system "ImageJ"

☆Sakamoto, Y.¹, K. Mori¹, W. Watanabe², Y. Matsuo¹, M. Chaya¹, T. Ozaki³, T. Nakao¹ (1.Nagasaki Agricultural and Forestry Technical Development Center, 2.Nagasaki Goto Development Bureau, 3.Nagasaki Agriculture & Forestry Department)

408 Effect of recurrent selection for widely-diversified outbred line family in sugar beet

○Taguchi, K.¹, Y. Kuroda¹, H. Iwata² (1.NARO Hokkaido Agric. Res. Cent., 2.University of Tokyo)

409 Genome-wide association study based on whole-genome sequencing enables rapid identification of novel agronomic trait genes in rice

☆Takeuchi, H.¹, K. Yano¹, K. Aya¹, L. Hu¹, M. Yamasaki², S. Yoshida³, K. Hirano¹, H. Kitano¹, M. Matsuoka¹ (1.Bioscience and Biotechnology Ctr.,Nagoya U., 2.Food Resources Education and Res. Ctr., Grad. Sch. Agric. Sci., Kobe U., 3.Hyogo Agric. Forest. Fish. Res. Ctr.)

410 Double-sized soybean achieved by knocking down MOG gene

○Ken, N.¹, K. Hirano², C. Buppa¹, Y. Takahashi¹, E. Ogiso¹, K. Takagi³, M. Ishimoto¹, A. Kaga¹, N. Tomooka¹ (1.NIAS, 2.Tokyo Univ. Agr., 3.NARO/ARC)

411 RNA-seq analysis of a novel extra early-flowering einkorn wheat mutant, extra early-flowering 5 (exe5)

☆Kitagawa, S.¹, T. LUU¹, N. Mizuno², S. Nasuda², N. Fujita³, Y. Kazama⁴, T. Abe⁴, K. Murai¹ (1.Dep. Biosci., Fukui Pref. Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.Dep. Biol. Prod., Akita Pref. Univ., 4.RIKEN, Nishina Cent.)

412 Exploitation of active transposons in wheat and related species

○Ubi, B.^{1,3}, Y. Gorafi^{1,4}, J. Kim¹, Y. Monden², H. Tsujimoto¹ (1.Arid Land Res. Cent., Tottori University, 2.Grad. Sch. Env. & Life Sci. Okayama Univ., 3.Dept. Biotech., Ebonyi State Univ. Nigeria, 4.Agr. Res. Corp., Sudan)

413 Plant Omics Data Center (PODC): The Integrated Web Repository for Interspecies Gene Expression Networks and high reliable functional annotation

☆Terashima, S.¹, T. Kudo¹, T. Takano¹, M. Kanno¹, M. Saito¹, S. Asano¹, Y. Sasaki¹, K. Yokoyama¹, M. Kobayashi¹, H. Ohyanagi^{1,2}, K. Yano¹ (1.Sch. of Agri., Meiji Univ, 2.King Abdullah Univ Sci & Technol)

414 A web database OryzaExpress Update: gene expression network based on public microarray data

☆Kudo, T., S. Terashima, Y. Takaki, M. Kanno, K. Yokoyama, K. Yano (Sch. Agri., Meiji Univ.)

415 CATchUP:A new web database providing information on genes specifically expressed in certain conditions

☆Nakamura, Y., T. Kudo, S. Terashima, M. Kanno, M. Saito, N. Matsuda, S. Asano, K. Yano (Sch. of Agri., Meiji Univ.)

416 Head detection of sorghum in the field by RGB images, the methods and applications

☆Guo, W., K. Watanabe, H. Iwata, S. Ninomiya (Grad.Sch.Agric.Life.Sci.,Univ.Tokyo)

417 Development of a simple language to script and simulate breeding schemes: the breeding scheme language

☆Yabe, S. ^{1,2}, H. Iwata ³, J. Jannink ⁴ (1.PRESTO, JST, 2.NARO Agricultural Research Center, 3.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 4.USDA-ARS)

418 Ininterspecific hybridization by ovule culture and embryo rescue in Sweetpea

○Morimoto, Y., Y. Mori (Okayama prefectural research institute for agriculture)

419 Development of the new Japanese radish cv. "Yuuhaku" and "Sara white" without containing 4-methylthio-3-but enyl glucosinolate

○Ishida, M. ¹, T. Kakizaki ¹, T. Kikuchi ², T. Ohara ¹, N. Fukino ¹, J. Kohori ¹, K. Hatakeyama ¹, S. Yoshiaki ¹, J. Ri ², T. Terada ² (1.NARO Institute of Vegetable and Tea Science, 2.Watanabenoji Company,Limited)

420 SNP of mitochondrial genome in *Brassica rapa* and *Brassica juncea*

○Yamagishi, H. ¹, S. Hatono ¹, K. Nishimura ¹, Y. Yamashita ², M. Tsujimura ^{1,2} (1.Fac. Life Sci., Kyoto Sangyo U.,, 2.Kyoto Sangyo U. Plant Organellar Genomics R. C.)

501 Functions of the two genes that suppress activity of transposon Tam3 in *Antirrhinum*

☆Hirata, M. ¹, R. Osawa ², H. Zhou ¹, I. Ebinuma ¹, K. Fujino ¹, Y. Kishima ¹ (1.Research Faculty of Agriculture, Hokkaido Univ., 2.Faculty of Engineering, Hokkaido Univ.)

502 Effects of DNA methylation on the binding activity of a rice autonomous transposable element *Ping*

○Tsukiyama, T. ¹, K. Onohara ¹, M. Tanaka ¹, H. Saito ¹, Y. Okumoto ¹, M. Teraishi ¹, K. Inouye ^{1,2}, T. Tanisaka ^{1,3} (1.Grad. Sch. Agr., Kyoto U., 2.Waki Pharma. Co., Ltd., 3.Dep. Agr. Region. Reclama., Kibi Int. U.)

503 Small RNA production and DNA methylation of soybean retrotransposon *SORE-1*

☆Mikuriya, S. ¹, A. Taneda ², J. Abe ¹, A. Kanazawa ¹ (1.Grad. Sch. Agr., Hokkaido Univ., 2.Grad. Sch. Sci. and Tech., Hirosaki Univ)

504 Qualitative improvement of potato by epigenome editing using grafting

☆Kasai, A., H. Hojo, T. Harada (Fac. Agric. Life Sci., Hirosaki Univ.)

505 Bi-allelic gene targeting in rice

○Endo, M. ¹, M. Mikami ^{1,2}, S. Toki ^{1,2,3} (1.Natl. Inst. Agrobiol. Sci., 2.Gra. Sch. Nanobiol., Yokohama City Univ., 3.Kihara Inst. Biological Res., Yokohama City Univ.)

506 Analysis of an *Arabidopsis* gene *FMT* that regulates mitochondrial distribution in the cell and its paralogs *FML*

☆Kawai, N. ¹, M. Fujimoto ¹, M. Shibamura ¹, K. Katayama ¹, Y. Fukao ², N. Tsutsumi ¹, S. Arimura ¹ (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.Col. Life Sci., Ritsumeikan Univ.)

507 Cell wall polysaccharide composition in *Arabidopsis* mitochondrial morphological mutants

☆Hajime, E. ¹, K. Katayama ¹, A. Nishimura ¹, N. Sakurai ², K. Suda ², M. Fujimoto ¹, N. Tsutsumi ¹, S. Arimura ¹ (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Dept.of Technology Development Kazusa DNA Research Institute)

508 Functional analyses of *LEAF LATERAL SYMMETRY1* involved in leaf morphogenesis

☆Honda, E. ¹, Y. Chow Lih ¹, Y. Nagato ¹, Y. Sato ², J. Itoh ¹ (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Grad. Sch. Bioagri. Sci., U. Nagoya)

509 Genetic regulation and jasmonate action that regulate spikelet development in rice

Hirokawa, T. ¹, D. Sato ¹, W. Tanaka ¹, K. Kurotani ², S. Hatanaka ², I. Takamure ³, S. Takeda ², ☆H. Hirano ¹ (1.Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Bioagri., Nagoya Univ., 3.Grad. Sch. Agric., Hokkaido Univ.)

510 Analysis of a rice mutant, which shows have partial defects in leaf epidermal tissues

☆Matsumoto, H. ¹, Y. Yasui ¹, T. Kumamaru ², H. Hirano ¹ (1.Grad. Sch. Sci., Univ. Tokyo, 2.Fac. Agri., Kyushu Univ.)

511 The difference of the regulation system between aerial stem and rhizome of *Oryza longistaminata*

☆Uehara, K. ¹, J. Nuguroho ¹, H. Kondo ¹, T. Omori ¹, R. Stefan ¹, T. Kawara ¹, T. Furuta ¹, T. Hachiya ^{1,2}, H. Sakakibara ², M. Ashikari ¹ (1.Bioscience and Biotechnology center, 2.RIKEN)

512 miR172 down-regulates the translation of cleistogamy 1 (*cly1*) in barley

Anwar, N. ¹, M. Ohta ¹, T. Yazawa ¹, Y. Sato ¹, A. Tagiri ¹, M. Sakuma ¹, T. Nussbaumer ², P. Bregitzer ³, M. Pourkheirandish ¹, J. Wu ¹, ○T. Komatsuda ¹ (1.National Institute of Agrobiological Sciences, 2.MIPS/IBIS, Germany, 3.USDA-ARS, Aberdeen)

513 Reverse mutation in the barley *cly1* locus converting cleistogamy to chasmogamy

○Kakeda, K. ¹, M. Tomokazu ¹, N. Wang ^{2,3}, C. Liu ^{2,4}, T. Komatsuda ² (1.Grad. Sch. Bioresour., Mie Univ., 2.NIAS, 3.Grad. Sch. Life Env. Sci., Univ. Tsukuba, 4.Crop Res. Inst., Shandong Acad. Agr. Sci.)

514 Effect of photoperiodic response gene *HvPhyC* and *Ppd-H1* on panicle differentiation and heading time in barley

○Aoki, E. ¹, H. Nishida ², T. Tonooka ³, K. Kato ², M. Taira ¹, T. Yanagisawa ¹ (1.NARO Institute of Crop Science, 2.Grad. Sch. Environ. Life Sci., Okayama U., 3.NARO/KARC)

515 Narrowing-down of the novel early-flowering gene region on 2H chromosome in barley

○Nishida, H. ¹, R. Tanabe ¹, K. Kobori ², K. Kato ¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Fac. Agr., Okayama U.)

516 Variation of histone methylation patterns of *VRN1* homoeologous gene in an alloplasmic wheat line showing late-flowering phenotype compared with a euplasmic line

☆Umekita, K. ¹, K. Nagaki ², M. Murata ², K. Murai ¹ (1.Dep. Biosci., Fukui Pref. Univ., 2.IPSR, Okayama Univ.)

517 A master gene BvBTC1, distinguishing annuals from biennial, controls early bolting of sugar beet

○Kuroda, Y., H. Takahashi, K. Okazaki, H. Matsuhira, K. Taguchi (Hokkaido Agricultural Research Center, NARO)

518 Analysis of regulatory mechanism of potato tuber formation

☆Taoka, K. ¹, C. Teo ², K. Takahashi ², A. Saito ², K. Shimizu ², K. Shimamoto ² (1.KIBR, YCU, 2.Grad. Sch. Biol. Sci, NAIST)

519 Genetic analysis of early heading gene located on 7A chromosome of wheat cultivar Ciano 67

○Kato, K. ¹, R. Tanabe ¹, M. Kishii ², H. Nishida ¹ (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.CIMMYT)

520 Epigenome profiling reveals unique cell-type specific patterns of DNA methylation in the root meristem

○Kawakatsu, T. ^{1,2}, T. Stuart ³, M. Valdes ⁵, B. Schmitz ², R. Lister ^{2,3}, P. Benfey ^{4,5}, J. Ecker ^{2,4} (1.NIAS, 2.Salk Institute, 3.UWA, 4.HHMI, 5.Duke Univ.)

521 Function of KNOTTED1 cofactors, the BEL1-like homeobox transcription factors in maize shoot development

☆Tsuda, K. ¹, A. Maeno ², T. Shiroishi ², K. Nonomura ¹, S. Hake ³ (1.National Institute of Genetics, Experimental Farm, 2.National Institute of Genetics, Mammalian Genetics Laboratory, 3.University of California, Berkeley)

601 Utilization of lower pasting characteristics derived from 'Akitasake44' for rice breeding

☆Kawamata, K., Y. Fukazawa, S. Higuchi, K. Okamoto (Plant Biotech. Inst., IBARAKI Agri. Cent)

602 Isolation of starch synthase IIa-deficient mutant rice with high water absorption property and low gelatinization temperature starch

○Fujita, N.¹, Y. Saito², S. Miura¹, Y. Hosaka¹, N. Crofts¹, T. Watanabe², T. Kumamaru³ (1.Facult. Biores. Sci., Akita Pref. Univ., 2.Rice Research Center, KAMEDA SEIKA Co. Ltd., 3.Facult. Agr., Kyushu Univ.)

603 Analyses of starch biosynthetic protein-protein complexes in rice double mutant line with significantly low soluble starch synthase activities

☆Hayashi, M., N. Crofts, M. Kodama, Y. Nakamura, N. Fujita (Dept. of Biol. Production, Akita Pref. Univ.)

604 The analyses of endosperm starch in novel rice lines, in which indica rice genes were introduced into high resistant starch containing BEIIb-deficient mutants

☆Itoh, Y., N. Crofts, M. Abe, N. Fujita (Dept. of Biol. Production, Akita Pref. Univ.)

605 Exploration of glycosyltransferases involved in soyasaponin biosynthesis by use of a high-density mutant library in soybean

☆Krishnamurthy, P.¹, R. Yano^{1,2}, Y. Fujisawa¹, S. Tochigi¹, S. Maita¹, A. Kaga¹, T. Anai³, C. Tsukamoto⁴, M. Ishimoto¹ (1.National Institute of Agrobiological Sciences, 2.Tsukuba University, 3.Saga University, 4.Iwate University)

606 Novel QTLs controlling saponin contents in soybean seed

○Teraishi, M.¹, Y. Tojo¹, N. Yamada², T. Tsukiyama¹, Y. Okumoto¹ (1.Graduate School of Agriculture, Kyoto University, 2.Nagano Vegetable and Ornamental Crops Experiment Station)

607 Annual variation in characteristics of boiled seeds and related components in black soybean landraces

○Hirota, T.¹, S. Yoshida², T. Sawada² (1.Hokubu Agr. Inst., Hyogo Pre. Tech. Cent. Agr. Forest. Fish., 2.Hyogo Pre. Tech. Cent. Agr. Forest. Fish.)

608 Effect of high grain protein content gene *Gpc-B1* on agricultural traits of spring wheat

☆Kurushima, M. ¹, Y. Yamashita ², N. Ashikaga ¹, H. Jinno ¹ (1.Kitami Agri. Exp. Stn., HRO., 2.Chuo Agri. Exp. Stn., HRO.)

609 Genetic interaction and pyramiding effect of QTLs for leaf photosynthesis efficiency detected between Japonica and Indica rice cultivars

○Yamamoto, T. ¹, T. Ueda ¹, S. Adachi ^{1,2}, K. Kondo ^{1,3}, T. Ookawa ², T. Hirasawa ² (1.National Institute of Agrobiological Sciences, 2.Tokyo University of Agriculture and Technology, 3.JIRCAS)

610 Development of RILs for the elucidation of molecular mechanism of heterosis in *Arabidopsis thaliana*

☆Kawanabe, T. ^{1,3}, N. Miyaji ², S. Takada ², E. Itabashi ³, T. Yasuda ³, R. Fujimoto ³ (1.Fac. Life Sci., Univ. Kyoto Sangyo, 2.Fac. Agri., Univ. Kobe, 3.Grad. Sch. Agri. Sci., Univ. Kobe)

611 Functional analysis of four copies of *Oma1*-like gene located in *Restorer-of-fertility 1* locus in sugar beet

☆Arakawa, T., H. Kagami, T. Mikami, T. Kubo (Grad. Sch. Sci., Univ. Hokkaido)

612 Segregation pattern of hybrid-sterility loci in cali derived from anther culture of hybrids between Asian and African rice cultivars

☆Kanaoka, Y., D. Kuniyoshi, I. Masuda, E. Inada, Y. Kishima (Res. Fac. Agr., Univ. Hokkaido)

613 Detailed genetic analysis of fertility restorer genes in eggplant

☆Gyawali, Y. ¹, T. Saito ², H. Fukuoka ², H. Yamagishi ³ (1.Kyoto Sangyo U. Plant Organellar Genomics R. C., 2.NIVTS/NARO, 3.Fac. Life Sci., Kyoto Sangyo U.)

614 Transcription factors for genes regulating small RNA biogenesis in meiotic anther tapetum in rice

☆Ono, S. ¹, K. Tsuda ^{1,2}, R. Komiya ³, E. Fukai ⁴, K. Nonomura ^{1,2} (1.Exp. Farm, Natl. Inst. Genet., 2.Dep. Life Sci., Grad. U. Adv. Study/SOKENDAI, 3.Okinawa Inst. Sci. Tech. Grad. U., 4.Fac. Agr., Niigata U.)

615 Production of alloplasmic *Raphanus sativus* and *Brassica juncea* through wide hybridization with *Brassica rapa* carrying *Dipotaxis erucoides* cytoplasm

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

616 Effects of heading time mutant genes on the canopy development in rice

☆Fushimi, E.¹, H. Saito¹, Y. Koide^{1,2}, W. Guo³, S. Ninomiya³, T. Tanisaka^{1,4}, Y. Okumoto¹ (1.Grad. Sch. Agri., Kyoto Univ., 2.Hakubi Center, Kyoto Univ., 3.Grad. Sch. Agri., Tokyo Univ, 4.Dep. Agric. Regional Reclamation., Kibi Int. Univ)

617 Genome editing using Cas9-gRNA driven by a mono-promoter in rice

☆Mikami, M.^{1,2}, M. Endo², S. Toki^{1,2,3} (1.Gra. Sch. Nanobiol., Yokohama City Univ., 2.Nalt. Inst. Agrobiol. Sci., 3.Kihara Inst. Biological Res., Yokohama City Univ.)

Poster presentations

P001 Characterization of wheat genotypes with high dietary fiber content

☆Tremmel-Bede, K., M. Rakszegi, L. Láng, Z. Bedő (Centre for Agricultural Research, Agricultural Institute, Hungarian Academy of Sciences)

P002 Black-box modeling using multi-task gaussian process for building a heading prediction model

☆Hori, T.¹, T. Aoike¹, A. Onogi^{1,2}, O. Ideta³, T. Yoshioka⁴, K. Ebana⁵, M. Yamazaki⁴, H. Nakagawa⁶, H. Iwata¹ (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.JST PRESTO, 3.Natl. Agr. Res. Ctr., Western Region, 4.Food Resources Education and Research Ctr., Grad. Sch. Agric. Sci., Kobe U., 5.Natl. Inst. Agrobiological Sci., 6.NARO/NARC)

P003 Genomic prediction and selection of seed protein content in soybean

☆Sekine, D.¹, M. Tsuda^{1,2}, T. Shimizu¹, S. Yabe^{3,4}, K. Machita¹, M. Saruta⁵, T. Yamada⁶, M. Ishimoto¹, H. Iwata⁴, A. Kaga¹ (1.NIAS, 2.Grad. Sch. Life&Env Sci., U. Tsukuba, 3.NARO/NARC, 4.Grad. Sch. Agr. Life Sci., U. Tokyo, 5.NARO/WARC, 6.NARO/NICS)

P004 Fluorescing seeds: visible markers for efficient screening of GM rice seeds

☆Akasaka, M. ¹, Y. Taniguchi ¹, M. Oshima ², Y. Tabei ², J. Tanaka ¹ (1.NARO/NICS, 2.NIAS)

P005 Possible selection for high yield wheat lines by using harvest index and canopy temperature

☆Ohnishi, S., H. Jinno (Kitami AES, HRO)

P006 Can historical data of crop performance trials accelerate data-driven breeding? An attempt in soybean

○Onogi, A. ^{1,2}, H. Iwata ², S. Ninomiya ² (1.JST PRESTO, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

P007 A database of rice irradiation mutants

☆Li, F., N. Nishimura, S. Niwa, H. Kato (Institute of Radiation Breeding, NIAS, MAFF)

P008 The application of Semantic Web Technology to contents of PGDBj (Plant Genome DataBase Japan)

○Ichihara, H. ¹, S. Shirasawa ¹, T. Shibaya ¹, A. Nakaya ², Y. Nakamura ¹, E. Asamizu ³, H. Hirakawa ¹, S. Tabata ¹ (1.Kazusa DNA Res. Inst., 2.Grad. Sch. Med. Osaka Univ., 3.Fac. Agri. Ryukoku Univ.)

P009 Quantitative evaluation of leaf color in field and greenhouse

Matsunaga, T. ¹, D. Ogawa ², F. Taguchi-Shiobara ², S. Matsunaga ¹, ○Y. Habu ² (1.Fac Sci Technol, Tokyo Univ Sci, 2.Agrogenomics Res Center, NIAS)

P010 QTL analysis and genomic prediction of seed morphology in a RIL population of sorghum

☆Sakamoto, R. ¹, M. Fujimoto ^{1,2}, H. Takanashi ^{1,2}, H. Kanegae ¹, M. Ishimori ¹, M. Kobayashi ^{2,3}, K. Yano ^{2,3}, F. Wacera ⁴, R. Hijiya ⁴, N. Ohnishi ⁴, N. Tsutsumi ^{1,2}, W. Sakamoto ^{2,4}, H. Iwata ^{1,2} (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.JST,CREST, 3.Sch. of Agri., Meiji Univ., 4.Inst. Plant Sci. Res., Okayama Univ.)

P011 Production of superior lines using cross breeding in Japanese lawn grass (Zoysia genus)

☆Chiba, S., Y. Matsuda, T. Murata (Grad.Sch.of Agri.Tokai U)

P012 Mutant breeding of a Japanese traditional black rice cultivar Yayoi-Murasaki to improve seed shattering trait

Tada, N., ☆S. Konishi-Sugita (Kagawa University)

P013 Breeding of a new waxy barley cultivars 'Waxy Fiber' with high beta-glucan content

○Yanagisawa, T.¹, E. Aoki¹, M. Taira¹, T. Yoshioka², T. Tonooka³ (1.NARO Institute of Crop Science, 2.NARO/WARC, 3.NARO/KARC)

P014 Soybean lines for narrow-row dense culture in south-western Japan

○Kono, Y.¹, M. Takahashi¹, N. Oki¹, M. Takahashi² (1.NARO, KARC, 2.NARO, NICS)

P015 Production of favorable line by using crossbreeding of yacon (*Smallanthus sonchifolius*)

☆Moriyama, R., Y. Matsuda, T. Murata (Grad.Sch.of Agri. Tokai U.)

P016 Breeding of a rice high-yielding variety "Oonari" by improving shattering habit of "Takanari"

○Kobayashi, N.¹, T. Ishii¹, M. Yamaguchi¹, H. Hirabayashi¹, Y. Takeuchi¹, M. Kuroki¹, A. Goto¹, H. Sato², H. Maeda³, H. Nemoto⁴, I. Ando¹, H. Ohta⁵, Y. Sunohara⁶, H. Tsunematsu¹, J. Tanaka¹, T. Ikegaya⁶, N. Tsuda⁵, H. Kato⁴ (1.NICS, NARO, 2.NARO/KARC, 3.NARO/ARC, 4.NIAS, 5.NARO/TARC, 6.NARO/HARC)

P017 Present circumstance and future of breeding sweetpotato for steamed and cured slices 'Hoshi-imo'

○Kuranouchi, T.¹, A. Takada², Y. Nakamura¹, T. Kumagai¹, M. Nakatani³, K. Katayama¹ (1.NARO Inst. of Crop Sci., 2.NARO Headquarters, 3.MAFF)

P018 "Satsuiku 2", the first LOX-less (with no lipoxygenase-1 activity) malting barley variety in Japan -II-

○Kanatani, R.¹, Y. Tokizono¹, W. Saito¹, T. Hoki¹, N. Hirota¹, M. Kihara¹, K. Takoi², T. Shinkai², A. Tanigawa², K. Ogushi¹ (1.Bioresources Research and Development Department, Sapporo Brew. Ltd., 2.Product & Technology Innovation Department, Sapporo Brew. Ltd.)

P019 Inheritance and estimating heritability of male sterility in the progenies of Satsuma mandarin

☆Goto, S., T. Yoshioka, M. Kita, S. Ohta, T. Shimizu (Inst. Fruit Tree Sci., NARO)

P020 Agronomic characteristics of the near-isogenic line about the leaf shape of soybean

○Saruta, M., Y. Takada, K. Yamashita (NARO/WARC)

P021 Breeding of a high-yielding glutinous rice variety "Yatanomochi"

○Goto, A.¹, M. Yamaguchi¹, T. Ishii¹, H. Hirabayashi¹, Y. Takeuchi¹, N. Kobayashi¹, M. Kuroki¹, I. Ando¹, H. Kato², H. Nemoto², T. Imbe³, Y. Sunohara⁴, H. Sato⁵, H. Ohta⁶, H. Maeda⁷, O. Ideta⁸, M. Hirayama⁹, M. Sakai³, H. Tsunematsu¹, J. Tanaka¹, K. Tamura¹⁰, N. Tsuda⁶, T. Ikegaya⁴, N. Aoki⁵ (1.NICS, NARO, 2.NIAS, 3.NARO, 4.NARCH, NARO, 5.KONARC, NARO, 6.TARC, NARO, 7.NARC, NARO, 8.WRARC, NARO, 9.Ibaraki Agric. Inst., 10.Iwate Biotech. Res. Center)

P022 Differences in the elongation speed of seminal root and coleoptile between rice varieties

○Ohmori, S., I. Nagaoka, A. Fukuda (Hokuriku Research Center, NARC)

P023 Varietal differences in growth-promoting effect appearing in rice seedlings which inoculated with biofertilizer bacteria *Bacillus pumilus* TUAT1 strain

○Higuma, S., M. Kanekatsu, T. Yamada, T. Yokoyama (Grad. Sch. Agr., Tokyo U. Agr. Tech.)

P024 Genetic mapping of "sinskajae syndrome"-related genes found in an accession of "Chernobyl radio mutant collection "in wheat

Amagai, Y.¹, L. Burdenyuk-Tarasevych², T. Kuboyama¹, ○N. Watanabe¹ (1.Coll. Agr., Ibaraki U., 2.Bila Tserkva Selection and Breeding Station, Ukraine)

P025 Exploration and Conservation of Plant Genetic Resources in Cambodia

○Okuzumi, H.¹, S. Ouch², E. Nonaka¹, S. Sakan² (1.National Institute of Agrobiological Sciences, 2.Cambodian Agricultural Research and Development Institute)

P026 Distribution of insertion sequences at upstream region of *Vrn-A3* locus among tetraploid wheat accessions

☆Nishimura, K., K. Katsura, H. Saito, T. Kawahara, A. Kitajima, T. Nakazaki (Grad. Sch. Agri., Univ. Kyoto)

P027 Pathogenicity and DNA polymorphism of SSR markers in the clubroot pathogen (*Plasmodiophora brassicae*)

○Kubo, N. ^{1,2}, K. Onnazaka ³, U. Ono ², G. Tsuji ¹ (1.Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ., 2.Biotechnol. Dept., Kyoto Pref. Agric. Forest. Fish. Technol. Cent., 3.Kyoto Pref. Kyoto Otokuni Agric. Ext. Cent.)

P028 Chromosome discrimination in diploid *Fragaria vesca*, *F. iinumae* and *F. nipponica* by BAC-FISH technique and its application to octoploid strawberry *F. X ananassa*

Nagayama, I. ¹, ○T. Koba ^{1,2}, S. Kikuchi ¹, H. Sassa ¹ (1.Grad. Sch. Hort., Chiba Univ., 2.Cen. Envi., Health, Field. Sci., Chiba Univ.)

P029 Analysis of genetic diversity among sugarcane genetic resources by array-marker technology

○Enoki, H. ¹, M. Mori ¹, M. Tanaka ², T. Hattori ² (1.TOYOTA Motor Corporation FP Div. Bio Research Lab., 2.NARO Kyushu Okinawa Agricultural Research Center)

P031 Diversity of ribosomal DNA and chromosome conformation gene in *Camellia*

☆Ogawa, S. ¹, S. Sugiyama ², S. Iida ^{2,3}, T. Ota ², N. Ohmido ⁴, K. Furukawa ² (1.National Institute of Technology, Numazu college, Advanced Engineering Course, 2.National Institute of Technology, Numazu college, 3.Department of Environmental and Life Sciences Toyohashi University of Technology, 4.Kobe University, Graduate school of human development and environment)

P032 Functioning of the Multilateral System of the ITPGRFA + recent progress in implementing the Nagoya Protocol to the CBD

○Yamamoto, A. (Environment Policy Office, Policy Planning Division, Minister's Secretariat, MAFF)

P033 QTL analysis for yield-related traits in F2 of a cross between *Oryza longistaminata* introgression line pLIA-4 and Koshihikari under low input conditions

☆Gichuhi, E.¹, M. Maekawa² (1.Graduate school of Environmental and Life Science, Okayama University, 2.Institute of Plant Science and Resources, Okayama University)

P034 Characterization of *spw1-cls2*, a cleistogamous mutant of rice, under field conditions

○Kuroki, M.¹, T. Ikegaya², H. Shimizu², T. Hayashi², A. Fukushima³, T. Yamaguchi⁴, S. Ohmori⁴, H. Yoshida¹ (1.NARO Inst. Crop Sci., 2.NARO Hokkaido Agri. Res. Cent., 3.NARO Tohoku Agri. Res. Cent., 4.NARO Agri. Res. Cent.)

P035 Evaluation of temperature responses of cleistogamy and cold tolerance in *spw1-cls* mutants using the temperature gradient chamber

○Hayashi, T.¹, T. Yamaguchi², S. Koike³, M. Kuroki⁴, T. Ikegaya¹, H. Shimizu¹, S. Ohmori², A. Fukushima³, H. Yoshida⁴ (1.NARO Hokkaido Agricultural Research Center, 2.NARO Agricultural Research Center, 3.NARO Tohoku Agricultural Research Center, 4.NARO Institute of Crop Science)

P036 Genetic variation for resistant to blast disease (*Pyricularia oryzae* Cavara) in rice (*Oryza sativa* L.) of Bangladesh

○Khan, M.¹, I. Koga², M. Khalequzzaman¹, M. Latif¹, M. Ali¹, Y. Fukuta² (1.Bangladesh Rice Research Inst., BRRI, 2.Tropical Agriculture Research Front, Japan International Research Center Agricultural Sciences (JIRCAS))

P037 Sequence variation of *Psy* and *Ccs* genes in "cheiro white", a white fruit pepper variety, and its carotenoid composition determined by TLC

☆Tsurumaki, K.¹, Y. Inaba², Y. Matsumoto², T. Sasanuma^{1,2} (1.United Grad. Sch. Agr. Sci., Iwate Univ., 2.Fac. Agr., Yamagata Univ.)

P038 Investigation of novel loci involved in the loss of seed shattering in Indica rice cultivar Kasalath

☆Oka, Y.¹, C. Inoue¹, T. Htun^{1,2}, Y. Takenaka¹, Y. Tsujimura¹, T. Ishii¹, R. Ishikawa¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Yezin Agr. Univ.)

P039 *gw2* mutation in Koshihikari background increases grain weight of brown rice and grain yield

☆Yamamoto, T.¹, S. Segami^{1,2}, M. Horikawa¹, K. Takehara¹, M. Nakamura¹, T. Hayashi³, F. Nakaoka³, A. Kobayashi³, K. Tomita³, H. Kitano⁴, K. Miura¹, Y. Iwasaki¹
(1.Dept. Biosci. Fukui Pref. Univ., 2.JSPS Research Fellow, 3.Fukui Agr. Exp. Stn.,
4.Biosci. Biotech. Cent. Nagoya Univ.)

P040 Evaluation of mutation in HIGOGIKU cv. 'Benifudou' induced by heavy ion-beam irradiation

☆Kuramoto, T.¹, Y. Matsuda¹, T. Murata¹, T. Abe² (1.Grad.Sch.of Agri. Tokai U,
2.RIKEN, Nishina Cent)

P041 Mutations on leaf organ differentiation cycle of rice found in tag lines which had been produced by using the endogenous transposon *mPing* as mutagen

○Horibata, A. (Fac. of BOST, Kinki Univ.)

P042 Approach to new cultivar breeding of "Sadowara" egg plant of Miyazaki origin vegetable using crossing method

☆Hiejima, T.¹, Y. Iwamoto¹, D. Toyomoto¹, L. Chen^{1,2} (1.Graduate School of Hort. Food Sci., Minami Kyushu U., 2.Fac. Environ. Hort. Sci., Minami Kyushu U.)

P043 Approach to new cultivar breeding of "Hyuga-kabocha" squash of Miyazaki original vegetable variety using interspecific crossing method

☆Iwamoto, Y.¹, D. Toyomoto¹, T. Hiejima¹, L. Chen^{1,2} (1.Graduate School of Hort. Food Sci., Minami Kyushu U., 2.Fac. Environ. Hort. Sci., Minami Kyushu U.)

P044 Sex type and genome size variation in backcross individuals derived from *Carica papaya* and *Vasconcellea cundinamarcensis* intergeneric crosses

○Tarora, K.¹, K. Yasuda¹, S. Kawano¹, H. Ueno², H. Matsumura³, N. Urasaki¹
(1.Okinawa Pref. Agric. Res. Ctr., 2.Dep. Biosci. Tex. Tech., Shinshu Univ., 3.Gene Res. Ctr., Shinshu Univ.)

P045 Estimation of genomic factors responsible for hybrid lethality expressed in hybrids between *Nicotiana tabacum* and five accessions of *N. occidentalis*

☆Ohya, Y.¹, M. Maekawa², T. Iizuka¹, T. Morikawa¹, M. Yanase¹, S. Yokoi¹, M. Oda¹, T. Tezuka¹ (1.Grad. Sch. Life Envi. Sci., Osaka Pref. U., 2.Sch. Life Envi. Sci., Osaka Pref. U.)

P046 Effects of the PAL inhibitor on hybrid lethality in the cross *Nicotiana suaveolens* × *N. tabacum*

Nakamura, R.¹, T. Yamada², W. Marubashi³, M. Oda¹, ○T. Tezuka¹ (1.Grad. Sch. Life Envi. Sci., Osaka Pref. U., 2.Grad. Sch. Agr., Tokyo U. Agr. Tec., 3.Sch. Agr., Meiji U.)

P047 Effects of ploidy level of *Nicotiana suaveolens* on reproductive isolation observed in crosses with *N. tabacum*

☆He, H.¹, T. Iizuka¹, M. Maekawa², T. Morikawa¹, M. Yanase¹, S. Yokoi¹, M. Oda¹, T. Tezuka¹ (1.Grad. Sch. Life Envi. Sci., Osaka Pref. U., 2.Sch. Life Envi. Sci., Osaka Pref. U.)

P048 Quantitative trait loci analysis in backcross progeny of amphidiploid festulolium

○Tamura, K.¹, Y. Sanada¹, K. Tase¹, A. Kubota², Y. Akiyama² (1.NARO/HARC, 2.NARO/TARC)

P049 Seed production of sweet potato using grafting method and establishment of direct gene transformation to sweet potato seeds using electroporation method -

○Chen, L.¹, S. Masuoka¹, Y. Nishimura¹, Y. Takahata² (1.Fac. Envir. Horti. Sci., Minami Kyushu U., 2.Kyushu Okinawa Agri. Res. Cent.)

P050 Approach to obtaining of transformants of ASG-1 using plant regeneration system from seed culture of sexual guinea grass-

☆Toyomoto, D.¹, Y. Iwamoto¹, T. Hiejima¹, K. Yoshida², T. Sugita³, L. Chen⁴ (1.Graduate School of Hort. Food Sci., Minami Kyushu U., 2.Fac. Agri., U. Tokyo, 3.Miyazaki Pref. Agri. Experi. Stan., 4.Fac. Environ. Hort. Sci., Minami Kyushu U.)

P051 Isolation of promoters regulating callus-specific gene expression in barley

☆Hisano, H., H. Ando, K. Sato (IPSR, Okayama Univ.)

P052 Genome editing on FAD2 gene in *Brassica napus*

○Okuzaki, A., J. Imamura, N. Koizuka (Fac. Agr., Tamagawa)

P053 Science communication between the public and researchers about NBT with establishing trust

○Sasakawa, Y.¹, Y. Sassa¹, Y. Tanaka² (1.Life&Bio plaza 21, 2.Faculty of Info., Osaka Gakuin Univ.)

P054 Evaluation of blast partial resistance genes and effect of accumulation focused on *pi21*

☆Suzuki, T.¹, M. Nakamura¹, S. Fukuoka², A. Ikeda¹ (1.Aichi Agri. Res. Cent. Mount. Reg. Agri. Res. Inst., 2.NIAS)

P055 The effective combinations of resistant QTLs to the three pathotypes of Wheat yellow mosaic virus in Japan

☆Kojima, H.¹, Z. Nishio², K. Hatta³, T. Sasaya², M. Seki⁴, C. Otobe¹, T. Takayama¹, Y. Fujita¹, M. Chono¹, H. Matsunaka², S. Oda¹ (1.NICS, 2.NARO/KARC, 3.NARO/HARC, 4.NARO/ARC)

P056 Development of the multi-desease resistant transgenic rice. IV Evaluation of bacterial leaf blight resistance in the field

○Yamazaki, M., S. Goto, F. Shimoda, H. Takatsuji (NIAS)

P057 Tandem repeated organization of NB-LRR genes in the clubroot resistant *CRb* locus in *Brassica rapa* L.

○Hatakeyama, K.^{1,2}, T. Niwa¹, T. Kato^{1,3}, T. Ohara¹, T. Kakizaki¹, S. Masumoto^{1,4} (1.NIVTS, 2.Fac. Agri., Iwate Univ., 3.Nippon Norin Seed Co., 4.TARC)

P058 Canceled

P059 Seed dormancy of wheat lines introduced MFT, 5AL-QTL and seed coat color related to pre-harvest sprouting resistance into durum wheat from Zenkoujikomugi

○Takata, K.¹, W. Funatsuki¹, M. Yanaka¹, H. Okusu² (1.NARO/WARC, 2.NIPPN)

P060 Genome wide association study of wheat heat tolerance in MSD population

☆Elbashir, A.^{1,3}, Y. Gorafi^{2,3}, J. Kim², H. Tsujimoto² (1.Graduate School of Agricultural Sciences, Tottori University, 2.Arid Land Research Center, Tottori University, 3.Agricultural Research Corporation, Sudan)

P061 Relationship between the overwintering ability of F9 and F10 RIL from "Fuyugoshi" (a domestic rice strain) × "Hoshinoyume" cross in Hokkaido

○Ushiki, J.¹, S. Matsuba¹, S. Hayashi¹, K. Okazaki² (1.Nat. Agr. Res. Cent. for Hokkaido Region, 2.Nat. Agr. Res. Cent.)

P062 Exploring rice genetic resources for seed germination and coleoptile elongation under anaerobic condition

☆Kuya, N., J. Sun, T. Yamamoto (NIAS)

P063 Evaluation on flooding tolerance of soybean cultivar's root system under oxygen deficient conditions

☆Fujimoto, S.¹, H. Takahashi¹, T. Mochizuki², R. Takahashi³, M. Nakazono¹ (1.Grad. Sch. Bioagri. Sch., Nagoya Univ., 2.Fac. Agri. Grad. Sch., Kyushu Univ., 3.NICS)

P064 Allele frequency of Mother of FT AND TFL1 (MFT) gene and their effects on seed dormancy in soft winter wheat lines in Hokkaido

☆Sonoda, T.¹, M. Chono², G. Ishikawa³, H. Jinno¹ (1.Kitami Agr. Exp. Stn.,HRO, 2.Inst. Crop Sci.,NARO, 3.Tohoku Agr. Res. Cent.,NARO)

P065 Correlation of F1-ATPase gene expression in the high temperature environment and damage to rice grain filling

Arisu, Y., L. Ou, R. Matsumoto, K. Tsujiuchi, J. Nakajima, H. Kusano, ○H. Shimada (Department of Biological Science and Technology, Tokyo University of Science)

P066 Performance of sorghum stay green introgression lines under different levels of post-flowering drought

☆Kamal, N.^{1,2}, Y. Gorafi¹, H. Tsujimoto¹, A. Ali^{2,3} (1.Arid Land Research Center, Tottori University, Japan, 2.Biotechnology and Biosafety Research Center, Agricultural Research Corporation, Sudan, 3.Plant Breeding and Genetics Laboratory, FAO/IAEA Joint Division, International Atomic Energy Agency (IAEA), Sibersdorf, Austria)

P067 Relationship between barrier to radial oxygen loss and suberin/lignin in *Zea nicaraguensis*

☆Watanabe, K.¹, S. Nishiuchi¹, S. Sato¹, F. Omori², H. Takahashi³, Y. Mano², M. Nakazono¹ (1.Grad. Sch. Bioagri. Sci., Nagoya Univ., 2.NARO Inst. Livest. Grassl. Sci.,

P068 Tolerance to high-temperature stress during ripening of rice Hokkaido cultivars

○Yasuda, H., R. Kaji, S. Matsuba, T. Ikegaya (NARO Hokkaido Agricultural Research Center)

P069 Water-saving drought stress tolerance of wheat due to enhancement of ABA signaling pathway

☆Mega, R.¹, F. Abe², J. Kim¹, K. Tanaka⁶, H. Kobayashi⁶, Y. Sakata⁵, H. Tsujimoto¹, K. Hanada³, M. Okamoto^{1,4} (1.Arid Land Research Center, Tottori University, 2.National Institute of Crop Science, NARO, 3.Frontier Research Academy for Young Researchers, Kyushu Institute of Technology, 4.JST, PRESTO, 5.Department of Bioscience, Tokyo University of Agriculture, 6.NODAI Genome Research Center)

P070 Physiological Response of Arabidopsis plants deficient in an unknown function gene At1g26580 to a combination of drought and heat stress

☆Nakano, R., M. Endo, N. Suzuki (Department of Materials and Life Sciences Faculty of Sciences and Technology Sophia University)

P071 Heat stress responses of Arabidopsis plants regulated by different heat sensors during vegetative stage

☆Kataoka, R., M. Takahashi, M. Fujii, N. Suzuki (Department of Materials and Life Sciences Faculty of Sciences and Technology Sophia University)

P072 Response of Arabidopsis plants deficient in salicylic acid or jasmonic acid signal to a combination of drought and heat stress

☆Kumazaki, A., N. Suzuki (Department of Materials and Life Sciences Faculty of Sciences and Technology Sophia University)

P073 Expression analysis of sugar metabolism related-genes during soybean secondary aerenchyma formation

○Takahashi, H.¹, A. Yanagawa¹, S. Hiraga², S. Shimamura³, M. Nakazono¹ (1.Grad. Sch. Agric. Sci., Nagoya U., 2.NARO Nat. Inst. Crop. Sci., 3.NARO Tohoku Agric. Res. Cent.)

P074 Response of *Arabidopsis* plants deficient in different heat sensors to heat stress during seedling and reproductive stages

☆Katano, K., N. Suzuki (Department of Materials and Life Sciences Faculty of Sciences and Technology Sophia University)

P075 QTL analysis of salt stress tolerance in wheat landraces

☆Tokunaga, A., K. Kawaura, S. Sakuma, Y. Ogihara (KIBR, Yokohama City Univ.)

P076 Genetic analysis of *qA1*, a locus for aluminum tolerance detected between wild rice (*Oryza rufipogon* W630) and cultivated rice (*O. sativa* Nipponbare)

Wada, M.¹, M. Iwata¹, K. Yokosho², S. Yoshida¹, P. Thanh¹, T. Ishii¹, J. Ma², ○R. Ishikawa¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.IPSR, Okayama Univ.)

P077 Improvement of cold tolerance in rice by cold induced expression of heat shock factor gene

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

P078 Functional analysis of potassium transporters from *S. virginicus*

○Tada, Y.¹, M. Katsuhara², C. Endo¹, T. Kurusu¹ (1.Sch of Biosci. Biotechnol., Tokyo Univ. of Technol., 2.Okayama Univ., Inst. of Plant Sci. Resources)

P079 Discrimination method for identifying a degree of sensitivity to the herbicide Benzobicyclon in various rice cultivars

○Kato, H.¹, M. Kawata³, K. Sekino⁴, Y. Yamada⁴, A. Yamazaki⁴, M. Ohshima³, H. Maeda² (1.National Institute of Agrobiological Sciences, 2.NARO National Agricultural Research Center, 3.NARO Institute of Crop Science, 4.SDS Biotech K.K.)

P080 Functional analysis of 4-HPPD inhibitory herbicide resistance gene from japonica rice

○Hirose, S.¹, M. Kawagishi-Kobayashi², H. Yoshida², Y. Taniguchi², A. Yamazaki³, K. Sekino³, Y. Yamada³, H. Maeda⁴, K. Murata⁵, H. Kato¹, M. Ohshima², M. Kawata², Y. Tozawa⁶ (1.National Institute of Agrobiological Sciences, 2.NARO Institute of Crop Science, 3.SDS Biotech K.K., 4.NARO National Agricultural Research Center, 5.Toyama Prefectural Agricultural, Forestry and Fisheries Research Center, 6.Saitama University, Graduate School of Science and Engineering)

P081 Influence of *MOTHER OF FT AND TFL1 (MFT-3A)*on pre-harvest sprouting related traits in wheat

○Nishimura, T. ^{1,2}, W. Nakane ³, H. Jinno ⁴, K. Nakamichi ⁵, M. Mori ³, H. Miura ³
(1.Kamikawa Agri.Exp.Stn.,HRO, 2.UGAS, Iwate Univ., 3.Obihiro Univ. Agric. & Vet. Med.,
4.Kitami Agri.Exp.Stn.,HRO, 5.Central Agri.Exp.Stn.,HRO)

P082 Rapid estimation of tofu property for breeding in soybean

○Takahashi, M. ¹, Y. Kono ¹, N. Oki ¹, M. Takahashi ² (1.NARO, KARC, 2.NARO, NICS)

P083 Response of amylose content of rice NIL (*qAC2*) to the seed maturing temperature

○Takemoto-Kuno, Y., H. Hirabayashi, T. Ishii, M. Yamaguchi, Y. Takeuchi (NARO Institute of Crop Science (NICS))

P084 Novel mutant alleles of the starch biosynthetic enzyme gene with altered characteristics of cocked rice texture

☆Nakata, M. ¹, T. Miyashita ¹, R. Kimura ¹, Y. Nakata ¹, T. Umemoto ², H. Yamakata ¹
(1.NARO/ARC, 2.NARO/HARC)

P085 Eating quality and starch characteristics of chromosome segment substitution lines of indica varieties, 'Bei Khe' or 'Tupa121-3', in Koshihikari

☆Hayashi, T. ¹, A. Kobayashi ¹, S. Fukuoka ², J. Yonemaru ², K. Tomita ¹, T. Shimizu ¹
(1.Fukui Agr. Exp. Stn., 2.NIAS)

P086 The relationship between Ppo-D1 gene and noodle sheet colour

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

P087 Differences in effects of top dressing to β -glucan contents in near isogenic barley lines

○Takahashi, A., T. Yoshioka (NARO/WARC)

P088 Genetic diversity and protein expression analysis of starch synthase genes in Asian common wheat

○Tanaka, H.¹, Y. Tanaka², C. Morris³, H. Tsujimoto⁴ (1.Fac. Agr., Tottori Univ., 2.Grad. Sch. Agr., Tottori Univ., 3.USDA/ARS, 4.ALRC, Tottori Univ.)

P089 Relationship between polyphenol oxidase genotypes involved in dough discoloration and a yellow mosaic disease resistance in wheat

○Ito, M.¹, T. Ikeda², Z. Nishio³, Y. Uehara⁴, H. Maejima⁴, G. Ishikawa⁵, T. Nakamura⁵, M. Saito⁵, Y. Terasawa¹, K. Nagasawa¹, K. Hatta¹ (1.NARO Hokkaido Agricultural Research Center, 2.NARO Western Region Agricultural Research Center, 3.NARO Kyushu Okinawa Agricultural Research Center, 4.Nagano Prefecture Agricultural Experiment Station, 5.NARO Tohoku Agricultural Research Center)

P090 Identification of quantitative trait loci controlling zinc concentration in seed using Australian wild rice, *Oryza meridionalis*

Iwata, M.¹, ☆K. Taniko¹, G. Monden¹, O. Chhourn¹, S. Yoshida¹, T. Ishii¹, J. Ma², R. Ishikawa¹ (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.IPSR, Okayama Univ.)

P091 Long-distance transport of glucosinolates in radish

○Kakizaki, T., N. Fukino, T. Ohara, M. Ishida (NARO Institute of Vegetable and Tea Science)

P092 Interaction among QTLs for flower color intensity of morning glory and polymorphisms of *InMYB1*, a candidate gene of *ADM2*, among strains

☆Miyamoto, K.¹, S. Okuno¹, H. Katsuyama¹, A. Hoshino², E. Nitashaka³, S. Iida⁴, N. Watanabe¹, T. Kuboyama¹ (1.Col. Agr., Uni. Ibaraki, 2.Natl. Inst., Basic Biol, 3.Grad. Sch. Sci., Uni. Kyushu, 4.Grad. Sch. Nutri. and Env. Sci. & Grad. Sch. Pharm. Sci., Uni. Shizuoka)

P093 Analysis of *qPBL6* regulating the primary rachis branch length in panicle of rice

☆Ota, S.¹, T. Hobo², K. Ando¹, R. Isihara¹, A. Agata¹, M. Ikeda², K. Doi¹, H. Kitano² (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U.)

P094 Development of a new type of wheat having starch characteristics reducing bread staling

☆Inokuma, T.¹, Y. Shinkai¹, Y. Taniguchi², M. Saito², A. Sunohara¹, T. Shimbata¹, P. Vrinten³, T. Nakamura² (1.Central Lab. Nippon Flour Mills Co., Ltd., 2.NARO/TARC,

P095 Estimation of QTL associated with increase in root volume at heading stage in rice, using chromosome segment substitution lines

○Fukuda, A.¹, J. Tanaka², K. Hori¹, T. Yamamoto¹ (1.National Institute of Agrobiological Sciences, 2.NARO Institute of Crop Science)

P096 Patterns of histone-methylation and expression of a class B MADS-box gene for flower development in bread wheat

☆Kuwabara, T.¹, M. Tanaka¹, K. Umekita¹, K. Nagaki², M. Murata², K. Murai¹ (1.Dep. Biosci., Fukui Pref. Univ., 2.IPSR, Okayama Univ.)

P097 Functional analysis of heterotrimeric G-protein γ2-subunit in rice

☆Fujita, M.¹, I. Sugita¹, S. Segami^{1,2}, K. Miura¹, Y. Iwasaki¹ (1.Dept. Biosci. Fukui Pref. Univ., 2.JSPS Research Fellow)

P098 Characterization of CYP78 regulating lateral organ and seed size in Rice

Mizuno, I., J. Itoh, ○K. Hibara (Grad.Sch.Agric.Life Sci., U.Tokyo)

P099 Expression and functional analyses of subtilisin-like proteases during early stages of rice seed development

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

P100 Allelic interaction at awning loci in the genetic backgrounds of wild and cultivated rice

☆Ikemoto, M., M. Otsuka, R. Ishikawa, T. Ishii (Grad. Sch. Agr. Sci., Kobe Univ.)

P101 Effects of air temperature on flowering signals of rice under short day conditions

☆Yoshitsu, Y.¹, M. Okada¹, D. Onodera¹, Y. Takahata¹, S. Yokoi² (1.Fac. Agri., Iwate Univ., 2.Grad.Sch. Lif. Envi. Sci., Osaka Pref. Univ.)

P102 Characterization of ssg6, a large amyloplast mutant of rice

○Matsushima, R.¹, M. Maekawa¹, M. Kusano², K. Tomita³, H. Kondo¹, H. Nishimura¹, N. Crofts⁴, N. Fujita⁴, W. Sakamoto¹ (1.Institute of Plant Science and Resources, Okayama University,, 2.Graduate School of Life and Environmental Sciences, University of Tsukuba, 3.Fukui Agricultural Experiment Station, 4.Department of Biological Production, Akita Prefectural University)

P103 The Juvenile - Adult phase change of soybean is regulated by photoperiod

☆Ozawa, S.¹, Y. Takahata¹, S. Yokoi² (1.Fac. Agr., Iwate Univ., 2.Grad. Sch. Lif. Envi. Sci., Osaka Pref. Univ.)

P104 Examination of indoor pollination conditions for the practical use of indoor seed production technique in *Cryptomeria japonica*

○Kurita, M.¹, Y. Hiraoka², T. Yamanobe², T. Hirao², M. Tamura³, M. Takahashi², A. Watanabe³ (1.Kyushu Regional Breeding Office, Forest Tree Breeding Center, FFPRI, 2.Forest Tree Breeding Center, FFPRI, 3.Faculty of Agriculture, Kyushu University)

P105 Evolutionary mechanism of restorer-of-fertility 1 gene inferred by its structural diversification in sugar beet

☆Ue, S., Y. Honma, Y. Yoshida, Y. Kamei (Grad. Sch. Agr., Hokkaido Univ.)

P106 Application of unfertilized ovule culture in doubled haploid production of foreign gentians

☆Takamura, Y.¹, T. Hikage², K. Hatakeyama¹, Y. Takahata¹ (1.Fac. Agri., Iwate Univ., 2.Hachimantai City Floricultural R & D Center)

P107 Identification of rice proteins interacting to germline-specific Argonaute protein MEL1

○Liu, H.¹, S. Ono¹, R. Hiratsuka², E. Fukai³, K. Nonomura^{1,4} (1.Exp. Farm, Natl. Inst. Genet., 2.Dpt. Nat. Sci, Jikei U., School Med., 3.Fac. Agr. Niigata U., 4.SOKENDAI, Life Sci.)

P108 DNA Polymorphism Annotation Database (DNApod): Toward an Integration of SRA-Driven Genotypic Data and Public Phenotypic Data

○Mochizuki, T.¹, Y. Tanizawa¹, T. Fujisawa¹, N. Nikoh², T. Shimizu³, A. Toyoda^{4,5}, A. Fujiyama^{4,5,6}, N. Kurata^{5,7}, H. Nagasaki¹, E. Kaminuma^{1,5}, Y. Nakamura^{1,5}

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P109 Development of Genome-wide Indel markers in foxtail millet -its distribution, mapping and diversity

Abe, Y.¹, Y. Shinkawa¹, N. Tanaka¹, Y. Nakayama¹, Y. Mukainari¹, H. Suga¹, H. Takagi², R. Terauchi², ○K. Fukunaga¹ (1.Fac.Life & Environ. Sci., Pref. U. Hiroshima, 2.Iwate Biotech.Res.Center)

P110 Detection of genetic polymorphisms by targeted re-sequencing in Soybean

☆Ogiso-Tanaka, E.¹, A. Kaga¹, T. Sayama¹, N. Kamei², M. Ishimoto¹ (1.National Institute of Agrobiological Sciences, 2.Thermo Fisher Scientific Life Technologies Japan Ltd.)

P111 Flesh color-specific RAD-derived markers for pineapple (*Ananas comosus*)

○Urasaki, N.¹, R. Kaneshima¹, K. Watanabe¹, S. Goeku¹, K. Tarora¹, M. Takeuchi², C. Moromizato², K. Yonamine², S. Tamashiro², F. Hosaka³, K. Nashima³, S. Terakami³, H. Matsumura⁴, T. Yamamoto³, M. Shoda¹ (1.Okinawa Pref. Agric. Res. Ctr., 2.Okinawa Pref. Agric. Res. Ctr., Nago, 3.NIFTS, 4.Gene Res. Ctr., Shinshu Univ.)

P112 Whole-genome sequencing for "late-maturity rice Koshihikari" integrated with *Hd16* gene by using Next-Generaion Sequencer

○Tomita, M.¹, K. Ishii², Y. Iwase¹ (1.Res. Inst. of Green Sci. & Tech., Shizuoka Univ., 2.Fac. Agr., Tokyo Univ., Agr. & Tech.)

P113 Analysis of the mitochondrial genome of onion(*Allium cepa*)—A normal type genome—

☆Izumotani, H.¹, M. Tsujimura², M. Shigyo³, T. Terachi⁴ (1.Grad.Sch.Life Sci., Kyoto Sangyo U., 2.Kyoto Sangyo U. Plant Organelle Genomics R.C., 3.Fac.Agr.,Yamaguchi U., 4.Fac.Life Sci.,Kyoto Sangyo U.)

P114 Sequence analysis of the mitochondrial genome of *Brachypodium distachyon*

☆Uemura, K.¹, M. Tsujimura², I. Nagashima², T. Terachi¹ (1.Fac. Life Sci., Kyoto Sangyo U., 2.Kyoto Sangyo U. Plant Organelle Genomics R. C.)

P115 Fine mapping of a QTL, *qGLT3-2*, enhancing effects of other QTLs on low-temperature germinability of rice

☆Satoh, T. ¹, K. Ueda ², K. Sakurai ², A. Watanabe ², H. Takahashi ², H. Akagi ² (1.Grad. Sch. Biores Sci. Akita Pref. Univ, 2.Akita Pref. Univ.)

P116 Development of Nested Association Mapping population of rice

☆Mori, J. ¹, A. Shimazu ¹, H. Sunohara ², M. Tasaki ², S. Nishiuchi ², K. Doi ² (1.School of agricultural Sciences, Nagoya University, 2.Graduate School of Bioagricultural Sciences, Nagoya University)

P117 Genotyping by sequencing of rice nested association mapping population

☆Shimazu, A. ¹, J. Mori ¹, H. Sunohara ², M. Tasaki ², S. Nishiuchi ², K. Doi ² (1.School of Agricultural Sciences, Nagoya University, 2.Graduate School of Bioagricultural Sciences, Nagoya University)

P118 Genetic analysis of agronomic traits in Japanese rice cultivars

○Yamasaki, M. ¹, O. I detta ², M. Maeda ¹, H. Iwata ³, K. Hori ⁴, K. Ebana ⁴, W. Yokoyama ¹, T. Yoshioka ¹, A. Garcia ⁵, T. Kataoka ⁶, R. Kaji ⁷, N. Yokogami ^{8,10}, H. Maeda ⁹, K. Murata ¹⁰, H. Nakagawa ¹¹, K. Doi ¹² (1.Food Resources Education and Research Ctr., Grad. Agric. Sci., Kobe U., 2.NARO Western Region Agric. Res. Ctr., 3.Grad. Sch. Agr. Life Sci., U. Tokyo, 4.NIAS, 5.USDA-ARS, 6.NARO Kyushu Okinawa Agric. Res. Ctr., 7.NARO Hokkaido Agric. Res. Ctr., 8.NARO Tohoku Agric. Res. Ctr., 9.NARO Agric. Res. Ctr., Hokuriku Res. Ctr., 10.Toyama Pref. Agric. Forest. Fish. Res. Ctr., 11.NARO Agric. Res. Ctr., 12.Grad. Sch. Bioagr. Sci., Nagoya U.)

P119 Genetic Analysis of Agronomic Traits in Japanese Rice Nested Association Mapping Population

☆Maeda, M. ¹, G. Tamiya ², S. Makino ², K. Hori ³, K. Ebana ³, K. Iijima ³, S. Nishiuchi ⁴, W. Yokoyama ¹, M. Suehiro ¹, S. Okada ¹, T. Goda ¹, M. Sasaki ¹, A. Garcia ⁵, K. Doi ⁴, M. Yamasaki ¹ (1.Food Resources Education and Research Ctr., Grad. Sch. Agric. Sci., Kobe U, 2.Tohoku Med. Megabank Org., Tohoku U, 3.Nat. Ins. Agr. Sci., 4.Grad. Sch. Bioagr. Sci., Nagoya U, 5.USDA-ARS)

P120 Construction of high-density genetic map in hexaploid wheat using DArt, SNPs and transposon markers

☆Gorafi, Y. ^{1,2}, A. Manickavelu ³, J. Kim ¹, B. Ubi ^{1,4}, T. Ban ³, H. Tsujimoto ¹ (1.Arid Land Research Center, Tottori University, Japan, 2.Agricultural Research Corporation, Wad Medani, Sudan, 3.Kihara Institute for Biological Research, Yokohama City University, Japan, 4.Ebonyi State University, Abakaliki, Ebonyi State, Nigeria)

P121 Fine mapping of qGF1 for lodging resistance in rice

○Hobo, T. ¹, R. Ishihara ², Y. Fujishiro ², Y. Takeda ², T. Kunishima ², S. Ota ², T. Kurotani ³, K. Nishitani ³, H. Kitano ¹ (1.Biosci. Biotech. Ctr., Nagoya U., 2.Grad. Sch. Bioagr. Sci., Nagoya U., 3.Grad. Sch. Life Sci., Tohoku U.)

P122 Genetic analysis for biorefinery traits in rice straw of the chromosomal segment substitution lines

☆Goda, T. ¹, H. Teramura ², S. Okada ¹, T. Sakamoto ¹, H. Koyanagi ¹, M. Suehiro ¹, C. Ogino ², A. Kondo ², M. Yamasaki ¹ (1.Food Resour. Educ. and Res. Cent., Grad. Sch. of Agric. Sci., Kobe Univ., 2.Grad. Sch. of Eng., Kobe Univ.)

P123 QTL analysis for panicle spreading using backcross populations between *Oryza rufipogon* and *O. sativa*

☆Nishioka, R., H. Mikazuki, Y. Tanaka, K. Numaguchi, R. Ishikawa, T. Ishii (Grad. Sch. Agr. Sci., Kobe Univ.)

P124 Genetic study for leaf traits related to early growth in rice using New Rice for Arica (NERICA)

☆Agata, A. ¹, T. Hobo ², S. Ota ¹, K. Doi ¹, Y. Inukai ³, D. Makihara ³, H. Kitano ² (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.ICCAE, Nagoya U.)

P125 Analysis of genes involved in the dominance and psuedo-over-dominance hypotheses in the hybrid vigor of sorghum

☆Yamaguchi, M. ¹, A. Fujii ², S. Nakamura-Araki ², S. Okamura ³, Y. Ito ², K. Sinohara-Ohmae ², H. Kitano ², M. Matsuoka ², S. Kasuga ⁴, T. Sazuka ² (1.Grad. Sch. Bioagri. Sci., Univ. Nagoya., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Fac. of Agr., Nagoya Univ., 4.AFC, Fac. of Agri., Shinshu Univ.)

P126 Positional cloning of *Heading date 18*, a homolog of *Arabidopsis FLOWERING LOCUS D*, involved in rice flowering pathway

☆Shibaya, T., K. Hori, E. Ogiso-Tanaka, U. Yamanouchi, K. Shu, N. Kitazawa, A. Shomura, T. Ando, K. Ebana, J. Wu, T. Yamazaki, M. Yano (NIAS)

P127 Detection of a heading time QTL in the Vrn-B3 region on the short arm of chromosome 7B of wheat

☆Cao, L. ^{1,2}, Y. Sakai ², M. Tokui ², H. Miura ², K. Onishi ² (1.UGAS, Iwate Univ., 2.Obihiro. Univ. Agric. & Vet. Med.)

P128 Analysis of QTLs for stigma exsertion rate in rice cultivar "Ma sho"

☆Kawaide, T., K. Toriyama (Grad. Sch. Agri. Sci. Tohoku Univ.)

P129 Characterization and development of functional in/del marker of short panicle allele *sp1* of 'Tachisuzuka'

○Tanaka, J. ¹, O. Ideta ², K. Matsushita ³, T. Ishii ¹ (1.NICS, 2.WARC, 3.ARC)

P130 Development of markers for ligulelessness locus *Lg* ₂ in *Triticum aestivum* L.

Amagai, Y., ☆T. Kuboyama, N. Watanabe (Col. Agri., Ibaraki U.)

P131 Sex linked DNA polymorphism in Mulberry (*Morus alba* L.)

☆Atsumi, R. ¹, R. Nishihara ¹, K. Tarora ², N. Urasaki ², H. Matsumura ³ (1.Grad. Sch. Sci. Tech., Univ. Shinshu, 2.Okinawa Pref. Agric. Res. Ctr., 3.Gene Res. Ctr., Univ. Shinshu)

P132 Sequence analysis of the type VIIb mitochondrial genome found in spelt wheat

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P133 Comparative analysis of orthologous genes among common wheat ancestors using RNA-Seq

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P134 RNA-seq analysis of cadmium responsive genes in the seedlings of *Oryza barthii*

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P135 Expression and functional analyses of a novel F-box protein gene, ESOFB1 during early phases of rice seed development

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P136 Analysis of expression pattern of heterotrimeric G protein $\gamma 1$ and $\gamma 2$ subunits in rice

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P137 Identification of $\gamma 1 \sim \gamma 5$ subunits of rice heterotrimeric G protein by LC/MS/MS

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P138 Application of *SRS5* gene regulating grain size independently from BR signal transduction in rice

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P139 Development of an artificial technique to control flowering time in gramineous crops

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P140 Comprehensive analysis of microbiome communities in root-knot nematode (*Meloidogyne incognita*) infected soils by 16S metagenomics

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P142 Predicting biomass and yield of rice: a new model unifying a crop model and a genomic prediction model

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P143 Collection and evaluation of genetic variation of coastal green foxtail *Setaria viridis* var. *pachystachys*

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P144 Insertion of transposable element in starch branching enzyme 1 of upland rice cultivar 'Hiderishirazu-D'

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P145 CRISPR/Cas9-mediated mutation induction in a Japanese maize inbred line

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P146 Co-differentiations of blast races and resistance of rice varieties in Japan

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P147 Resistance expression of resistant rice cultivars against rice-ear bugs in release experiments

○Sugiura, K.¹, M. Kato¹, A. Ito¹, Y. Ide¹, A. Hamagashira¹, T. Nonoyama² (1.Aichi Agri. Res. Cent., 2.Mount. Reg. Agri. Inst., Aichi Agri. Res. Cent.)

P148 Cytoplasmic effects on submergence stress response in common wheat

○Nakamura, C., S. Takenaka (Faculty of Agriculture, Ryukoku University)

P149 Effect of grain polyphenol oxidase on flour color and noodle color in wheat

○Yanaka, M. ¹, H. Okusu ², K. Takata ¹, W. Funatsuki ¹ (1.NARO/WARC, 2.Nippon Flour Mills)

P150 Growth of sugar beet F1 lines showing different degrees of heterosis in root weight

○Matsuhira, H., Y. Kuroda, K. Okazaki, K. Taguchi, S. Ueda, H. Takahashi (NARO-HARC)

P151 Isolation and characterization of a candidate sex-determining gene in *Asparagus officinalis*

☆Tsugama, D. ¹, M. Hayashi ², K. Matsuyama ², M. Ide ², K. Fujino ¹, K. Masuda ¹ (1.Res. Fac. Agr., Hokkaido Univ., 2.Grad. Sch. Agr., Hokkaido Univ.)

P152 QTL mapping of flowering time in morning glory using RAD sequencing

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P153 Culture system of somatic embryos of tea tree (*Camellia sinensis*) for the transformation process

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