

**Title of Papers Presented at the 120th Meeting of The JAPANESE SOCIETY OF BREEDING at Fukui Prefectural University, Fukui, Japan September 23–24, 2011**

- 101 Chromosomal distribution of functionally characterized genes in rice and comparative analysis with QTL regions. ☆E. Yamamoto, J. Yonemaru, T. Yamamoto, M. Yano (National Institute of Agrobiological Sciences)
- 102 Mapping of quantitative trait loci for biomass-related traits using recombinant inbred lines between high-yielding rice varieties, Tachisugata and Hokuriku 193 ☆K. Matsubara<sup>1</sup>, J. Tanaka<sup>1</sup>, H. Tsunematsu<sup>1</sup>, T. Yamamoto<sup>2</sup>, J. Yonemaru<sup>2</sup>, R. Mizobuchi<sup>2</sup>, E. Yamamoto<sup>2</sup>, M. Yano<sup>2</sup>, H. Kato<sup>1</sup> (1.NICS2.NIAS)
- 103 Identification and genetic diagnosis of rice novel QTL associating with both semidwarfism and late-maturity. ☆M. Tomita, T. Yamaguchi (Mol. Genet. Lab., Fac. of Agr., Tottori U.)
- 104 Synteny analysis of QTL regions for root thickness between *Raphanus sativus* and *Brassica rapa*. ☆K. Tonosaki, F. Li, H. Kitashiba, T. Nishio (Grad. Sch. Agric. Sci., Tohoku Univ.)
- 105 The relationship among seed shape, seed weight and developmental periods of soybean revealed by QTL analysis OK. Komatsu<sup>1</sup>, M. Takahashi<sup>2</sup>, T. Sayama<sup>3</sup>, N. Oki<sup>2</sup>, H. Funatsuki<sup>4</sup>, M. Ishimoto<sup>3</sup> (1.Nat. Agri. Res. Cent. Hokkaido Reg.2.Nat. Agri. Res. Cent. Kyushu Okinawa Reg.3.Nat. Inst. Agribiol. Sci.4.Nat. Agri. Res. Cent. Western Reg.)
- 106 QTL analysis of wheat yellow mosaic virus resistance derived from Sumai 3 OT. Suzuki<sup>1</sup>, S. Kobayashi<sup>2</sup>, Y. Yoshimura<sup>2</sup> (1.Chuo Agri. Exp. Stn., HRO.2.Kitami Agri. Exp. Stn., HRO.)
- 107 Analysis of QTLs for the spike morphology and related traits in an interspecific hybrid of diploid wheat relatives (*Aegilops longissima* × *Ae. sharonensis*) ☆A. Ohta<sup>1</sup>, T. Kawahara<sup>2</sup>, K. Yamane<sup>1,3</sup> (1.Grad. Sch. Bio. Env. Sci., Osaka Pref. U.2.Grad. Sch. Agr., Kyoto U.3.Bio. Sci., Gifu U.)
- 108 Interorganellar DNA transfer in wheat: dynamics and phylogenetic origin
- 109 Identification of responsive transcripts under Pi-starved and Pi-sufficient stressed in rice using mRNA-Seq ☆Y. Oono<sup>1</sup>, Y. Kawahara<sup>1</sup>, H. Kanamori<sup>1</sup>, H. Mizuno<sup>1</sup>, H. Yamagata<sup>1</sup>, M. Yamamoto<sup>1</sup>, S. Hosokawa<sup>1</sup>, H. Ikawa<sup>2</sup>, Z. Zhu<sup>1</sup>, J. Wu<sup>1</sup>, T. Itoh<sup>1</sup>, T. Matsumoto<sup>1</sup> (1.National Institute of Agrobiological Sciences2.Forestry and Fisheries, Institute of the Society for Techno-innovation of Agriculture)
- 110 Transcriptome analysis of female gamete development in rice ☆T. KUBO<sup>1,2</sup>, M. FUJITA<sup>1</sup>, H. TAKAHASHI<sup>3</sup>, M. NAKAZONO<sup>3</sup>, N. Tsutsumi<sup>4</sup>, N. KURATA<sup>1,2</sup> (1.Natl. Inst. Genet.2.SOKENDAI, Life Science3.Grad. Sch. Bioagr. Sci., Nagoya U.4.Grad. Sch. Agric. Life Sci., U. Tokyo)
- 111 Comparison of the expression patterns of repetitive sequences between somatic and germ cells in rice. ☆S. Ishiguro<sup>1</sup>, K. Ogasawara<sup>1</sup>, M. Ezawa<sup>1</sup>, Y. Sato<sup>2</sup>, Y. Kishima<sup>1</sup> (1.Res. Fac. Agric., Hokkaido U.2.NARCH)
- 112 Elimination of tight linkage between rice seeds lipoxgenase-3 null gene and easily preharvest sprouting characteristics using DNA markers OY. Suzuki<sup>1</sup>, K. Shirasawa<sup>1,2</sup>, A. Shigemune<sup>3</sup>, H. Sasahara<sup>3</sup>, H. Ohta<sup>3,4</sup>, Y. Uehara<sup>3</sup>, T. Ishikawa<sup>3</sup>, K. Miura<sup>3</sup> (1.NARO, Inst. Crop Sci.2.(Present address) Kazusa DNA Res. Inst.3.NARO, Agirc. Res. Cent.4.(Present address) NARO, Tohoku Agirc. Res. Cent.)
- 113 Development of chromosome segment substitution lines in soybean. ☆W. Satoshi<sup>1</sup>, A. Kaga<sup>1</sup>, T. Shimizu<sup>1</sup>, k. Machita<sup>1</sup>, Y. Tsubokura<sup>2</sup>, Z. Xia<sup>1</sup>, B. Eduardo<sup>2</sup>, T. Yamada<sup>2</sup>, K. Hirata<sup>2</sup>, N. Oki<sup>3</sup>, N. Yamada<sup>2</sup>, M. Hajika<sup>2</sup>, K. Harada<sup>1</sup>, M. Ishimoto<sup>1</sup> (1.NIAS2.NICS3.NARC for Kyusyu Okinawa Region)
- 114 Genome-wide association study and genomic prediction of rice grain shape OH. Iwata<sup>1</sup>, K. Ebana<sup>2</sup>, Y. Uga<sup>2</sup>, T. Hayashi<sup>3</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo2.NIAS3.NARC)

- 115 Genetic relationships among estimated parental haplotypes of commercial F1 varieties in tomato ☆A. Suzuki<sup>1</sup>,H. Matsunaga<sup>2</sup>,A. Ohyama<sup>2</sup>,H. Fukuoka<sup>2</sup>,K. Shirasawa<sup>3</sup>,H. Iwata<sup>1</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo<sup>2</sup>.NIVTS<sup>3</sup>.Kazusa DNA Research Institute)
- 116 mRNA-seq for identification of unannotated transcripts in pathogen-infected sorghum ☆H. Mizuno<sup>1</sup>,H. Kawahigashi<sup>1</sup>,Y. Kawahara<sup>2</sup>,H. Kanamori<sup>1</sup>,H. Minami<sup>3</sup>,S. Mori<sup>1</sup>,H. Sasaki<sup>1</sup>,T. Itoh<sup>2</sup>,T. Matsumoto<sup>1</sup> (1.Plant Genome, NIAS<sup>2</sup>.Bioinformatics, NIAS<sup>3</sup>.MSS)
- 117 A rapid chemical method for lysing Arabidopsis cells ☆D. Tsugama,T. Takano(ANESC., U.Tokyo)
- 118 Genome-wide association mapping in *Cryptomeria japonica* –Amount of male strobili and wood property traits (1)– ☆K. Uchiyama<sup>1</sup>,T. Ihara<sup>1</sup>,H. Iwata<sup>2</sup>,M. Tsubomura<sup>3</sup>,K. Mishima<sup>3</sup>,T. Iki<sup>3</sup>,A. Watanabe<sup>3</sup>,N. Futamura<sup>1</sup>,K. Shinohara<sup>1</sup>,Y. Tsumura<sup>1</sup> (1.FFPRI<sup>2</sup>.Grad. Sch. Agric. Life Sci., U. Tokyo<sup>3</sup>.Forest Tree Breeding Center, FFPRI)
- 119 Structural polymorphism of cucumber mitochondrial genome which could be related with the short dispersed repeat sequences S. Kodani<sup>1</sup>,T. Yamamoto<sup>2</sup>,Y. Akashi<sup>1</sup>,K. Tanaka<sup>3</sup>,H. Nishida<sup>1</sup>,O.K. Kato<sup>1</sup> (1.Grad. Sch. Natural Sci. Tech., Okayama U.<sup>2</sup>.Hagihara Farm<sup>3</sup>.Fac. Humanities, Hirosaki U.)
- 120 Rice ubiquitin-related modifier-1 RURM1 is required for stable chromosome behavior in mitosis. ☆M. Kadotani,T. Tsukiyama,S. Nasuda,M. Teraishi,T. Tanisaka,Y. Okumoto(Grad.Sch.Agric,Kyoto Univ.)
- 201 A high-resolution linkage map of EST-based SNP markers in *Raphanus sativus* and its application in genomic analysis O.H. Kitashiba,F. Li,Z. Zou,K. Tonosaki,T. Nishio(Grad. Sch. Agric. Sci., U. Tohoku)
- 202 Fine mapping of the clubroot resistance gene,CRb, in *Brassica rapa*. ☆T. Kato<sup>1,2</sup>,S. Matsumoto<sup>2</sup>,K. Hatakeyama<sup>2</sup>,N. Fukino<sup>2</sup> (1.Grad. Sch. Bioresour., Mie Univ.<sup>2</sup>.NIVTS, NARO)
- 203 Mapping of restorer of fertility gene in RT102C carrying male sterile cytoplasm. ☆H. Murata<sup>1</sup>,T. Kazama<sup>1</sup>,K. Motomura<sup>2</sup>,K. Toriyama<sup>1</sup> (1.Graduate School of Agricultural Science, Tohoku University<sup>2</sup>.College of Agriculture, University of the Ryukyus)
- 204 Mapping of resistance to peanut stunt virus in soybean cultivar “Hyuga” ☆M. Saruta<sup>1</sup>,Y. Takada<sup>1</sup>,T. Yamada<sup>2</sup>,K. Komatsu<sup>3</sup>,T. Sayama<sup>4</sup>,M. Ishimoto<sup>4</sup> (1.NARO/WARC<sup>2</sup>.NICS<sup>3</sup>.NARO/HARC<sup>4</sup>.NIAS)
- 205 Molecular mapping of a high lysine mutant gene (*lys3a*) in barley ☆Y. Yamashita<sup>1</sup>,A. Takahashi<sup>2</sup>,T. Yanagisawa<sup>3</sup>,S. Taketa<sup>1</sup> (1.IPSR, Okayama U. <sup>2</sup>.WeNARC, NARO<sup>3</sup>.Natl. Inst. Crop Sci., NARO)
- 206 Fine mapping and character expression of the short awn 2 (*lks2*) gene on barley chromosome 7H O.S. Taketa<sup>1</sup>,T. Yuo<sup>1</sup>,Y. Yamashita<sup>1</sup>,Y. Sakurai<sup>2</sup>,S. Miyake<sup>2</sup>,M. Ichii<sup>3</sup> (1.IPSR, Okayama U.<sup>2</sup>.Fac.Agric., Kagawa U.<sup>3</sup>.Kagawa U.)
- 207 Screening of markers closely linked to a recessive nuclear male sterility gene using a high density linkage map in *Cryptomeria japonica*. ☆Y. Moriguchi<sup>1</sup>,T. Ihara<sup>1</sup>,K. Uchiyama<sup>1</sup>,N. Futamura<sup>1</sup>,M. Saito<sup>2</sup>,S. Ito<sup>3</sup>,Y. Higuchi<sup>3</sup>,A. Matsumoto<sup>1</sup>,N. Tani<sup>4</sup>,H. Taira<sup>5</sup>,K. Shinohara<sup>1</sup>,Y. Tsumura<sup>1</sup> (1.FFPRI<sup>2</sup>.Toyama For. Res. Inst.<sup>3</sup>.Niigata For. Res. Inst.<sup>4</sup>.JIRCAS<sup>5</sup>.Ex. Grad. Sch. Tec., Niigata U.)
- 208 Detection of adaptive genes, its correlation with environmental variables and the location on linkage map in *Cryptomeria japonica* using SNP genotyping. O.Y. Tsumura,K. Uchiyama,Y. Moriguchi,S. Ueno,T. Ihara(Forestry and Forest Products Research Institute)
- 209 Analysis of the Chinese cabbage clubroot resistant locus CRa ☆H. Ueno<sup>1</sup>,D. Aruga<sup>1</sup>,H. Matsumura<sup>2</sup>,E. Matsumoto<sup>3</sup>,N. Hayashida<sup>4</sup> (1.Dep.Biosci.Tex.Tech., U.Shinshu<sup>2</sup>.Gene.Res.Ctr., U.Shinshu<sup>3</sup>.Nag.Veg.Orna.Crop.Expt.Stn. <sup>4</sup>.Div.Appl.Biol., U.Shinshu)

- 210 Exploration of DNA markers linked to resistance for root rot of lettuce race 2 using crisphead type lettuces. ☆D. Aruga<sup>1</sup>, N. Tsuchiya<sup>2</sup>, H. Ueno<sup>1</sup>, H. Matsumura<sup>3</sup>, E. Matsumoto<sup>4</sup>, N. Hayashida<sup>5</sup> (1. Dep. Biosci. Tex. Tech., U. Shinshu<sup>2</sup>, Nag. Agri. Experi. Stat. 3. Gene. Res. Ctr., U. Shinshu<sup>4</sup>, Nag. Veg. Orna. Crop. Expt. Stn. 5. Div. Appl. Biol., U. Shinshu)
- 211 Euchromatin targeted SNP discovery by sequence capture procedure in eggplant (*Solanum melongena* L.) OH. Fukuoka<sup>1</sup>, K. Shirasawa<sup>2</sup>, H. Hirakawa<sup>2</sup>, S. Sato<sup>2</sup>, K. Miyatake<sup>1</sup>, S. Negoro<sup>1</sup>, A. Ohyama<sup>1</sup>, T. Nunome<sup>1</sup>, H. Yamaguchi<sup>1</sup> (1. NIVTS2. KDRI)
- 212 Genome-wide genotyping of bitter melon (*Momordica charantia*) by modified restriction-assisted DNA tag analysis OH. Matsumura<sup>1</sup>, N. Miyagi<sup>2</sup>, H. Ando<sup>1</sup>, N. Taniai<sup>2</sup>, K. Tarora<sup>2</sup>, A. Shudo<sup>2</sup>, N. Urasaki<sup>2</sup> (1. Gene Res. Ctr., Shinshu U. 2. Okinawa Pref. Agric. Res. Ctr.)
- 213 Development of DNA markers linked to the *Fusarium* wilt-resistance gene in strawberry. OF. Hashizume<sup>1</sup>, T. Tsuji<sup>1</sup>, Y. Yamamoto<sup>1</sup>, K. Kakeda<sup>2</sup>, K. Hashimoto<sup>2</sup>, Y. Seko<sup>2</sup>, J. Kohori<sup>1</sup>, H. Kitamura<sup>1</sup>, T. Mori<sup>1</sup> (1. Mie Pref. Agr. Res. Inst. 2. Grad. Sch. Bioresour., Mie U.)
- 214 Effect of extremely long paired-end reads on the whole genome shotgun analysis of barley O K. Sato, Y. Motoi, N. Yamaji (IPSR, Okayama U.)
- 215 Sequence analysis of 24,783 barley (Haruna Nijo) full-length cDNAs and database construction. OT. Matsumoto<sup>1</sup>, T. Tanaka<sup>1</sup>, H. Sakai<sup>1</sup>, N. Amano<sup>1</sup>, H. Kanamori<sup>1,2</sup>, K. Kurita<sup>1,2</sup>, A. Kikuta<sup>2</sup>, K. Kamiya<sup>2</sup>, M. Yamamoto<sup>2</sup>, K. Ikawa<sup>2,3</sup>, N. Fujii<sup>4</sup>, K. Hori<sup>1</sup>, T. Itoh<sup>1</sup>, K. Sato<sup>5</sup> (1. National Institute of Agrobiological Sciences 2. Institute of Society for Techno-Innovation of Agriculture, Forestry, and Fisheries 3. Mitsubishi Space Software Co. Ltd. 4. Hitachi Government & Public Corporation System Engineering, Ltd. 5. Institute of Plant Science and Resources, Okayama University)
- 216 Characterization of a new transposon, GeST (Genome Surfing Trader), found in Tamyb10-A1 for grain color of wheat ☆E. Himi, M. Maekawa (Inst. Plant Sci. Res., Okayama Univ.)
- 217 Alteration of expression levels of stress-responsive genes using active transposable element mPing in rice ☆K. Yasuda, T. Tsukiyama, H. Saito, M. Teraishi, T. Tanisaka, Y. Okumoto (Grad. Sch. Agr., Kyoto U.)
- 218 Whole genome sequence analysis of somaclonal variation of rice. V. Detection of transposition of transposon OA. Miyao, M. Nakagome, H. Yamagata, H. Kanamori, H. Ikawa, Y. Katayose, A. Takahashi, T. Matsumoto, H. Hirochika (NIAS)
- 219 Identification of genomic regions linked to phenotype by whole genome sequencing of bulked DNA in rice. ☆A. Abe<sup>1</sup>, S. Kosugi<sup>2</sup>, K. Yoshida<sup>2</sup>, H. Takagi<sup>2</sup>, S. Natsume<sup>2</sup>, M. Tamiru<sup>2</sup>, Y. Ochiai<sup>2</sup>, T. Sasaki<sup>1</sup>, R. Terauchi<sup>2</sup> (1. Iwate Agricultural Research Center 2. Iwate Biotechnology Research Center)
- 220 Diversification and Evolution of three wild accessions of *Oryza rufipogon* revealed by high-throughput DNA sequencing ☆H. Ohyanagi<sup>1,2</sup>, H. Nagasaki<sup>3</sup>, T. Nagata<sup>1</sup>, T. Mochizuki<sup>3</sup>, E. Kaminuma<sup>3</sup>, Y. Nakamura<sup>3</sup>, S. Takeshita<sup>2</sup>, T. Aizu<sup>4</sup>, A. Toyoda<sup>4</sup>, A. Fujiyama<sup>4</sup>, Q. Zhao<sup>5</sup>, B. Han<sup>5</sup>, N. Kurata<sup>1</sup> (1. Plant Genetics Laboratory, National Institute of Genetics 2. Tsukuba Division, Mitsubishi Space Software Co., Ltd. 3. Genome Informatics Laboratory, National Institute of Genetics 4. Comparative Genomics Laboratory, National Institute of Genetics 5. National Center for Gene Research and Institute of Plant Physiology and Ecology, Chinese Academy of Sciences)
- 221 Use of next-gen DNA sequencer for genome analyses of agricultural products of North Tohoku region of Japan ☆S. Natsume<sup>1</sup>, K. Yoshida<sup>1</sup>, S. Kosugi<sup>1</sup>, C. Mitsuoka<sup>1</sup>, A. Uemura<sup>1</sup>, A. Abe<sup>2</sup>, K. Nakade<sup>1</sup>, Y. Sakamoto<sup>1</sup>, M. Nakajima<sup>1</sup>, T. Takeda<sup>1</sup>, R. Terauchi<sup>1</sup> (1. Iwate Biotechnology Research Center 2. Iwate Agricultural Research Center)
- 301 Production of B-genome monosomic addition lines of auto- and alloplasmic *Brassica napus* with single chromosome of *B. juncea*. ☆M. Takashima<sup>1,2</sup>, S. Bang<sup>1</sup>, Y. Kaneko<sup>1</sup> (1. Fac. Agric., Utsunomiya U. 2. Unit. Grand Sch. Agric., Tokyo U. Agric. Tech.)

- 302 Production and characteristics of *Raphanus sativus*-*Brassica oleracea* var. *italica* monosomic addition lines ☆M. Ogata<sup>1</sup>,M. Ishida<sup>2</sup>,S. Bang<sup>1</sup>,Y. Kaneko<sup>1</sup> (1.Fac. Agric., Utsunomiya U.2.NIVTS, NARO)
- 303 LET-dependent effect on DNA mutations in *Arabidopsis thaliana* (2) ☆T. Hirano<sup>1</sup>,Y. Kazama<sup>2</sup>,S. Ohbu<sup>2</sup>,Y. Shirakawa<sup>2</sup>,Y. Hayashi<sup>2</sup>,T. Abe<sup>1,2</sup> (1.RIKEN Innovation Center 2.RIKEN Nishina Center)
- 304 Detection of mutations in M1 generation of *Arabidopsis thaliana* for analysis of LET-dependent effect on mutation frequency ☆Y. Kazama<sup>1</sup>,L. Ma<sup>1,2</sup>,T. Hirano<sup>3</sup>,S. Ohbu<sup>1</sup>,Y. Shirakawa<sup>1</sup>,Y. Hayashi<sup>1</sup>,T. Abe<sup>1,3</sup> (1.RIKEN Nishina Cent.2.Grad.Sch.Sci.Eng.Saitama U.3.RIKEN Innovation Cent.)
- 305 Activation of Dart, DNA transposon, by Ion beam irradiation in rice ○M. Maekawa<sup>1</sup>,H. Nishimura<sup>1</sup>,E. Himi<sup>1</sup>,S. Iida<sup>2</sup>,K. Tsugane<sup>3</sup> (1.Inst. Plant Sci. Res., Okayama U.2.Grad.Sch.Nutr.Envir.,U.Shizuoka3.Natl.Inst. Basic Biol.)
- 306 Identification of Darts activated by 5azaC treatment in rice. ○H. Nishimura<sup>1</sup>,E. Himi<sup>1</sup>,S. Iida<sup>2</sup>,K. Tsugane<sup>3</sup>,M. Maekawa<sup>1</sup> (1.Inst. Plant Sci. Res., Okayama U.2.Grad.Sch.Nutr.Envir.,U.Shizuoka 3.Natl. Inst. Basic Biol.)
- 307 An insertion mutation in Hd3a gene induced by a rice transposable element mPing ☆M. Ito,<sup>H. Saito</sup>,K. Mustafa,<sup>Y. Yoshitake</sup>,T. Asami,<sup>S. Asano</sup>,T. Yokoo,<sup>Q. Xu</sup>,H. Izumi,<sup>Y. Okumoto</sup>(Grad.Sch.Agric, U.Kyoto)
- 308 Screening of rice oleosin mutants by TILLING method ☆H. Matsusaka,<sup>M. Satoh</sup>,H. Satoh,<sup>T. Kumamaru</sup>(Fac. Agric., U. Kyushu)
- 309 Development of a TILLING platform for analysis of tomato important traits. ☆Y. Okabe,<sup>E. Asamizu</sup>,T. Saito,<sup>C. Matsukura</sup>,T. Ariizumi,<sup>T. Mizoguchi</sup>,H. Ezura(Grad. Sch. Life. Env. Sci., U. Tsukuba)
- 310 Allergenicity test of hypo-allergenic rice seed proteins with serum derived from rice allergy patients ☆Y. Wakasa<sup>1</sup>,K. Hirano<sup>2</sup>,A. Urisu<sup>3</sup>,T. Matsuda<sup>2</sup>,F. Takaiwa<sup>1</sup> (1.NIAS2.Grad. Sch. Bioagric. Sci., Nagoya U.3.Dep. Pediatrics, Fujita-Health U.)
- 311 Development of new generation of transgenic rice having therapeutic function against Japanese cedar pollen allergy ○F. Takaiwa,<sup>L. Yang</sup>,H. Takagi,<sup>Y. Wakasa</sup>,M. Oota(Functional Crop, NIAS)
- 312 Transgenic *Panicum meyerianum* producing CoQ10 M. Seo<sup>1,4</sup>,S. Takahashi<sup>2</sup>,K. Kadowaki<sup>2</sup>,M. Kawamukai<sup>3</sup>,M. Takahara<sup>4</sup>,☆T. Takamizo<sup>4</sup> (1.Natl. Inst. of Livestock and Grassl. Sci.2.Natl. Inst. Agrbiol. Sci.3.Fac. Life and Env. Sci, Shimane Univ.4.Natl. Acad. of Agr. Sci.)
- 313 Optimized *Agrobacterium*-mediated gene targeting system and targeted knockouts lacking  $\beta$  1,2-xylotransferase in rice (*Oryza sativa* L.) ○K. Ozawa<sup>1</sup>,Y. Ogo<sup>1</sup>,K. Matsuo<sup>2</sup>,F. Takaiwa<sup>1</sup> (1.National Institute of Agrobiological Sciences2.National Institute of Advanced Industrial Science and Technology)
- 314 *Agrobacterium* mediated genetic transformation in chamomile. ☆E. Maruyama,<sup>Y. Takahara</sup>(Dept. Bioengn., Nagaoka U.T.)
- 315 Production and application of smaller gold particles for plastid transformation in Tobacco ☆A. Okuzaki<sup>1</sup>,J. Watanabe<sup>2</sup>,S. Takahashi<sup>1,3</sup>,I. Hirasawa<sup>2</sup>,Y. Tabei<sup>1</sup> (1.NIAS2.Grad. Sch. Appl. Chem., U. Waseda3.Grad. Sch. Front. Sci., U. Tokyo)
- 316 Comparative studies on the transplastomic tobacco plants containing different genes encoding ROS scavenging enzymes ☆T. Tsujimura<sup>1</sup>,Y. Ohya<sup>2</sup>,H. Yamamoto<sup>2</sup>,T. Terachi<sup>2</sup> (1.Grad.Sch.Fac.Eng.,Kyoto Sangyo U.2.Fac.Life Sci.,Kyoto Sangyo U.)
- 317 Regulation of flavonoid biosynthetic genes in transgenic soybean seeds harboring LjMyb12. ☆A. Torii,<sup>M. Arai</sup>,J. Abe,<sup>K. Kitamura</sup>,T. Yamada(Grad. Sch. Agric.,Hokkaido U.)
- 318 Antagonistic actions of HLH/bHLH proteins are involved in grain length and weight in rice ☆D. Heang,<sup>H. Sassa</sup>(Grad. Sch. Hort., Chiba U.)

- 319 Induction mechanisms of RNA silencing of the drug-resistance gene introduced with a transgene inducing co-suppression ☆M. Kasai<sup>1</sup>,A. Taneda<sup>2</sup>,A. Kanazawa<sup>1</sup> (1.Res. Fac. Agr., Hokkaido U.2.Grad. Sch. Sci. Technol., Hirosaki U)
- 320 Acceleration of epigenetic changes required for producing a plant that does not carry a transgene but has altered traits ○A. Kanazawa,J. Inaba,M. Kasai,H. Shimura,C. Masuta(Res. Fac. Agr., Hokkaido U.)
- 401 Search for regulatory regions of heading on the short arm of wheat chromosome 7D using deletion lines ○H. Handa<sup>1,2</sup>,H. Ui<sup>3</sup>,R. Kikuchi<sup>4</sup>,H. Kawahigashi<sup>1</sup>,T. Ogawa<sup>1</sup> (1.Natl.Inst.Agrobiol.Sci.2.Grad.Sch.Life & Env.Sci., U.Tsukuba3.Dept.Biol.Sci. & Technol., Tokyo U.Sci.4.Kihara Inst.Biol.Res., Yokohama City U.)
- 402 Analysis of heading time stability in barley using sequence polymorphism in heading time genes ○H. Nishida<sup>1</sup>,M. Tsuchiya<sup>1</sup>,E. Aoki<sup>2</sup>,T. Tonooka<sup>2,3</sup>,T. Yoshioka<sup>2,4</sup>,T. Yanagisawa<sup>2</sup>,K. Kato<sup>1</sup> (1.Grad. Sch. Nat. Sci. Tech., Okayama U.2.Natl. Inst. Crop. Sci., NARO3.AFFRC4.Nat. Agric. Res. Cent. Western Region, NARO)
- 403 Sequence variation of photoperiod sensitivity gene Ppd-1 affects its expression pattern in wheat ☆K. Tanaka,Y. Iuchi,H. Nishida,K. Kato(Grad. Sch. Nat. Sci. Tech., Okayama U.)
- 404 Natural variation of vernalization requirements in domesticated barley: Higher grades of vernalization requirements are biasedly distributed in East Asia. ☆D. Saisho <sup>1</sup>,M. Ishii <sup>1</sup>,K. Hori<sup>2</sup>,K. Sato <sup>1</sup> (1.IPSR, Okayama U. 2.Natl. Inst. Agrobiol. Sci.)
- 405 Isolation of a novel photoperiod sensitive gene which regulates the expression of Ehd1 ☆T. Yokoo,H. Saito,T. Asami,Y. Yoshitake,Q. Xu,S. Asano,H. Izumi,M. Ito,K. Mostafa,T. Tanisaka,Y. Okumoto(Grad.Sch.Agriculture Kyoto univeristy)
- 406 Functional analysis of Florigen Activation Complex ☆H. Tsuji<sup>1</sup>,K. Taoka<sup>1</sup>,I. Ohki<sup>1</sup>,C. Nakashima<sup>1</sup>,C. Kojima<sup>1,2</sup>,K. Shimamoto<sup>1</sup> (1.Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol. (NAIST)2.Inst. Protein Res., Osaka Univ.)
- 407 The analysis of juve e-adult phase change mutants in rice. ☆N. Tanaka<sup>1,4</sup>,H. Itoh<sup>2</sup>,N. Sentoku<sup>2</sup>,H. Sakakibara<sup>3</sup>,M. Kojima<sup>3</sup>,T. Izawa<sup>2</sup>,J. Itoh<sup>1</sup>,Y. Nagato<sup>1</sup> (1.Graduate School of Agricultural and Life Sciences, University of Tokyo2.National Institute of Agrobiological Sciences3.RIKEN Plant Science Center4.Japan Society for the Promotion of Science Research Fellow)
- 408 Research on bulb formation mechanism in wild barley *Hordeum bulbosum* L. by histological analysis ☆N. Asama,M. Furukawa,E. Sagata,T. Ban(Kihara Inst. Bio. Res., Yokohama City U.)
- 409 Genetic analysis of the dense panicle 3 (dn3) mutant affecting development of panicle and spikelet in rice ○I. Takamura,K. Shioaku,H. Nagano(Grad. Sch. Agr., Hokkaido U.)
- 410 Developmental analysis of the spikelet in twin eyes mutant.
- 411 GYPSY EMBRYO regulates panicle branching and floral meristem determinacy in rice. ☆S. Yamaki<sup>1</sup>,Y. Nagato<sup>2</sup>,K. Nonomura<sup>1,3</sup>,N. Kurata<sup>1,3</sup> (1.Natl.Inst.Genet.2.Grad.Sch.Agric.Life Sci., U.Tokyo3.Sch.Life Sci., Sokendai)
- 412 Analysis of the tongariboushi (tob) mutant that causes pleiotropic phenotype in rice spikelet and isolation of its responsible gene. ☆W. Tanaka<sup>1</sup>,T. Toriba<sup>1</sup>,Y. Ohmori<sup>1</sup>,A. Kawai<sup>1</sup>,A. Yoshida<sup>2</sup>,N. Mitsuda<sup>3</sup>,M. Takagi<sup>3</sup>,T. Tsuchida<sup>4</sup>,H. Ichikawa<sup>4</sup>,H. Hirano<sup>1</sup> (1.Dept. Biol. Sci., Grad. Sch. Sci., Univ. Tokyo2.Grad. Sch. Agric. Life. Sci., Univ. Tokyo3.AIST4.NIAS)
- 413 Analysis of the function of OsHMA2 (*Oryza sativa* heavy metal ATPase 2) by characterizing three allelic mutant lines generated by retrotransposon Tos17 ☆N. Satoh-Nagasawa<sup>1</sup>,M. Mori<sup>1</sup>,T. Kawamoto<sup>2</sup>,Y. Nagato<sup>3</sup>,K. Sakurai<sup>1</sup>,H. Takahashi<sup>1</sup>,A. Watanabe<sup>1</sup>,H. Akagi<sup>1</sup> (1.Akita Prefectural University2.Akita Pref. Agri., Forestry and Fisheries Res. Center3.Grad.Sch.Agric.Life Sci., U.Tokyo)

- 414 Identification of target genes of the tomato MADS-box transcription factor RIN by transcriptome analysis ☆M. Fujisawa<sup>1</sup>, Y. Shima<sup>1</sup>, N. Higuchi<sup>2</sup>, T. Nakano<sup>1</sup>, Y. Koyama<sup>2</sup>, T. Kasumi<sup>2</sup>, Y. Ito<sup>1</sup> (1.Natl. Food Res. Inst., NARO<sup>2</sup>.Dept. Agric. Biol. Chem., Nihon Univ.)
- 415 Physiological study of repetitive high concentration sucrose treatment on somatic embryogenesis in Carrot ☆M. Makino(Dept. Bioengn., Nagaoka U.T.)
- 416 miR171a regulates plant developmental processes ☆H. Sumiyoshi<sup>1</sup>, H. Takanashi<sup>1,2</sup>, S. Arimura<sup>1</sup>, n. Tsutsumi<sup>1</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo<sup>2</sup>.Grad.Sch.Sci., Nagoya U.)
- 417 Rice SLENDER LEAF 1 gene involves in cytokinesis ☆T. Yoshikawa, K. Hibara, J. Ito, Y. Nagato(Grad. Sch. Agric. Life Sci., U. Tokyo)
- 418 Analysis of rice precocious mutant that promotes adult phase initiation ☆M. Isono, k. Hibara, J. Ito, Y. Nagato(Grad.Sch.Agric.Life Sci., U.Tokyo)
- 419 The analysis of a rice mutant defective apical meristems ☆M. Takeyama, K. Hibara, J. Ito, Y. Nagato(Grad.Sch.Agric.Life Sci., U.Tokyo)
- 420 *REDUCED EMBRYO2 gene is involved in rice embryo size. OK. Hibara<sup>1</sup>, N. Nagasawa<sup>2,3</sup>, J. Takeda<sup>4</sup>, H. Sakai<sup>2</sup>, Y. Nagato<sup>1</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo<sup>2</sup>.DuPont<sup>3</sup>.Fac.BioSci., Akita Pref.U. <sup>4</sup>.Fac.Agr., U.Tokyo )*
- 501 Improvement of multi-disease resistant rice by optimal constitutive WRKY45 expression ☆S. Goto, F. Sasakura-Shimoda, M. Shimono, S. Sugano, H. Takatsuji(Natl. Inst. Agrobiol. Sci.)
- 502 Fine mapping of Rsdv1, a major gene controlling Soybean dwarf virus resistance derived from "WILIS" ☆Y. Yamashita<sup>1</sup>, S. Ohnishi<sup>1</sup>, T. Takeuchi<sup>2</sup> (1.Central Agr. Exp. Stn., HRO<sup>2</sup>.Kitami Agr. Exp. Stn., HRO)
- 503 *BROAD-SPECTRUM RESISTANCE 1 gene confers disease resistance in monocotyledonous and dicotyledonous crops ☆S. Maeda<sup>1</sup>, N. Yokotani<sup>2</sup>, S. Sugano<sup>1</sup>, K. Oda<sup>2</sup>, M. Matsui<sup>3</sup>, H. Hirochika<sup>1</sup>, H. Takatsuji<sup>1</sup>, M. Mori<sup>1</sup> (1.National Institute of Agrobiological Sciences<sup>2</sup>.RIBS Okayama<sup>3</sup>.RIKEN PSC)*
- 504 Classification of genotypes of the Target leaf spot-resistant gene (ds1) in Sorghum OH. Kawahigashi<sup>1</sup>, S. Kasuga<sup>2</sup>, H. Okuizumi<sup>1</sup>, H. kanamori<sup>1</sup>, T. Ando<sup>1</sup>, J. Yonemaru<sup>1</sup>, J. Wu<sup>1</sup>, T. Sazuka<sup>3</sup>, T. Matsumoto<sup>1</sup> (1.National Institute of Agrobiological sciences<sup>2</sup>.Shinshu University<sup>3</sup>.Nagoya University)
- 505 Detection of quantitative trait loci for partial blast resistance by using next generation genome sequencer in the japonica rice cultivar Nortai ☆H. Takagi<sup>1,2</sup>, A. Abe<sup>3</sup>, S. Kosugi<sup>2</sup>, K. Yoshida<sup>2</sup>, R. Terauchi<sup>1,2</sup> (1.United Grad. Sch. Agric. Sci., Iwate U. <sup>2</sup>.Iwate Biotech. Res. Center<sup>3</sup>.Iwate Agric. Res. Center)
- 506 Production of a transgenic rice cultivar for whole crop silage with yam tuber lectin DB1 and mutant ALS to confer insect and herbicide resistance ☆S. Yoshimura<sup>1</sup>, K. Kaku<sup>2</sup>, M. Komatsu<sup>2</sup>, Y. Ito<sup>1</sup>, K. Toriyama<sup>1</sup> (1.Grad.Sch.Agric.Sci.Tohoku U.<sup>2</sup>.Kumiai Chemical Industry)
- 507 Specific recognition between rice blast AVR-Pik alleles and rice Pik alleles. OH. Kanzaki, K. Yoshida, R. Terauchi(Iwate Biotech. Res. Cent.)
- 508 The problem of selecting resistant soybean cultivar to aphid species. ☆M. Kobayashi<sup>1</sup>, T. Murai<sup>2</sup> (1.United graduate school of agricultural science, Tokyo university of Agriculture and technology<sup>2</sup>.Faculty of agriculture, Utsunomiya Univ.)
- 509 Detailed genetic analysis and genomic sequencing toward the isolation of insect resistance gene in mungbean OM. Ishimoto<sup>1</sup>, M. Teraishi<sup>2</sup>, S. Liu<sup>3</sup>, T. Sayama<sup>1</sup>, A. Hirose<sup>3</sup>, Y. Nakamoto<sup>3</sup>, Y. Yokota<sup>1</sup>, S. Sato<sup>4</sup>, H. Hirakawa<sup>4</sup>, A. Kaga<sup>1</sup> (1.NIAS<sup>2</sup>.Grad. Sch. Agric., Kyoto Univ.<sup>3</sup>.NARCH<sup>4</sup>.Kazusa DNA Res. Inst.)
- 510 Characterization of rice RCN1/OsABCG5 in early seedling growth under low temperature condition ☆K. Furukawa<sup>1</sup>, S. Matsuda<sup>1</sup>, N. Komori<sup>1</sup>, Y. Tokuji<sup>1</sup>, I. Takamura<sup>2</sup>, K. Kato<sup>1</sup> (1.Obihiro Univ.Agric & Vet.Med<sup>2</sup>.Grad.Sch.Agr.,Hokkaido U.)

- 511 Genetic variation in root growth response to nitrate in rice ☆M. Kawahara<sup>1</sup>,Y. Hori<sup>2</sup>,A. Shimizu<sup>1,2</sup>,H. Hasagawa<sup>1,2</sup> (1.Grad. Sch. Environ. Sci., Univ. Shiga Pref. (Graduate School of Environmental Science, the University of Shiga Prefecture))<sup>2</sup>.Sch. Environ. Sci., Univ. Shiga Pref. (School of Environmental Science, the University of Shiga Prefecture))
- 512 Transcriptome analysis of genes related to ethylene-inducible aerenchyma formation in maize roots. ☆H. Takahashi<sup>1</sup>,T. Yamauchi<sup>1</sup>,I. Rajhi<sup>2</sup>,Y. Nagamura<sup>3</sup>,N. Tsutsumi<sup>2</sup>,N. K. Nishizawa<sup>2,4</sup>,M. Nakazono<sup>1</sup> (1.Grad. Sch. Bioagric Sci., Nagoya U.<sup>2</sup>.Grad. Sch. Agric. Life Sci., U.Tokyo<sup>3</sup>.Nat. Inst. Agrobio. Sci.<sup>4</sup>.Res. Insti. Biores. Biotech., Ishikawa Prefectural U.)
- 513 Functional analysis of a NAM transcriptional factor involved in suberin biosynthesis in rice ☆ S. Nishiuchi<sup>1</sup>,K. Watanabe<sup>2</sup>,T. Yamauchi<sup>1</sup>,H. Takahashi<sup>1</sup>,K. Shiono<sup>3</sup>,T. Tsuchida-Mayama<sup>4</sup>,N. Mitsuda<sup>5</sup>,M. Ohme-Takagi<sup>5</sup>,H. Ichikawa<sup>4</sup>,M. Nakazono<sup>1</sup> (1.Grad.Sch.Bioagri. Sci., Nagoya Univ.<sup>2</sup>.Sch. Agr. Sci., Nagoya Univ.<sup>3</sup>.Fukui Prefectural Univ.<sup>4</sup>.NIAS<sup>5</sup>.AIST)
- 514 Identification of wheat chromosome related to ABA responsiveness at seedling stage using chromosome substitution lines ☆M. Iehisa,S. Takumi(Grad.Sch.Agric.Sci., Kobe U.)
- 515 Chilling tolerance and agronomic traits of the transgenic feed rice overexpressing the wheat 1-SSTgene ○Y. Sato,M. Yoshida,Y. Masuta,S. Murayama,E. Shimosaka(National Agricultural Research Center for Hokkaido Region)
- 516 The transgenic Arabidopsis over-expressing a salt stresses induced chloride channel gene (OsCLC8) exhibit higher salt tolerance and longer hypocotyl ☆X. Li<sup>1</sup>,d. tsugama<sup>1</sup>,S. Liu<sup>2</sup>,T. Takano<sup>1</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo<sup>2</sup>.Northeast Forestry U. China)
- 517 Water relations of salt-tolerant and sensitive black gram (*Vigna mungo*) varieties grown under salt stress conditions W. KHIN THUZAR<sup>1</sup>,O. AUNG ZAW<sup>2</sup>,T. OOKAWA<sup>3</sup>,Y. HIRATA<sup>3</sup>,☆T. HIRASAWA<sup>4</sup> (1.UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE<sup>2</sup>.UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE<sup>3</sup>.UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE<sup>4</sup>.UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE<sup>5</sup>.UNITED GRADUATE SCHOOL OF AGRICULTURAL SCIENCE)
- 518 Effects of essential metals in a growth medium on Cd uptake/accumulation in a Cd hyper-tolerator, *Athyrium yokoscense* ○T. Yoshihara<sup>1,2</sup>,M. Kitazaki<sup>1,2</sup>,N. Suzui<sup>3</sup>,S. Ishii<sup>3</sup>,Y. Kawachi<sup>3</sup>,H. Yamazaki<sup>2,3</sup>,S. Fujimaki<sup>3</sup>,S. Hashida<sup>1</sup>,H. Shimada<sup>2</sup>,K. Kitazaki<sup>1</sup>,K. Shoji<sup>1</sup>,F. Goto<sup>1</sup> (1.Lab. Environ. Sci., CRIEPI<sup>2</sup>.Indust. Sci. Tech., TUS<sup>3</sup>.RI imaging, JAEA)
- 519 Functional analysis of rice mitochondrial PPR gene MPR25 which affecting photosynthesis. ☆ T. Toda<sup>1</sup>,S. Fujii<sup>2</sup>,K. Noguchi<sup>3</sup>,S. Arimura<sup>4</sup>,T. Kazama<sup>1</sup>,K. Toriyama<sup>1</sup> (1.Grad.Sch.Life Sci., U.Tohoku<sup>2</sup>.Grad.Sch.Sci., U.Kyoto<sup>3</sup>.Grad.Sch.Sci., U.Tokyo<sup>4</sup>.Grad.Sch.Life Sci., U.Tokyo)
- 520 Effects of improvement of midrib formation by modified DROOPING LEAF gene on rice yield
- 521 Heterosis is observed in shoots at early developmental stages of *Arabidopsis thaliana* and Chinese cabbage ☆R. Fujimoto<sup>1,2</sup>,T. Kawanabe<sup>3</sup>,S. Konno<sup>3</sup>,M. Kaji<sup>3</sup>,W. Peacock<sup>1</sup>,E. Dennis<sup>1</sup> (1.CSIRO Plant Industry<sup>2</sup>.Grad. Sch. Sci. Tech., Niigata U.<sup>3</sup>.Watanabe Seed Co., Ltd.)
- 601 Evaluation of soybean diversity preserved in NIAS Genebank. 1.Geographical distribution of several known alleles for agronomic traits. ☆A. Kaga,T. Shimizu,S. Watanabe,Y. Tsubokura,Y. Katayose,K. Harada,D. Vaughan,I. Masao,N. Tomooka(NIAS)
- 602 Roothairless 2 (*rth2*) mutant represents a loss-of-function allele of the cellulose synthase-like gene *OsCSLD1* in rice (*Oryza sativa* L.) ☆T. Yuo<sup>1</sup>,K. Shiotani<sup>2</sup>,A. Miyao<sup>3</sup>,H. Hirochika<sup>3</sup>,M. Ichii<sup>4</sup>,S. Taketa<sup>1</sup> (1.Institute of Plant Science and Resources., U. Okayama<sup>2</sup>.Faculty of Agriculture., U. Kagawa<sup>3</sup>.National Institute for Agrobiological Sciences<sup>4</sup>.U. Kagawa)

- 603 Comprehensive transcriptome analysis for exploring gene networks associated with the development and functions of the rice root system ☆H. Takehisa<sup>1</sup>, Y. Sato<sup>1</sup>, M. Igarashi<sup>1,2</sup>, T. Abiko<sup>3,4</sup>, B. Antonio<sup>1</sup>, N. Namiki<sup>5</sup>, Y. Inukai<sup>6</sup>, M. Nakazono<sup>6</sup>, Y. Nagamura<sup>1</sup> (1.NIAS<sup>2</sup>.Bioscience, NAIST<sup>3</sup>.Grad. Sch. Agric. Life Sci., U. Tokyo<sup>4</sup>.JIRCAS<sup>5</sup>.MSS<sup>6</sup>.Grad. Sch. Bioagr. Sci., Nagoya U.)
- 604 Evaluation of strawberry fruit quality based on analysis of images photographed under visible and ultraviolet lights ○Y. Yoshioka<sup>1</sup>, H. Horie<sup>1</sup>, E. Kitadani<sup>2</sup>, M. Nakayama<sup>3</sup>, Y. Noguchi<sup>1</sup> (1.NIVTS, NARO<sup>2</sup>.KONARC, NARO<sup>3</sup>.NIFS, NARO)
- 605 QTL analysis for the occurrence of milky-white grains due to high temperature during ripening period of rice M. Tsubone, ○T. Wada, T. Inoue (Fukuoka Agric. Res. Cent.)
- 606 Quantitative evaluation by Standard-Images of whitened areas in rice grains caused by high temperature in filling period. S. Hamamura<sup>1</sup>, I. Kazuhiko<sup>2</sup>, ○Y. Takahara<sup>1</sup> (1.Dept. Bioengn., Nagaoka U.T.2.Crop Res. Center, Niigata Agric. Res. Inst.)
- 607 Apparent quality of brown rice of Niigatawase s introduced QTL associated with resistance to heat-induced quality decline from Hana-echizen ○A. Kobayashi<sup>1</sup>, K. Sugimoto<sup>2</sup>, M. Yano<sup>2</sup>, K. Tomita<sup>1</sup> (1.Fukui Agr. Exp. Stn.<sup>2</sup>.NIAS)
- 608 Characterization and evaluation of NIAS rice core collection in grain quality with high temperature during the ripening period ○J. Sonoda<sup>1</sup>, m. Kondo<sup>2</sup>, T. Umemoto<sup>3</sup> (1.Kagoshima Prefectural Institute for Agricultural Development<sup>2</sup>.National Institute of Crop Science<sup>3</sup>.National Agricultural Research Center for Hokkaido Region)
- 609 QTL analysis for appearance quality of rice grain using chromosome segment substitution lines of Habataki in the genetic background of Koshihikari ○T. Ebitani, K. Murata, T. Yamaguchi, Y. Iyama, H. Ozaki, H. Maeda (Toyama Pref. Agri. Fore. Fish. Res. Cent. )
- 610 Properties of rice bread made from low gelatinization mutants ○N. Aoki<sup>1</sup>, K. Okamoto<sup>2</sup>, T. Umemoto<sup>1,3</sup>, Y. Suzuki<sup>1</sup> (1.NARO National Institute of Crop Science<sup>2</sup>.Ibaraki Agricultural Center, Plant-Biotechnology Institute<sup>3</sup>.NARO Hokkaido Agricultural Research Center)
- 611 Visualization of Starch Grains; A Rapid Observation Method to Isolate Mutants with Defects in Starch Grain Morphology ☆R. Matsushima<sup>1</sup>, M. Maekawa<sup>1</sup>, N. Fujita<sup>2</sup>, J. Yamashita<sup>1</sup>, W. Sakamoto<sup>1</sup> (1.Institute of Plant Sciences and Resources, Okayama University<sup>2</sup>.Department of Biological Production, Akita Prefectural University)
- 612 Natural variation of phytin content in rice bran ☆K. Hatanaka<sup>1</sup>, M. Suehiro<sup>1</sup>, K. Yoshida<sup>2</sup>, M. Yamasaki<sup>1</sup> (1.Food Resources Education and Research Center, Graduate School of Agricultural Science, Kobe University<sup>2</sup>.Graduate School of Agricultural Science, Kobe University)
- 613 Genetic and phenotypic analysis of BADH2 gene based on phylogenetic analysis of Japanese fragrant rice ☆K. Otsuka<sup>1</sup>, T. Itani<sup>2</sup>, R. Ishikawa<sup>1</sup> (1.Laboratory of Plant Breeding and Genetics, Faculty of Agriculture and Life Science, Hirosaki University<sup>2</sup>.Hiroshima Prefectural University, 562 Nanatsuka, Shobara, Hiroshima)
- 614 Effect of expression level and structure in seed storage protein on dough strength in alien chromosome addition wheat ○H. Tanaka<sup>1</sup>, T. Arakawa<sup>1</sup>, H. Tsujimoto<sup>2</sup> (1.Fac. Agr., Tottori U.<sup>2</sup>.ALRC, Tottori U.)
- 615 Contents of functional free amino acids in Dadacha-bean lines of vegetable-type soybean. ○ T. Abe (Fac. Agr. Yanagata U.)
- 616 Changes in glucosinolate content and composition of null 4MTB-GSL radish line in growth stage.
- 617 Difference of fruit texture between Japanese and foreign cucumber cultivars. ☆K. Shimomura, Y. Yoshioka, M. Sugiyama (NIVTS, NARO)

- 618 Breeding of [Itomakidaikon] to promote Miyazaki Prefectural conventional vegetable. II. New trains and their DNA analysis ☆Y. Tanaka<sup>1</sup>,K. Kumamoto<sup>2</sup>,Y. Nishimura<sup>1</sup>,H. Tominaga<sup>3</sup>,L. Chen<sup>1,2</sup> (1.Grad. Sch. Horti. & Food Sci. Minami Kyushu U.2.Fac. Environment & Horti. Minami Kyushu U.3.Miyazaki Pref. Agri. Exper. Sta.)
- 619 Approach to breeding of new variety of [Hyuga-kabocha] using methods of interspecific hybridization and RAPD-PCR ☆K. Goto<sup>1</sup>,Y. Hodouchi<sup>2</sup>,Y. Tanaka<sup>1</sup>,Y. Nishimura<sup>1</sup>,L. Chen<sup>1,2</sup> (1.Grad. Sch. Horti. & Food Sci. Minami Kyushu U.2.Fac. Environment & Horti. Minami Kyushu U.)
- 620 The development of the high isoflavone-contained and SMV-resistant black soybean line ON. Furutani<sup>1</sup>,Y. Shizukawa<sup>1</sup>,M. Matui<sup>2</sup> (1. Kyoto Prefectural Agriculture,Forestry and Fisheries Technology CenterBiotechnology Research Department2.Kyoto Prefectural University )
- 621 Breeding of a new soybean cultivar "Kyosirotanba" with soybean mosaic virus resistance, large seed size and good eating quality OR. Takisawa<sup>1</sup>,Y. Minamiyama<sup>2</sup>,N. Hurutani<sup>1</sup>,Y. Kosaka<sup>1</sup>,H. Iwakawa<sup>3</sup>,T. Asida<sup>4</sup>,D. Todoroki<sup>5</sup>,M. Matsui<sup>6</sup>,S. Matsumoto<sup>1</sup> (1.Kyoto Prefectural Agriculture Forestry and Fisheries Technology Center Biotechnology Research Department2.Faculty of Education, Wakayama University3.Kyoto Prefectural Agriculture Forestry and Fisheries Technology Center Agriculture and Forestry Technology Department 4.Department of Agriculture, Forestry and Fisheries5.Kyoto Prefectural Nantan Agricultural Extension Center6.Graduate School of Life Environmental Science, Kyoto Prefectural University)
- 622 Practicability of genomic selection in breeding of allogamous crops ☆S. Yabe<sup>1</sup>,R. Ohsawa<sup>2</sup>,H. Iwata<sup>1</sup> (1.Grad.Sch.Agric.Life Sci., U.Tokyo2.Grad.Sch.Life Envi.Sci., U.Tsukuba)
- 623 The effects of CO<sub>2</sub> application, root restriction, and offshoot removal on the days to rice heading in accelerated generation advance by incubator. ☆J. Tanaka(National Institute of Crop Science (NICS), NARO)
- 624 Fine-mapping domestication-related genes towards Neo-domestication of Wild Vigna species ☆K. Naito<sup>1</sup>,A. Kaga<sup>1</sup>,S. Isobe<sup>2</sup>,K. Shirasawa<sup>2</sup>,H. Hirakawa<sup>2</sup>,S. Tabata<sup>2</sup>,N. Tomooka<sup>1</sup> (1.National Institute of Agrobiological Sciences2.Kazusa DNA Research Institute)
- 701 Analysis of weak self-incompatibility of a Japanese pear cultivar 'Natsuhikari' ☆M. Kato<sup>1</sup>,S. Kato<sup>2</sup>,M. Kitaguchi<sup>2</sup>,H. Sassa<sup>1</sup> (1.Grad.Sch.Hort.Chiba U.2.Chiba pref.Agr.and Forest.Res.Cen.)
- 702 Analysis of pollen behavior on Brassica self-incompatibility ☆K. Hiroi<sup>1</sup>,S. Takayama<sup>2</sup>,G. Suzuki<sup>3</sup>,K. Suwabe<sup>4</sup>,M. Watanabe<sup>1</sup> (1.Grad. Sch. Life Sci., U. Tohoku2.Grad. Sch. Biol. Sci., NAIST3.Div. Natl. Sci., U. Osaka Kyoiku4.Grad. Sch. Bioresour., U Mie)
- 703 Comparison of spontaneous hybridization frequency in Brassica juncea × B. napus under field condition for two years ☆M. Tsuda<sup>1</sup>,A. Okuzaki<sup>1</sup>,K. Konagaya<sup>1,2</sup>,Y. Nanasato<sup>1</sup>,Y. Tabei<sup>1</sup> (1.NIAS2.Forest Bio-Research Center, FFPRI)
- 704 Distorted segregation caused by a rice transposon, mPing, at the long arm of chromosome 12 OT. Kato,Y. Kakikubo,A. Horibata(Fac. BOST, Kinki U.)
- 705 Characterization of mitochondrial respiration of sugar beet with Owen type cytoplasm ☆M. Matsunaga,T. Kubo,T. Mikami(Grad.Sch.Agr., Hokkaido Univ.)
- 706 A sequence analysis of mitochondrial genome of radish (Raphanus sativus) using next-generation sequencer 2: Comparison of Normal and Ogura-type genomes ☆Y. Tanaka<sup>1</sup>,M. Tsuda<sup>2</sup>,K. Yasumoto<sup>2</sup>,H. Yamagishi<sup>1</sup>,T. Terachi<sup>1</sup> (1.Fac. Life Sci., Kyoto Sangyo U.2.Fac. Eng., Kyoto Sangyo U.)
- 707 Function of a pollen fertility restorer gene found in a black radish variety on the mitochondrial orf138 ☆Y. Mori<sup>1</sup>,K. Yasumoto<sup>2</sup>,L. Zang<sup>3</sup>,H. Yamagishi<sup>1</sup> (1.Grad. Sch. Fac. Eng., Kyoto Sangyo U.2.Fac. Eng., Kyoto Sangyo U.3.Nat. Eng. Res. Center for Veg.)

- 708 Comparison of mitochondrial genome structures and restorer fertility genes in 8 wild rice carrying cytoplasm of male sterility ☆T. Kano,T. Kazama,K. Toriyama(Grad Sch Agri Sci,Tohoku Univ,Japan)
- 709 The analysis of repeated sequences and cytoplasmic male-sterility of the mitochondrial genome in Brassica ☆A. Ohmine,Y. Hirata,S. Kawai(Grad.Sch.Agr., TUAT)
- 710 Quantification of copy numbers of orf125 sublimon detected in fertility restored Brassica napus ☆M. Watanabe,J. Imamura(Fac.Agr.Tamagawa U.)
- 711 Comparative study on the mitochondrial genomes of alloplasmic wheat lines with Aegilops mutica cytoplasm ☆Y. Gyawali ,Y. Tanaka,M. Tsujimura,T. Terachi(Fac. Life Sci., Kyoto Sangyo U.)
- 712 Analysis of mitochondrial genome of somatic hybrids between Arabidopsis thaliana and cabbage(Brassica oleracea) ☆M. Tsuda<sup>1</sup>,Y. Tanaka<sup>2</sup>,K. Yasumoto<sup>3</sup>,T. Terachi<sup>1</sup>,H. Yamagishi<sup>1</sup> (1.Gra.Sch.Fac.Eng.,Kyoto Sangyo U.2.Fac.Life Sci.,Kyoto Sangyo U.3.Fac.Eng.,Kyoto Sangyo U.)
- 713 Transcriptome analysis of the rice female gametophytic cells by RNA-seq ☆H. Takanashi<sup>1,5,6</sup>,Y. Hirata<sup>1</sup>,H. Ohyanagi<sup>2,3</sup>,J. Kawarama<sup>2</sup>,T. Nagata<sup>3</sup>,A. Toyoda<sup>4</sup>,A. Fujiyama<sup>4</sup>,N. Kurata<sup>3</sup>,N. Tsutsumi<sup>1</sup> (1.Grad. Sch. Agric. Life Sci., U. Tokyo<sup>2</sup>.Mitsubishi Space Software Co., Ltd.<sup>3</sup>.Plant Genetics Lab., NIG<sup>4</sup>.Comparative Genomics Lab., NIG<sup>5</sup>.Grad. Sch. Sci., U. Nagoya<sup>6</sup>.Research Fellow of the JSPS)
- 714 Timing and the place of domestication in wheats and barley clarified by charred remains from archeological sites ☆K. Tanno<sup>1</sup>,G. Willcox<sup>2</sup> (1.Fac. Agrc. Yamaguchi U., Japan<sup>2</sup>.Archeorient, CNRS, France)
- 715 Free-threshing emmer wheat may have originated several times. ☆S. Takenaka,T. Kawahara(Grad.Sch.Agric., Kyoto U.)
- 716 Genetic diversity of organellar genome in Aegilops umbellulata and its relation to the phylogeny of Ae. neglecta and Ae. columnaris ON. Mori<sup>1</sup>,Y. Yasugi<sup>1</sup>,S. Ohta<sup>2</sup> (1.Lab.Plant Genet.,Grad.Sch.Agric.Sci., Kobe U.2.Dept. BioSci, Fukui Pref. U.)
- 717 Genetic relationships among wild common buckwheat Fagopyrum esculentum ssp. ancestrale and its self-compatible relative F. homotropicum B. Tian<sup>1</sup>,C. Li<sup>2</sup>,OT. Ohsako<sup>1</sup> (1.Grad.Sch.Life Environmental Sci., Kyoto Pref.U.2.National Center for Agro-biodiversity, Yunnan Agr.U.)
- 718 *GS3* participates in stigma exsertion as well as seed length in rice. ☆N. Takano-Kai<sup>1</sup>,K. Doi<sup>1,2</sup>,A. Yoshimura<sup>1</sup> (1.Fac. Agr., Grad. Sch., Kyushu Univ.2.Grad. Sch. Bioagr. Sci., Nagoya Univ.)
- 719 Genetic variation of rice cultivars in Japan. III. Classification based on the resistant to blast disease (Pyricularia oryzae Cavara) ☆A. Tanaka-Kawasaki<sup>1,2</sup>,N. Hayashi<sup>3</sup>,Y. Fukuta<sup>1,2</sup> (1.JIRCAS<sup>2</sup>.Uni. Grad. Sch. Agri. Sci., U. Tottori<sup>3</sup>.NIAS)
- 720 The genetic diversity for ancestral varieties of sugar beet(Beta vulgaris L.) breeding in Japan ☆K. Taguchi,K. Okazaki,Y. Kuroda,H. Takahashi(Natl. Agr. Res. Cent. Hokkaido)
- 721 Production of allotriploid hybrids between diploid Iris setosa and diploid I. laevigata OT. Yabuya,S. Harada,A. Hanazaki,K. Inoue(Fac. Agr., U. Miyazaki)
- 722 Genetic studies on Bambuseae species in Japan. XXXI. Bamboos as an important useful plant group growing in the satoyama landscape. OM. Muramatsu(Prof. Emeritus, U. Okayama)
- 723 The role played by farm stands and the trend of the cultural geography in wasabi based on interviews with roadside station employees OK. Yamane(Fac. Appl. Biol. Sci., U. Gifu)
- P001 Breeding of new malting barley cultivar "Sai no Hoshi" with high quality and multiple disease resistance. S. Arai<sup>1</sup>,OR. Kanatani<sup>1</sup>,W. Saito<sup>1</sup>,T. Hoki<sup>1</sup>,M. Kihara<sup>1</sup>,S. Takahashi<sup>1</sup>,C. Kobayashi<sup>2</sup>,M. Nanamori<sup>2</sup>,S. Yosida<sup>3</sup>,S. Yamada<sup>1</sup> (1.Bioresources Research and Development Department, Sapporo Breweries Ltd<sup>2</sup>.Gunma Plant Production Department ,SBL<sup>3</sup>.Product and Technology Development Center, SBL.)

- P002 Breeding of "Wheat Norin-PL 9 (Akakabikei 3)", a cleistogamous wheat line with Fusarium head blight resistance OK. Kubo1,N. Kawada1,M. Fujita1,K. Hatta1,H. Matsunaka1,S. Oda2,T. Hatano1,M. Seki3,T. Yoshioka4,C. Otobe2,T. Nakajima1 (1.NARO/KARC2.NARO/NICS3.NARO/NARC4.NARO/WARC)
- P003 Breeding of a new sweetpotato cultivar "Satsumamasari" for Shochu (spirits) with good root shape and high storage ability. OK. Katayama1,Y. Kai2,T. Sakai2,T. Kumagai3,K. Ishiguro4,Y. Nakazawa2,m. Yoshinaga2 (1.NICS2.KONARC3.NARO4.NARCH)
- P004 A simple and versatile hydroponics method for rice seed production in a plant incubator OM. Kuroda,S. Ikenaga(NARO Agric. Res. Cent.)
- P005 OryzaExpress: An Integrated Database for Gene Expression Networks in Rice ☆K. Hamada1,K. Fukazawa1,T. Nagayama1,K. Yokoyama1,H. Tsuchida1,K. Igarashi1,N. Kurata2,K. Yano1 (1.Bioinf., Sch. Agri., Meiji Univ.2.Natl. Inst. Genet.)
- P006 Development of Brassica rapa cDNA resources for the systematic consolidation of Brassica and Arabidopsis OH. ABE1,I. SASAKI1,K. HATAKEYAMA2,M. NARUSAKA3,T. TAMURA4,K. FUKAMI-KOBAYASHI1,Y. NARUSAKA3,M. KOBAYASHI1 (1.RIKEN BioResource Center2.National Institute of Vegetable and Tea Science3.Research Institute for Biological Sciences4.BITS Co., Ltd.)
- P007 Cultivation and traditional utilization of emmer wheat (*Triticum turgidum* subsp. *dicoccum*) in India OS. Ohta1,N. Mori2,H. Chiba3,V. Shinde4,T. Osada5 (1.Dep. Biosci., Fukui Pref. U.2.Grad. Sch. Agric. Sci., Kobe U.3.Tohoku Gakuin U.4.Post-Grad. & Res. Inst., Decan College5.RIHN)
- P008 Morphological characteristics in the progenies from Nagai type of Japanese garden iris (*Iris ensata* Thunb.) ☆K. Kitahara (Sakai)1,4,Y. Murai2,3,S. Bang1,T. Iwashina3,Y. Kaneko1 (1.Fac. Agric., Utsunomiya U.2.Dept. Chem., Keio Univ.3.Dept. Bot., Natl. Mus. Nature Sci.4.Unit. Grad. Sch. Agric., Tokyo U. Agric. Tech.)
- P009 Phylogenetic differentiation in soybean landraces Dadacha-mame. ☆S. Konishi,T. Sasanuma,T. Abe(Fac. Agr. Yamagata U.)
- P010 Variation of polyphenol oxidase(PPO) gene in foxtail millet landraces and its relationship with phenol color reaction ☆T. Inoue1,E. Hitomi1,K. Ichitani2,M. Kawase3,K. Fukunaga1 (1.Fac.Life Environ.Sci., Pref.U.Hiroshima2.Fac.Agr., Kagoshima U.3.NIAS Genebank)
- P011 Origin of waxy common millet, *Panicum miliaceum* L. in Japan M. Araki1,A. Numaoka1,M. Kawase2,OK. Fukunaga1 (1.Fac.Life Environ.Sci., Pref.U.Hiroshima2.NIAS Genebank)
- P012 Research for CMS cytoplasm based on the variations of chloroplast genome in cruciferous plants. ☆K. Tsutsui1,2,S. Bang1,Y. Kaneko1 (1.Fac. Agric., Utsunomiya U.2.Unit. Grad. Sch. Agric., Tokyo U. Agric. Tech.)
- P013 Trace of genetic change of modern Japanese soybean varieties according to genomic and chloroplastic SSR polymorphisms ☆T. Sayama,Y. Yokota,T. Suwama,H. Sasama,A. Kaga,M. Ishimoto(NIAS)
- P014 Genetic diversity of wild soybeans and its relationship with metabolic profiling of seed components ☆Y. Yokota1,T. Sayama1,H. Sasama1,A. Hirose2,K. Komatsu2,A. Kaga1,M. Ishimoto1 (1.NIAS2.NARCH)
- P015 Diversity of Seed hardness on Single Kernel Characterization System in durum wheat. OK. Hatta1,H. Matsunaka1,K. Kubo1,M. Fujita1,K. Tanno2 (1.NARO/KARC2.Fac.agr.,Yamaguchi)
- P016 Natural variation of root growth direction in rice OE. Hanzawa1,K. Sasaki1,Y. Uga2,T. Sato1 (1.Grad. Sch.Life. Sci., U. Tohoku2.Natl. Inst. Agrobiol. Sci.)
- P017 Screening of peanut lines lacking a major allergen induced by heavy-ion beam irradiation ☆C. Cabanos1,H. Katayama1,H. Urabe1,C. Kuwata2,Y. Murota2,T. Abe3,Y. Okumoto1,N. Maruyama1 (1.Grad.Sch.Agric. U. Kyoto2.Chiba Prefectural Agriculture and Forestry Research Center3.RIKEN)

- P018 Analysis of temperature-sensitive virescent mutant in rice. ☆R. Morita<sup>1,2</sup>, M. Nakagawa<sup>3</sup>, Y. Hayashi<sup>2</sup>, S. Kogure<sup>2</sup>, H. Takehisa<sup>2,4</sup>, H. Tokairin<sup>2</sup>, T. Sato<sup>5</sup>, T. Abe<sup>1,2</sup> (1. Innovation Center, RIKEN<sup>2</sup>. Nishina Center, RIKEN<sup>3</sup>. Grad. Sch. Bioagric. Sci., U. Nagoya<sup>4</sup>. NIAS<sup>5</sup>. Grad. Sch. Life. Sci., U. Tohoku)
- P019 Activity of transposable elements inserted into OsMADS6 and phenotypic variation of the revertants. ☆S. Saito, R. Ishikawa (Faculty of Agric. and Life Sci., Hirosaki U.)
- P020 Transient expression assay of HWC1 using a biolistic ☆Y. Okiyama<sup>1</sup>, K. Ichitani<sup>2</sup>, N. Watanabe<sup>1</sup>, T. Kuboyama<sup>1</sup> (1. Col. Agr., Ibaraki U<sup>2</sup>. Fac. Agr., Kagoshima U)
- P021 Identification of the genome responsible for hybrid lethality in reciprocal-interspecific hybrids between *Nicotiana nudicaulis* and *N. tabacum* ○H. Liu, M. Hoshio, Y. Masaki, Y. Mori, W. Marubashi (Sch. Agr. Meiji U.)
- P022 Production and versatility of the CMS Brassica rapa line carrying *B. oxyrrhina* cytoplasm ○S. Shim, S. Bang, Y. Kaneko (Utsunomiya University)
- P023 Classification of Brassica oleracea-Diplotaxis tenuifolia monosomic addition lines by cytogenetical and molecular biological characteristics ☆Y. Okamoto, S. Bang, Y. Kaneko (Fac. Agric., Utsunomiya U.)
- P024 Morphological and cytological characteristics of Brassica napus-Raphanus sativus disomic addition lines ☆Y. Ozeki<sup>1</sup>, M. Takahashi (Akaba)<sup>1,2</sup>, A. Kondo<sup>1,3</sup>, K. Tsutsui<sup>1,4</sup>, S. Bang<sup>1</sup>, Y. Kaneko<sup>1</sup> (1. Fac. Agric., Utsunomiya U<sup>2</sup>. Fac. Agric., Iwate U<sup>3</sup>. Kihara Inst. Bio. Res., Yokohama City U<sup>4</sup>. Unit. Grad. Sch. Agric., Tokyo U. Agric. Tech.)
- P025 Knockdown of the genes related to cell division by RNA interference causes necrotic cell death in transgenic Arabidopsis ☆N. Mizuno<sup>1,2,3</sup>, N. Shitsukawa<sup>4</sup>, S. Takumi<sup>3</sup> (1. Grad. Sch. Agric. Sci., Kyoto U<sup>2</sup>. JSPS Research Fellow<sup>3</sup>. Grad. Sch. Agric. Sci., Kobe U<sup>4</sup>. Inst. Plant Sci. Resources, Okayama U.)
- P026 Preliminary isolation of aposporous embryo sac initial cell in facultative apomictic guineagrass (*Panicum maximum*) ○L. Chen<sup>1,2</sup>, Y. Nishimura<sup>2</sup> (1. Fac. Environment & Horti. Minami Kyushu U<sup>2</sup>. Grad. Sch. Horti. & Food Sci. Minami Kyushu U.)
- P027 Screening of the mutants for the factors participating in the localization on the specific ER of prolamin-mRNA in rice by TILLING method. ☆K. Taniguchi<sup>1</sup>, W. Hujimoto<sup>1</sup>, T. Okita<sup>2</sup>, T. Kumamaru<sup>1</sup> (1. Grad. Sch. Agric., Kyushu U<sup>2</sup>. WSU)
- P028 Functional analysis of apomixis specific genes: attempt to do introgression of ASG-1 gene into Arabidopsis ○Y. Nishimura<sup>1</sup>, T. Tetsumura<sup>2</sup>, L. Chen<sup>1,3</sup> (1. Grad. Sch. Horti. & Food Sci. Minami Kyushu U<sup>2</sup>. Fac. Agri. U. Miyazaki<sup>3</sup>. Fac. Environment & Horti. Minami Kyushu U.)
- P029 Analysis of Carotenoid biosynthetic genes in the mature fruit color variation induced interspecific-grafting in pepper ☆C. Yamaguchi, Y. Hirata, S. Kawai (Grad. Sch. Agric. IEAS, TUAT)
- P030 Comparative analysis of homologs of rice blast resistance gene Pit in gramineous species ○K. Hayashi<sup>1</sup>, N. Yasuda<sup>1</sup>, H. Yoshida<sup>2</sup> (1. Natl. Agric. Res. Ctr. <sup>2</sup>. Natl. Inst. Crop. Sci)
- P031 Increased disease tolerance to *Magnaporthe oryzae* in synthetic hexaploid wheat showing hybrid chlorosis ☆H. Nakano, Y. Tosa, S. Takumi (Grad. Sch. Agric. Sci., Kobe U.)
- P032 Evaluation of rice stripe resistance genes using near-isogenic lines of Koshihikari. ○H. Maeda<sup>1</sup>, O. Ideta<sup>2</sup>, K. Matsushita<sup>2</sup>, Y. Sunohara<sup>1</sup> (1. NICS<sup>2</sup>. WeNARC)
- P033 Effect of soybean cyst nematode resistance gene rhg1-b from PI 88788 ○N. Yamada<sup>1</sup>, T. Sayama<sup>2</sup>, H. Sasama<sup>2</sup>, M. Takahashi<sup>3</sup>, Y. Tsubokura<sup>1</sup>, T. Yamada<sup>1</sup>, K. Hirata<sup>1</sup>, M. Ishimoto<sup>2</sup>, M. Hajika<sup>1</sup> (1. NICS<sup>2</sup>. NIAS<sup>3</sup>. KONARC)
- P034 Production of abiotic stress tolerant GM potato by antioxidants recycle and reuse approach ☆A. Eltayeb<sup>1</sup>, M. Eltayeb<sup>2</sup>, T. Hisashi<sup>1</sup>, T. Kiyoshi<sup>2</sup> (1. Arid Land Research Center, Tottori U<sup>2</sup>. Unit. Grad. Sch. Agric. Sci., Tottori U.)

- P035 Expression analysis of aerenchyma formation-related genes in rice using the rcn1 mutant ☆ T. Yamauchi<sup>1</sup>, K. Shiono<sup>2</sup>, I. Takamura<sup>3</sup>, Y. Nagamura<sup>4</sup>, N. Tsutsumi<sup>5</sup>, N. Nishizawa<sup>5,6</sup>, K. Kato<sup>7</sup>, M. Nakazono<sup>1</sup> (1. Grad. Sch. Bioagr. Sci., Nagoya U. 2. Department of Bioscience, Fukui Pref. U. 3. Grad. Sch. Agr., Hokkaido U. 4. Genome Resource Center, Natl. Inst. Agr. Sci. 5. Grad. Sch. Agric. Life Sci., U. Tokyo 6. Res. Inst. Bioresource Biotech., Ishikawa Pref. U. 7. Obihiro Univ. Agric. & Vet. Med.)
- P036 Environmental Biosafety Assessment on Salt-Tolerant Transgenic Eucalyptus in Isolated Field ☆ Y. Kashimura<sup>1</sup>, X. Yu<sup>1</sup>, T. Oguchi<sup>1</sup>, E. Matsunaga<sup>2</sup>, K. Nanto<sup>2</sup>, M. Oishi<sup>2</sup>, A. Kikuchi<sup>1</sup>, K. Watanabe<sup>1</sup> (1. Grad. Sch. Life & Env. Sci., U. Tsukuba 2. Agri-Biotechnology Research Laboratory Nippon Paper Industries Co., Ltd.)
- P037 A new method for assessment of resistance to cracking of rice kernel. Artificial repeated wetting and drying test. ☆ T. Hayashi, A. Kobayashi, K. Tomita (Fukui Agri. Exp. Sta.)
- P038 Expression patterns and subcellular localizations of Arabidopsis U-box E3 ligases, PUB20 & 21. OS. Kobayashi, D. Tsugama, T. Takano (ANESC, U. Tokyo)
- P039 Analysis of drought responsive genes from *Jatropha curcas* OY. Tada<sup>1</sup>, Y. Katsumata<sup>2</sup>, Y. Yoshida<sup>2</sup> (1. Sch. Biosci. Biotechnol., Tokyo Univ. of Technol. 2. Grad. Sch. Bionics, Tokyo Univ. of Technol.)
- P040 Analysis of secondary aerenchyma formed in soybean hypocotyl under waterlogged conditions. ☆ A. Yanagawa<sup>1</sup>, H. Takahashi<sup>2</sup>, S. Hiraga<sup>3</sup>, S. Shimamura<sup>4</sup>, M. Nakazono<sup>2</sup> (1. Sch. Agric. Sci., Nagoya U. 2. Grad. Sch. Bioagric Sci., Nagoya U. 3. Nat. Inst. Crop. Sci. 4. Nat. Agr. Res. Cent. Tohoku Reg.)
- P041 Isolation and identification of novel partners interacted with Arabidopsis type 2 C protein phosphates 52 (AtPP2C52) using yeast two-hybrid system OH. Liu<sup>1</sup>, D. Tsugama<sup>1</sup>, S. Liu<sup>2</sup>, T. Takano<sup>1</sup> (1. Grad. Sch. Agric. Life Sci., U. Tokyo 2. Northeast Forestry U. China)
- P042 Evaluation of soybean salt tolerance for near-isogenic lines carrying a salt tolerant gene in field condition OD. Xu<sup>1</sup>, D. Tuyen<sup>1</sup>, E. Hanzawa<sup>2</sup>, T. Sato<sup>2</sup> (1. JIRCAS 2. Grad. Sch. Life Sci., Tohoku U.)
- P043 A comprehensive expression analysis of members of the half size ATP binding cassette protein G subfamily in rice OS. Matsuda<sup>1</sup>, N. Komori<sup>1</sup>, K. Furukawa<sup>1</sup>, A. Funabiki<sup>1</sup>, Y. Tokujii<sup>1</sup>, I. Takamura<sup>2</sup>, K. Kato<sup>1</sup> (1. Obihiro Univ. Agric. & Vet. Med. 2. Grad. Sch. Agr., Hokkaido U.)
- P044 Effects of acclimation on chilling tolerance in Asian cultivated and wild rice A. Baruah<sup>1</sup>, Y. Oguma<sup>1</sup>, N. Ishigo-Oka<sup>1</sup>, N. Uwatoko<sup>1</sup>, Y. Sano<sup>1</sup>, OK. Onishi<sup>1,2</sup> (1. Res. Fac. Agr., Hokkaido U. 2. Obihiro U. Agric. & Vet. Med.)
- P045 Transition of chilling-sensitivity during germination and postgermination in radish (*Raphanus sativus*) ON. Shimomura<sup>1</sup>, T. Ishikawa<sup>2</sup>, T. Okada<sup>3</sup>, T. Fukaya<sup>4</sup>, R. Shishido<sup>5</sup>, K. Nomura<sup>6</sup> (1. Coll. Bioresource Sci., Nihon U. 2. Coll. Bioresource Sci., Nihon U. 3. Coll. Bioresource Sci., Nihon U. 4. Coll. Bioresource Sci., Nihon U. 5. Coll. Bioresource Sci., Nihon U. 6. Coll. Bioresource Sci., Nihon U.)
- P046 Isolation and characterization of wheat myo-inositol 1-phosphate synthase gene, TaMIPS. OE. Shimosaka, S. Murayama (NARO. Agr. Res. Cent. Hokkaido)
- P047 Difference of pre-maturity sprouting resistance in Japanese wheat. OH. Matsunaka<sup>1</sup>, M. Chono<sup>2</sup>, K. Hatta<sup>1</sup>, K. Kubo<sup>1</sup>, M. Fujita<sup>1</sup> (1. NARO/KONARC 2. NARO/NICS)
- P048 Seed components and gene expression of soybean in response to temperature. OT. Yamada<sup>1</sup>, H. Kobayashi<sup>2</sup>, Y. Yamashita<sup>1</sup>, Y. Mori<sup>1</sup>, A. Torii<sup>1</sup>, T. Agata<sup>1</sup>, J. Abe<sup>1</sup> (1. Grad. Sch. Agric., Hokkaido U. 2. Fac. Agric., Hokkaido U.)
- P049 Selection of high  $\beta$ -glucan content lines using a DNA marker linked to the high amylose (amo1) gene in barley. ☆ a. takahashi<sup>1</sup>, s. taketa<sup>2</sup>, k. sato<sup>2</sup>, t. yoshioka<sup>1,3</sup>, t. yanagisawa<sup>1,3</sup> (1. WeNARC, NARO 2. IPSR, Okayama U. 3. NICS, NARO)

- P050 Water absorption of pearled barley using in near isogenic lines with starch and  $\beta$ -glucan. OT. Yanagisawa<sup>1,2</sup>, E. Aoki<sup>1</sup>, A. Takahashi<sup>2</sup>, T. Nagamine<sup>2,3</sup> (1.NICS,NARO2.WeNARC,NARO3.NARC,NARO)
- P051 Genetic characterization of high-sucrose trait in a soybean cultivar, "Toyoshirome". OT. Anai, D. Inoue, H. Koga (Fac. Agric., Saga Univ.)
- P052 Chemical structural analysis of new saponin components accumulated in hybrid seeds between mutant wild soybean (*Glycine soja*) and cultivar (*Glycine max*) OT. Kon<sup>1</sup>, N. Honda<sup>1</sup>, Y. Takada<sup>2</sup>, S. Kato<sup>3</sup>, A. Kikuchi<sup>3</sup>, M. Ishimoto<sup>4</sup>, H. Muraoka<sup>5</sup>, S. Ogawa<sup>5</sup>, C. Tsukamoto<sup>1</sup> (1.Faculty of Agriculture, Graduate School of Iwate University2.National Agricultural Research Center for Western Region3.National Agricultural Research Center for Tohoku Region4.National Institute of Agrobiological Sciences5.Faculty of Engineering, Iwate University)
- P053 Varietal differences in basic 7S globulin secretion from soybean seeds by a hot water treatment OK. Fujiwara, Y. Kobayashi, N. Maruyama (Grad.Sch.Agric., U.Kyoto)
- P054 A large genetic variation in phenolic compound contents of seed coat among black soybean cultivars ☆S. Phommalath, m. teraishi, t. tsukiyama, y. okumoto (Grad.Sch.Agric. Kyoto University)
- P055 Identification of candidate genes conferring structural diversity at C-21 position of soybean saponins ☆K. Takagi<sup>1</sup>, Y. Takada<sup>2</sup>, A. Kikuchi<sup>3</sup>, S. Kato<sup>3</sup>, T. Suwama<sup>4</sup>, H. Sasama<sup>1</sup>, T. Sayama<sup>1</sup>, S. Tochigi<sup>1</sup>, C. Tsukamoto<sup>5</sup>, M. Ishimoto<sup>1</sup> (1.NIAS2.WeNARC3.NARCT4.NARCH5.Grad. Sch. Agric., Iwate U.)
- P056 Why is the tofu curd processing aptitude of 7S deficiency soybean unstable? OM. Hajika, N. Yamada, T. Yamada, K. Hirata (NARO Institute of Crop Science)
- P057 Analysis of genes showing different expression pattern during seed development between different oil content lines of *Brassica napus* ☆H. Doi, M. Akaba, H. Yamada-Akiyama, Y. Akasaka-Kennedy, S. Yokoi, Y. Takahata (Fac. Agri., Iwate U.)
- P058 Improvement of grain shape in tetraploid and hexaploid wheat revealed by principal component analysis of seed shape-related traits ☆Y. Okamoto, S. Takumi (Grad.Sch.Agric.Sci., Kobe U.)
- P059 Variation of depression of grain quality in Japanese rice varieties grown at 32degree during filling period ☆M. Mizunaga<sup>1</sup>, A. Kobayashi<sup>2</sup>, K. Okuno<sup>1</sup> (1.Grad.Sch.Life and Envi.Sci., U.Tsukuba2.Fukui Agric.Exp.Sta.)
- P060 Differential regulation of gene expression for starch synthesis to alteration of source-sink balance in rice endosperm OT. Inukai (Res. Fac. Agri., Hokkaido Univ.)
- P061 Quality of wheat flour and bread making in near-isogenic lines carrying different Wx genes ○ M. Seki<sup>1</sup>, H. Matsunaka<sup>2</sup>, H. Kojima<sup>3</sup>, M. Fujita<sup>2</sup>, C. Kiribuchi-Otobe<sup>3</sup>, S. Oda<sup>3</sup>, T. Nakamura<sup>4</sup>, M. Saito<sup>4</sup> (1.NARC,NARO2.KNARC,NARO3.NICS,NARO4.NARCT,NARO)
- P062 Use of cross breeding and irradiation of gamma rays for the selection of standing type sweetpotato plants OT. Kuranouchi<sup>1</sup>, T. Fujita<sup>1</sup>, T. Kumazaki<sup>2</sup>, T. Kumagai<sup>3</sup>, K. Katayama<sup>1</sup> (1.Natl. Inst. of Crop Sci.2.Toyohashi Univ. of Technol.3.Natl. Agric. Res. Org.)
- P063 Phenotypic characterization of a rice mutant, NM3-631 expressing hyper-tillering in the late vegetative and reproductive stages. ☆T. Hobo<sup>1</sup>, Y. Nagato<sup>2</sup>, H. Kitano<sup>1</sup> (1.Bioscience and Biotechnology Center, Nagoya University2.Grad.Sch.Agric.Life Sci., U.Tokyo)
- P064 Effects of the genes affecting grain number per panicle of rice on yield related traits in different fertilizer condition. ☆T. Nakano<sup>1</sup>, H. Honjo<sup>2</sup>, N. Saka<sup>2</sup>, T. Oga<sup>2</sup>, M. Ikeda<sup>3</sup>, T. Hobo<sup>3</sup>, H. Kitano<sup>3</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya U. 2.Aichi Agric. Res. Ctr.3.Biosci. Biotech. Ctr., Nagoya U.)

- P065 Heterosis at early developmental stages in *Arabidopsis thaliana* is independent of flowering time. ☆T. Kawanabe<sup>1</sup>, E. Dennis<sup>2</sup>, R. Fujimoto<sup>3</sup> (1.Watanabe seed Co., Ltd. 2.CSIRO Plant Industry 3.Graduate school of Science and Technology, Niigata university, )
- P066 Identification of a novel mutant with ectopic expression of a KNOX gene in rice ☆M. Ishibashi, Y. Ito (Grad.Sch.Agric. Sci., Tohoku U.)
- P067 Expression analysis and splicing variants in the *Brassica rapa* FLC genes of a late bolting breeding material, Leafy Green Parental Line No.2. ☆N. Kitamoto<sup>1</sup>, S. Yui<sup>2</sup>, Y. Takahata<sup>1</sup>, S. Yokoi<sup>1</sup> (1.Faculty of Agric., U. Iwate 2.NARC)
- P068 Genetic analysis of photoperiodic insensitive mutant accessions found in the natural population of *Aegilops tauschii* ☆K. Koyama, Y. Okumura, S. Takumi (Grad.Sch.Agric.Sci., Kobe U.)
- P069 Gene cloning and expression analysis of MADS box protein gene and monodehydroascorbate reductase gene on the papaya sex chromosomes ○N. Urasaki<sup>1</sup>, K. Tarora<sup>1</sup>, A. Shudo<sup>1</sup>, M. Tamaki<sup>1</sup>, H. Ueno<sup>2</sup>, K. Yoshida<sup>3</sup>, S. Adaniya<sup>4</sup>, H. Matsumura<sup>2</sup> (1.Okinawa Pref. Agric. Res. Ctr. 2.Gene Res. Ctr. Shinshu Univ. 3.Gene Res. Ctr. Shinshu Univ. 4.Fac. Agric., U. Ryukyus)
- P070 *Arabidopsis heterotrimeric G protein β subunit (AGB1)* is involved in brassinosteroid signaling D. Tsugama, ○T. Takano (ANESC., U.Tokyo)
- P071 Production of transformation-competent sugar beet with annual habitat: a basis for sugar beet reproduction research. ☆H. Kagami<sup>1</sup>, H. Matsuhira<sup>2</sup>, T. Kubo<sup>1</sup>, T. Mikami<sup>1</sup> (1.Grad. Sch. Agr., Hokkaido U. 2.NARCH)
- P072 Highly expressed genes in sugar beet callus with good regeneration ability. ☆H. Matsuhira<sup>1</sup>, H. Kagami<sup>2</sup>, K. Taguchi<sup>1</sup>, T. Kubo<sup>2</sup>, T. Mikami<sup>2</sup> (1.NARO Hokkaido Agr. Res. Ctr. 2.Grad. Sch. Agr., Hokkaido Univ. )
- P073 Identification of a novel restorer-of-fertility gene for Owen cytoplasmic male sterility (CMS) in sugar beet ☆Y. Honma<sup>1</sup>, K. Taguchi<sup>2</sup>, H. Hiyama<sup>1</sup>, R. Yui-Kurino<sup>1</sup>, T. Kubo<sup>1</sup>, T. Mikami<sup>1</sup> (1.Grad. Sch. Agr., Hokkaido U. 2.Natl. Agr. Res. Cent. Hokkaido)
- P074 Mapping of a fertility restorer gene Rft for Ogura cytoplasmic male sterility in radish. ☆K. Yasumoto<sup>1</sup>, T. Terachi<sup>2</sup>, H. Yamagishi<sup>2</sup> (1.Fac. Eng., Kyoto Sangyo U. 2.Fac. Life Sci., Kyoto Sangyo U.)
- P075 Allelism tests of genes associated with male and monoecious characters in spinach ☆K. Yamamoto, Y. Onodera, T. Mikami (Grad. Sch. Agr., Hokkaido U.)
- P076 Histological observation of shoot formation process in petal cultures of HIGOGIKU ○Y. Matsuda, Y. Takamiya, H. Kaneko, T. Murata (Sch.Agric., Tokai U.)
- P077 Factors affecting the natural hybridization rates in domestic rice cultivators. – Variation of flowering phenology – ☆A. Mizuguti<sup>1</sup>, H. Shibaie<sup>2</sup>, S. Ohmori<sup>1</sup>, K. Yokoyama<sup>1</sup>, Y. Kominami<sup>1</sup>, H. Aoki<sup>1</sup>, O. Yatou<sup>1</sup> (1.NARO Agricultural Research Center 2.National Institute for Agro-Environmental Sciences)
- P078 Mapping of QTLs of controlling luster of boiled rice in Japonica cultivar, Sasanishiki using chromosome segment substitution lines ○H. Hayasaka (Miyagi Pref. Furukawa Agric. Exp. Stn. )
- P079 Estimation for chromosome regions controlling sake-brewing traits in parental lines of Yamadanishiki ☆T. Hachiken<sup>1</sup>, S. Yoshida<sup>2</sup>, T. Ishii<sup>3</sup>, A. Ota<sup>4</sup>, T. Akashi<sup>4</sup>, A. Nishimura<sup>4</sup>, N. Mori<sup>1</sup> (1.Lab.Plant Genet., Grad.Sch.Agric.Sci., Kobe U. 2.Hyogo Institute of Agriculture, Forestry and Fishery 3.Lab. Plant Breeding, Grad.Sch.Agric.Sci., Kobe U. 4.Res. & Development Dept., Hakutsuru Sake Brewing Co., Ltd.)
- P080 QTL analysis for panicle traits in rice using a long-panicle line ☆K. Ando<sup>1</sup>, T. Hobo<sup>2</sup>, M. Ikeda<sup>2</sup>, M. Ashikari<sup>2</sup>, M. Matsuoka<sup>2</sup>, H. Kitano<sup>2</sup>, K. Doi<sup>1</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya U. 2.Biosci. Biotec. Ctr., Nagoya U.)
- P081 A high-throughput phenotyping software for measuring size of rice seeds ☆T. Tanabata, T. Shibaya, K. Ebana, M. Yano (Natl. Inst. Agrobiol. Sci.)

- P082 QTL analysis of grain shape in Koshihikari / Nipponbare BILs by using new software for measuring rice grains ☆T. Shibaya,T. Tanabata,K. Hori,M. Yano(Natl. Inst. Agrobiol. Sci.)
- P083 QTL analysis of rice annual growth habit by using *Oryza glaberrima* chromosome segment substitution lines ☆A. Kume<sup>1</sup>,N. Komeda<sup>2</sup>,S. Kawara<sup>3</sup>,T. Takashi<sup>4</sup>,H. Kitano<sup>2</sup>,K. Doi<sup>1</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya U.2.Biosci. Biotech. Ctr., Nagoya U.3.Fac. Agr., Nagoya U.4.HRI-JP)
- P084 QTL analysis for cold tolerance and other agronomic traits in rice; cross between NERICA parent variety, WAB56-104 and cold tolerant variety, Hananomai ☆C. Wainaina<sup>1</sup>,Y. Inukai<sup>1</sup>,Y. Nakajima<sup>2</sup>,Y. Mizukami<sup>3</sup>,M. Nakamura<sup>3</sup>,S. Asanuma<sup>4</sup>,H. Kitano<sup>5</sup>,D. Makihara<sup>4</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya U. 2.Aichi Agric. Res. Ctr.3.MARI., Aichi Agric. Res. Ctr.4.ICCAE, Nagoya U.5.Biosci., Biotech. Ctr., Nagoya U.)
- P085 QTL mapping of regrowth ability of sudangrass and development of an evaluation method for the number of culm at the second harvest. ○J. Yonemaru<sup>1</sup>,S. Kasuga<sup>2</sup>,E. Ichikawa<sup>2,4</sup>,N. Higuchi<sup>2,5</sup>,H. Nagayama<sup>2,6</sup>,R. Matsumoto<sup>2,7</sup>,T. Ando<sup>1,3</sup>,I. Kono<sup>3,8</sup> (1.Natl. Inst. Agrobiol. Sci.2.Shinshu Univ. AFC3.STAFF4.Nagoya Univ.5.Hakubaku Co. Ltd.6.JA Kamiina7.Masuda Seed Co. Ltd.8.RIKEN)
- P086 QTL analysis for cleistogamy in bread wheat by using DH lines derived from the cross "U24" and "Ayahikari" M. Fujita<sup>1</sup>,H. Matsunaka<sup>1</sup>,K. Kubo<sup>1</sup>,K. Hatta<sup>1</sup>,A. Hamada<sup>2</sup>,Y. Okumoto<sup>2</sup>,M. Nitta<sup>2</sup>,○S. Nasuda<sup>2</sup> (1.NARO/KARC2.Grad. Sch. Agric., Kyoto U.)
- P087 Genetic analysis of early flowering genes in Nepal wheat landraces and Shiroganekomugi ☆A. Ngyuen<sup>1</sup>,N. Mizuno<sup>1,2</sup>,M. Nitta<sup>2</sup>,S. Nasuda<sup>2</sup>,S. Takumi<sup>1</sup> (1.Grad.Sch.Agric.Sci., Kobe U.2.Grad.Sch.Agric., Kyoto U.)
- P088 A QTL for high isoflavone contents in seeds of the soybean cultivar 'Tamahomare' is closely linked to the hilum color Inhibitor locus. ☆S. Miranda<sup>1</sup>,M. Teraishi<sup>2</sup>,T. Yoshikawa<sup>3</sup>,T. Tsukiyama<sup>4</sup>,Y. Okumoto<sup>5</sup> (1.Graduate School of Agriculture, Kyoto University2.Graduate School of Agriculture, Kyoto University3.Graduate School of Agriculture and Life Science, University of Tokyo4.Graduate School of Agriculture, Kyoto University5.Graduate School of Agriculture, Kyoto University)
- P089 QTL analysis of number of seeds per pod in EDAMAME variety. ○Y. Takada,M. Saruta(WeNARC)
- P090 Refinement of QTL region for paternal inheritance of mitochondrial plasmid in *Brassica napus*. ☆M. Oshima<sup>1</sup>,H. Handa<sup>1,2</sup> (1.Grad. Sch. Life & Env. Sci., U Tsukuba2.NIAS)
- P091 Isolation of MSH1 gene homologs that involves stability of mitochondrial genome in *Brassica* species ☆Y. Terao,Y. Kawahara,T. Ando,J. Imamura(Fac. Agric. Tamagawa U.)
- P092 QTL analysis of glucosinolate content in *Raphanus sativus* ☆Z. Zou<sup>1</sup>,M. Ishida<sup>2</sup>,S. Suzuki<sup>1</sup>,T. Kakizaki<sup>2</sup>,f. Li<sup>1</sup>,H. Kitashiba<sup>1</sup>,T. Nishio<sup>1</sup> (1.Grad. Sch. Agric. Sci., Tohoku.Univ.2.National Institute of Vegetable and Tea science(NIVTS).)
- P093 High-density linkage map of *Raphanus sativus* with EST-SSR markers. ○K. Shirasawa<sup>1</sup>,M. Oyama<sup>2</sup>,H. Hirakawa<sup>1</sup>,S. Sato<sup>1</sup>,S. Tabata<sup>1</sup>,T. Fujioka<sup>2</sup>,C. Kimizuka-Takagi<sup>3</sup>,T. Sakai<sup>2</sup>,S. Isobe<sup>1</sup> (1.Kazusa DNA Res. Inst.2.Mikado Kyowa Seed Co., Ltd.3.Kimizuka Vegetable Farm)
- P094 Construction of linkage maps of foxtail millet(*Setaria italica* (L.) P. Beauv.) based on transposon display markers. ☆K. Sato<sup>1</sup>,K. Naito<sup>2</sup>,K. Fukunaga<sup>1</sup> (1.Fac.Life Environ.Sci., Pref. U. Hiroshima2.NIAS Genebank)
- P095 Mapping of the gene for monoecism in *Spinacia oleracea* L. ☆Y. Oda,Y. Onodera,T. Mikami(Grad.Sch.Agr.,Hokkaido Univ.)
- P096 Fine mapping of the spineless gene of eggplant (*Solanum melongena* L.) ○K. Miyatake,S. Negoro,H. Yamaguchi,T. Nunome,A. Ohyama,H. Fukuoka(NIVTS)
- P097 Detection of SNPs in synthetic hexaploid wheat lines using real-time PCR and its application of linkage map construction R. Matsuda,M. Iehisa,○S. Takumi(Grad.Sch.Agric.Sci., Kobe U.)

- P098 Genetic Analysis of Early Growth in Sorghum Bicolor (L.) Moench ○E. Ichikawa<sup>1</sup>, S. Kasuga<sup>2</sup>, K. Omae<sup>1</sup>, K. Ohara<sup>2</sup>, C. Tsugui<sup>2</sup>, Y. Wakako<sup>2</sup>, Y. Yamashita<sup>2</sup>, J. Yonemaru<sup>3</sup>, T. Sazuka<sup>1</sup> (1.Biosci. and Biotech. Ctr, Nagoya Univ.2.Edu. Res. Ctr. of Alp. Field Sci., Shinshu Univ.3.Natl. Inst. Agrobiol. Sci.)
- P099 The chromosomal region of a teosinte (*Zea mays* ssp. *huehuetenangensis*) causing small ear of Maize. ○T. Kikawada, Y. Mano, H. Tamaki, S. Mitsuhashi, H. Sato (NARO Institute of Livestock and Grassland Science)
- P100 Development and utility evaluation of DNA markers linked to late bolting in Chinese cabbage parental line Nou 6 gou. ☆T. Kakizaki<sup>1</sup>, T. Kato<sup>1,2</sup>, N. Fukino<sup>1</sup>, M. Ishida<sup>1</sup>, K. Hatakeyama<sup>1</sup>, S. Matsumoto<sup>1</sup> (1.NIVTS, NARO2.Grad. Sch. Bioresour., Mie Univ.)
- P101 Detection of SSR markers linked to the everbearing gene in cultivated strawberry ○M. Honjo<sup>1</sup>, T. Nunome<sup>2</sup>, S. Kataoka<sup>1</sup>, S. Yui<sup>1</sup>, T. Yano<sup>1</sup>, M. Hamano<sup>1</sup>, H. Yamazaki<sup>1</sup>, M. Morishita<sup>1</sup>, T. Yamamoto<sup>3</sup> (1.NARO/TARC2.NIVTS3.NIFTS)
- P102 Development of STS markers for the selection of sporeless mutants in *Pleurotus eryngii*
- P103 Global analysis of gene expression in male strobili of *Cryptomeria japonica* conferring male sterility ○N. Futamura<sup>1</sup>, M. Saito<sup>2</sup>, K. Shinohara<sup>1</sup> (1.For. and Forest Prod. Res. Inst.2.Toyama For. Res. Inst.)
- P104 Exploration of host plant genes related to gall-inducing insects using wheat-barley chromosome addition lines. 2 ☆K. Yoshida<sup>1</sup>, K. Kawaura<sup>1</sup>, M. Tokuda<sup>2</sup>, S. Kumashiro<sup>2</sup>, K. Matsukura<sup>3</sup>, M. Matsumura<sup>3</sup>, Y. Jikumaru<sup>4</sup>, Y. Ogihara<sup>1</sup> (1.KIBR, Yokohama City U.2.Kyushu U.3.KONARC/NARO4.RIKEN PSC)
- P105 Functional analysis of genes based on large-scale SNP data in tomato cultivars ○H. Hirakawa, K. Shirasawa, S. Sato, S. Isobe, S. Tabata (Kazusa DNA Res. Inst.)