

# Title of Papers Presented at the 123rd Meeting of The JAPANESE SOCIETY Oral presentations

## Oral Presentations

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**101** QTL-seq identified a genomic region related to booting stage low temperature tolerance in rice.

☆Abe, A.<sup>1</sup>, H. Takagi<sup>1,2</sup>, H. Yaegashi<sup>1</sup>, H. Sugawara<sup>3</sup>, A. Fukushima<sup>4</sup>, R. Terauchi<sup>1</sup> (1.Iwate Biotech. Res. Ctr., 2.United Grad. Sch. Agric. Sci., Iwate Univ., 3.Iwate Agric. Res. Ctr., 4.NARO/TARC)

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**102** MutMap+: the new method for identification of mutagenized gene without crossing in rice

☆Yaegashi, H.<sup>1</sup>, R. Fekih<sup>1</sup>, H. Takagi<sup>1,2</sup>, M. Tamiru<sup>1</sup>, A. Abe<sup>1</sup>, S. Natsume<sup>1,2</sup>, A. Uemura<sup>1</sup>, R. Terauchi<sup>1</sup> (1.Iwate Biotech. Res. Center, 2.United Grad. Sch. Agric. Sci., Iwate U.)

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**103** A new method for rapid identification of mutant causal gene without complete reference sequence in rice.

☆Takagi, H.<sup>1,2</sup>, H. Yaegashi<sup>1</sup>, A. Uemura<sup>1</sup>, A. Abe<sup>1</sup>, S. Natsume<sup>1,2</sup>, H. Utsushi<sup>1</sup>, R. Terauchi<sup>1,2</sup> (1.Iwate Biotech. Res. Cent., 2.United Grad. Sch. Agric. Sci., Iwate U.)

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**104** Fine mapping of *HWA1* and *HWA2*, complementary hybrid weakness genes in rice

○Ichitani, K.<sup>1</sup>, C. Urata<sup>1</sup>, S. Taura<sup>2</sup>, T. Tezuka<sup>3</sup>, Y. Okiyama<sup>4</sup>, T. Kuboyama<sup>4</sup>, M. Sato<sup>1</sup> (1.Fac. Agr., Kagoshima Univ., 2.Inst. Gene Res., Kagoshima Univ., 3.Grad. Sch. Life Envi. Sci., Osaka Pref. Univ., 4.Col. Agr., Ibaraki Univ.)

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**105** Identification of novel QTLs promote plant height from extremely tall *d1* mutant, Xhinheiguai.

☆Miura, K.<sup>1</sup>, S. Segami<sup>1</sup>, M. Sasaki<sup>1</sup>, M. Nakamura<sup>1</sup>, M. Ashikari<sup>2</sup>, H. Kitano<sup>2</sup>, Q. Qian<sup>3</sup>, Y. Iwasaki<sup>1</sup> (1.Dept. Biosci. Fukui Pref. Univ., 2.Biosci. Biotech. Cent. Nagoya Univ., 3.China national rice reserach institute)

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**106** Phenotype annotation of introgressed regions derived from indica varieties in Japanese high-biomass rice cultivars

○Yonemaru, J.<sup>1</sup>, R. Mizobuchi<sup>1</sup>, H. Kato<sup>2</sup>, T. Yamamoto<sup>1</sup>, E. Yamamoto<sup>1</sup>, K. Matsubara<sup>2</sup>, H. Hirabayashi<sup>2</sup>, Y. Takeuchi<sup>2</sup>, H. Tsunematsu<sup>2</sup>, T. Ishii<sup>2,3</sup>, H. Ohta<sup>2,4</sup>, H. Maeda<sup>2,5</sup>, K. Ebana<sup>1</sup>, M. Yano<sup>1</sup> (1.NIAS, 2.NICS,NARO, 3.WARC,NARO, 4.TARC,NARO, 5.Agriculture, Forestry and Fisheries Research Council, MAFF)

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**107** Development of an efficient program for detection of mutations using data of next generation sequencing. II. Case of F2 individuals

○Miyao, A., M. Nakagome, E. Solovieva, Y. Nagamura, T. Itoh, K. Hori, T. Yamamoto (Agrogenomics Res. Cent. NIAS)

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**108** Genomic regions involving cold tolerance at booting stage inherited in Japanese rice cultivars revealed by pedigree haplotype information

○Yamamoto, T.<sup>1</sup>, K. Saeki<sup>2</sup>, T. Endo<sup>2</sup>, T. Mizubayashi<sup>1</sup>, T. Ando<sup>1</sup>, S. Fukuoka<sup>1</sup> (1.National Institute of Agrobiological Sciences, 2.Miyagi Prefectural Furukawa Agricultural Experiment Station)

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**109** Exploitation of genome discrimination methods in common wheat transcripts using diploid ancestor RNA-seq

☆Mishina, K.<sup>1</sup>, K. Kawaura<sup>1</sup>, Y. Kamiya<sup>1</sup>, K. Mochida<sup>2</sup>, H. Tarui<sup>3</sup>, N. Suzuki<sup>3</sup>, J. Kawai<sup>3</sup>, K. Igarashi<sup>4</sup>, K. Yano<sup>4</sup>, Y. Ogiwara<sup>1</sup> (1.KIBR, Yokohama City U., 2.RIKEN PSC, 3.RIKEN OSC, 4.Bioinf., Sch. of Agri., Meiji Univ.)

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**110** Construction of a high density genetic map of bread wheat by the array based marker system for detecting DNA polymorphism

○Kimura, T.<sup>1</sup>, H. Enoki<sup>1</sup>, S. Nishimura<sup>1</sup>, R. Ohno<sup>2</sup>, M. Iehisa<sup>2</sup>, S. Takumi<sup>2</sup>, S. Nasuda<sup>3</sup> (1.Future Project Div., TOYOTA MOTOR CORPORATION, 2.Grad. Sch. Agric. Sci., Kobe Univ., 3.Grad. Sch. Agric., Kyoto Univ.)

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**111** QTL analysis for intraspecific differentiation of spike and grain shape-related traits in *Aegilops tauschii*

Okamoto, Y., R. Nishijima, Y. Kuki, K. Sakaguchi, M. Yoshioka, ○S. Takumi (Grad. Sch. Agri. Sci., Kobe Univ.)

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**112** Genome-wide Determination of the Active Retrotransposon Insertion Sites for Wheat Chromosome Deletion Lines Analyzed by the Next-generation Sequencer

☆Takai, T.<sup>1</sup>, M. Tahara<sup>2</sup>, Y. Monden<sup>2</sup> (1.Grad. Sch. Nat. Sci. & Tech., 2.Grad. Sch. Env. & Life Sci.)

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**113** Construction of a high-density map and analysis of malting quality QTLs on Mikamo golden × Harrington doubled haploid population in barley (*Hordeum vulgare* L.)

○Zhou, T.<sup>1</sup>, T. Iimure<sup>1</sup>, M. Kihara<sup>1</sup>, K. Sato<sup>2</sup>, S. Yamada<sup>1</sup> (1.Sapporo Breweries Ltd., 2.IPSR, Okayama Univ.)

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**114** The QTL for barley malt extract on chromosome 2H

○Iimure, T.<sup>1</sup>, T. Zhou<sup>1</sup>, T. Hoki<sup>1</sup>, M. Kihara<sup>1</sup>, K. Sato<sup>2</sup>, S. Yamada<sup>1</sup> (1.BRDD, Sapporo Brew. Ltd., 2.IPSR, Okayama U.)

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**115** Barley Expression Database: bex-db

○Tanaka, T.<sup>1</sup>, H. Sakai<sup>1</sup>, N. Fujii<sup>2</sup>, S. Nakamura<sup>3</sup>, J. Wu<sup>1</sup>, T. Itoh<sup>1</sup>, T. Matsumoto<sup>1</sup> (1.National Institute of Agrobiological Sciences, 2.Hitachi Government and Public Corporation System Engineering, Ltd., 3.National Institute of Crop Science)

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**116** A wheat bin map of PLUG markers and its comparative analysis with the barley genome

☆Saito, M.<sup>1</sup>, T. Shimbata<sup>2</sup>, A. Sunohara<sup>2</sup>, T. Tanaka<sup>3</sup>, G. Ishikawa<sup>1</sup>, T. Inokuma<sup>2</sup>, T. Takiya<sup>2</sup>, T. Nakamura<sup>1</sup> (1.NARO/TARC, 2.Central Lab., Nippon Flour Mills Co., Ltd., 3.NIAS)

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**117** Construction of a high-density linkage map and QTL analysis in common buckwheat.

☆Hara, T.<sup>1</sup>, S. Yabe<sup>2</sup>, M. Ueno<sup>3</sup>, H. Enoki<sup>4</sup>, T. Kimura<sup>4</sup>, S. Nishimura<sup>4</sup>, Y. Yasui<sup>3</sup>, H. Iwata<sup>2</sup>, R. Ohsawa<sup>1</sup> (1.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.Grad. Sch. Agr., Univ. Kyoto, 4.Future Project Div., TOYOTA MOTOR CORPORATION)

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**118** Linkage disequilibrium in a breeding population and prospects for genomic selection in common buckwheat

☆Yabe, S.<sup>1</sup>, T. Hara<sup>2</sup>, M. Ueno<sup>3</sup>, H. Enoki<sup>4</sup>, T. Kimura<sup>4</sup>, S. Nishimura<sup>4</sup>, Y. Yasui<sup>3</sup>, R. Ohsawa<sup>2</sup>, H. Iwata<sup>1</sup> (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 3.Grad. Sch. Agr., Univ.

**201** Fine mapping of *Dt2* locus coactively controlling plant shapes with different loci.

☆Sayama, T.<sup>1</sup>, N. Yamaguchi<sup>2</sup>, H. Sasama<sup>1</sup>, Y. Yokota<sup>1</sup>, T. Miyoshi<sup>2</sup>, M. Ishimoto<sup>1</sup> (1.NIAS, 2.HRO Tokachi Agric. Exp. Stn.)

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**202** Development and evaluation of a 6K SNP array for Japanese soybeans

○Kaga, A.<sup>1</sup>, T. Shimizu<sup>1</sup>, T. Matsumoto<sup>1</sup>, S. Watanabe<sup>1,2</sup>, H. Kanamori<sup>1</sup>, H. Uenishi<sup>1</sup>, Y. Katayose<sup>1</sup>, M. Ishimoto<sup>1</sup> (1.National Institute of Agrobiological Sciences, 2.Saga University)

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**203** QTL analysis of salt tolerance in *Vigna*.

☆Ogiso, E.<sup>1</sup>, Y. Yoshida<sup>2</sup>, T. Isemura<sup>1</sup>, A. Kaga<sup>1</sup>, K. Naito<sup>1,3</sup>, K. Okuno<sup>2</sup>, N. Tomooka<sup>1</sup> (1.National Institute of Agrobiological Sciences, Biodiversity Research Unit, 2.Tsukuba University, Life and Environmental Sciences, 3.JST PRESTO)

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**204** QTL analysis of turnip formation in *Brassica rapa* L.

☆Takahashi, Y.<sup>1</sup>, S. Yokoi<sup>1</sup>, K. Hatakeyama<sup>2</sup>, H. Hukuoka<sup>2</sup>, S. Matsumoto<sup>2</sup>, Y. Takahata<sup>1</sup> (1.Fac. Agr., Iwate Univ., 2.NIVTS, NARO)

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**205** Development of EST-SSR markers and construction of a linkage map in faba bean

○ISOBE, S.<sup>1</sup>, W. El-Rodeny<sup>2</sup>, M. Kimura<sup>1</sup>, H. Hirakawa<sup>1</sup> (1.Kazusa DNA Res. Inst., 2.ARC, Egypt)

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**206** Fine mapping seedpod dehiscence gene in Azuki bean

☆Naito, K., C. Muto, H. Sakai, E. Ogiso, A. Kaga, N. Tomooka (Nat. Inst. Agrobiological Sci.)

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**207** Genome Structure, Evolution and Diversity in Common bean (*Phaseolus vulgaris*) and its Relatives

☆Iwata, A.<sup>1</sup>, A. Tek<sup>2</sup>, A. Pedrosa-Harand<sup>3</sup>, V. Geffroy<sup>4</sup>, K. Nagaki<sup>2</sup>, S. Jackson<sup>1</sup> (1.Univ. Georgia, 2.Univ. Okayama, 3.Federal Univ. Pernambuco, 4.Univ.Paris-Sud)

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**208** Fine mapping of a resistance gene *rxp* to bacterial pustule in soybean

○Yamada, N.<sup>1</sup>, T. Sayama<sup>2</sup>, A. Kaga<sup>2</sup>, H. Sasama<sup>2</sup>, T. Yamada<sup>3</sup>, K. Hirata<sup>3</sup>, M. Ishimoto<sup>2</sup>, M. Hajika<sup>3</sup> (1.Nagano Vegetable and Ornamental Crops Exp. Stn., 2.NIAS, 3.NICS)

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**209** Identification of the parthenocarpic fruit 2 (*pat-2*) gene in tomato.

○Nunome, T.<sup>1</sup>, I. Honda<sup>2</sup>, A. Ohyama<sup>1</sup>, K. Miyatake<sup>1</sup>, H. Yamaguchi<sup>1</sup>, H. Fukuoka<sup>1</sup> (1.NARO Institute of Vegetable and Tea Science, 2.Maebashi Institute of Technology)

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**210** Genome-wide SNP identified by whole-genome resequencing in tomato

○Shirasawa, K.<sup>1</sup>, H. Fukuoka<sup>2</sup>, H. Matsunaga<sup>2</sup>, Y. Kobayashi<sup>3</sup>, I. Kobayashi<sup>3</sup>, H. Hirakawa<sup>1</sup>, S. Isobe<sup>1</sup>, S. Tabata<sup>1</sup> (1.Kazusa DNA Res. Inst., 2.NIVTS, 3.Mie U.)

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**211** Development of a SNP marker for gynoecey in bitter melon (*Momordica charantia*)

○Matsumura, H.<sup>1</sup>, N. Taniai<sup>2</sup>, N. Miyagi<sup>2</sup>, M. Fukushima<sup>1</sup>, K. Tarora<sup>2</sup>, A. Shudo<sup>2</sup>, N. Urasaki<sup>2</sup> (1.Gene Res. Ctr., Shinshu Univ., 2.Okinawa Pref. Agric. Res. Ctr.)

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**212** Single nucleotide polymorphism in genes accounting for ethylene biosynthesis and perception in melon

☆Shibata, C., K. Hiwasa-Tanase, T. Ariizumi, H. Ezura (Grad Sci.Life and Envi.Sci., Univ.Tsukuba)

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**213** Large-scale analysis of DNA polymorphism in *Morus* spp. using RAD-seq analysis

☆Nishihara, R.<sup>1</sup>, H. Matsumura<sup>2</sup> (1.Grad. Sch. Sci. Tech., Univ. Shinshu, 2.Gene Res. Ctr., Univ. Shinshu)

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**214** Phylogenetic analysis of local edible chrysanthemum varieties in Niigata and Yamagata prefecture using SSR markers

○Egashira, H.<sup>1</sup>, N. Ogasawara<sup>1</sup>, Y. Takeda<sup>2</sup>, Y. Saito<sup>3</sup>, T. Takashina<sup>3</sup>, S. Endo<sup>3</sup>, H. Kanamori<sup>4</sup>, A. Sato<sup>5</sup> (1.Fac. Agric. Yamagata U., 2.Yamagata Nishi-Okitama Agri.Tech.Pop.Div., 3.Hort. Exp.Stan. Yamagata Integrated Agric. Res. Cent., 4.NIAS, 5.Crop. Prod. Hort. Div. Niigata Pref. Gov.)

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**215** Mitochondrial genome analysis of *Triticum* and *Aegilops* species II. Mitochondrial genome of an alloplasmic line of common wheat with *Ae. speltooides* cytoplasm

☆Tsumijima, M.<sup>1</sup>, N. Mori<sup>2</sup>, H. Yamagishi<sup>1</sup>, T. Terachi<sup>1</sup> (1.Fac. Life Sci., Univ. Kyoto Sangyo, 2.Grad. Sch. Agric. Sci., Kobe Univ.)

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**216** Application of linkage disequilibrium and association analysis for the enhancement of abiotic stress tolerance in sorghum

☆Shehzad, T.<sup>1</sup>, S. Sakhi<sup>1,2</sup>, T. Fukuda<sup>1</sup>, K. Okuno<sup>1</sup> (1.Grad. Sch. Life & Envi. Sci., U.Tsukuba, 2.Dept. Plant Sci. Kohat Univ. Sci. & Tech. Kohat, Pakistan)

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**301** Simplified Biotron Breeding System (sBBS): an efficient rapid generation advancement system without embryo rescue and removal of tillers for rice breeding

○Tanaka, J.<sup>1</sup>, T. Hayashi<sup>2</sup> (1.NARO Institute of Crop Science, 2.NARO Research Center)

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**302** Predictions of segregation for heading date in rice F<sub>2</sub> populations based on a genomic selection model

○Iwata, H.<sup>1,2</sup>, T. Yoshioka<sup>3</sup>, A. Onogi<sup>1,2</sup>, K. Ebana<sup>4</sup>, T. Hayashi<sup>5</sup>, M. Yamasaki<sup>3</sup> (1.Grad. Sch. Agr. Life Sci., U. Tokyo, 2.JST, CREST, 3.Grad. Sch. Agr. Sci., Kobe U., 4.NIAS, 5.NARO/ARC)

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**303** Quantification of phenotypic influence of flowering time on other traits using structural equation models: application to a bi-parental population in rice

☆Onogi, A.<sup>1,2</sup>, K. Hori<sup>3</sup>, K. Ebana<sup>3</sup>, H. Iwata<sup>1,2</sup> (1.Grad. Sch. Agric. Life Sci., 2.JST CREST, 3.Natl. Inst. Agrobiological Sci.)

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**304** Whole genome prediction and QTL based prediction of flowering phenology in backcross inbred line of rice

☆Watanabe, M.<sup>1</sup>, T. Mochizuki<sup>2</sup>, T. Hayashi<sup>3</sup>, H. Nakagawa<sup>3</sup>, T. Hasegawa<sup>4</sup>, H. Iwata<sup>1</sup> (1.Dept. Agr. Life Sci, U. Tokyo, 2.Fac. Agr., Kyushu U., 3.NARO/ARC, 4.NIAES)

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**305** Development of rapid estimation method for allele number of *H1* and selection of multiplex lines in potato

☆Asano, K., S. Tamiya (NARO Hokkaido Agricultural Research Center)

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**306** Development of resources and technologies for promotion of research on a model grass, *Brachypodium distachyon*

○Himuro, Y.<sup>1</sup>, K. Ishiyama<sup>2</sup>, K. Mochida<sup>1,3</sup>, F. Takahashi<sup>1,3</sup>, T. Gondo<sup>4</sup>, R. Akashi<sup>4</sup>, M. Kobayashi<sup>1,2</sup>, K. Shinozaki<sup>1,3</sup> (1.BMEP, Riken, 2.BRC Plant Div., Riken, 3.PSC, Riken, 4.FSRC, Univ. Miyazaki)

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**307** Constructing an integrated database of DNA polymorphisms from NGS Archive DB and its analytical workflow

☆Mochizuki, T.<sup>1,2</sup>, H. Nagasaki<sup>1</sup>, E. Kaminuma<sup>1</sup>, H. Ohyanagi<sup>3,4</sup>, T. Shimizu<sup>5</sup>, A. Toyoda<sup>6</sup>, A. Fujiyama<sup>6</sup>, N. Kurata<sup>3</sup>, N. Nikoh<sup>2</sup>, Y. Nakamura<sup>1</sup> (1.Genome Informatics., Natl.Inst.Genet., 2.Dept. of Liberal Arts, The Open Univ. of Japan, 3.Plant Genetics., Natl. Inst. Genet., 4.Mitsubishi Space Software Co., Ltd., 5.Okitsu group, Natl. Inst. Fruit Tree Science, 6.Comparative Genomics., Natl. Inst. Genet.)

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**308** Global transcriptome profile of rice root in response to three major nutrient deficiencies

☆Takehisa, H., Y. Sato, B. Antonio, Y. Nagamura (National Institute of Agrobiological Sciences)

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**309** Microarray analysis of barley proanthocyanidin-free mutants

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

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**310** Modification of soybean storage protein mediated by artificial microRNA

☆Mori, Y.<sup>1</sup>, K. Yasue<sup>2</sup>, N. Maruyama<sup>3</sup>, J. Abe<sup>1</sup>, T. Yamada<sup>1</sup> (1.Grad.Sch.Agric.,Hokkaido U., 2.Fac.Agric.,Hokkaido U., 3.Grad.Sch.Agr.,Kyoto U.)

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**311** Studies on Physiological Function of Phosphoenolpyruvate Carboxykinase (PEPCK) in Tomato Plant

☆HUANG, Y., A. Sanuki, Y. Yin, K. Honda, N. Fukuda, H. Ezura, C. Matsukura (Grad. Sch. Life Env. Sci., Univ. Tsukuba)

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**312** Additive effect of QTLs controlling for cold tolerance at fertilization stage in rice

○Shinada, H.<sup>1</sup>, N. Iwata<sup>2</sup>, T. Sato<sup>1</sup>, K. Fujino<sup>3</sup> (1.Kamikawa Agriculture Experimental Station, 2.HOKUREN Federation of Agricultural Cooperatives, 3.NARO Hokkaido Agricultural Research Center)

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**313** Production of transgenic Arabidopsis plants showing the growth vigor

Makabe, S.<sup>1</sup>, Y. Honda<sup>2</sup>, ☆I. Nakamura<sup>1</sup> (1.Grad. Sch. Hort., Chiba U., 2.Fac. Hort., Chiba U.)

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**314** Novel techniques for identifying active retrotransposon family using high-throughput sequencing of PBS sites

☆Monden, Y.<sup>1</sup>, K. Yamaguchi<sup>2</sup>, M. Tahara<sup>1</sup> (1.Grad. Sch. Env., Univ. Okayama, 2.Grad. Sch. Nat., Univ. Okayama)

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**315** Expression analysis of *CmAP1* in chrysanthemum by direct introduction of florigen (Hd3a)

☆Asao, H.<sup>1</sup>, H. Tsuji<sup>2</sup>, H. Washida<sup>2</sup>, K. Shimamoto<sup>2</sup> (1.Nara Pref. Agri. Center, 2.Grad. Sch. Biol. Sci., NAIST)

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**316** Genome-wide exploitation for selected genes in the paths of varietal differentiations in peach

☆Akagi, T.<sup>1,2</sup>, I. Henry<sup>2</sup>, T. Gradziel<sup>2</sup>, L. Comai<sup>2</sup> (1.Grad. Sch. Agric. Kyoto Univ., 2.Univ. California Davis)

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**317** Searching for genes related to gall-induction by the orange leafhopper using wheat-barley chromosome addition lines

○Kawaura, K.<sup>1</sup>, K. Yoshida<sup>1</sup>, S. Kumashiro<sup>2</sup>, M. Tokuda<sup>3</sup>, K. Matsukura<sup>4</sup>, M. Matsumura<sup>4</sup>, Y. Ogihara<sup>1</sup> (1.KIBR, Yokohama City U., 2.United Grad. Sch. Agric. Sci., Kagoshima U., 3.Fac. Agric., Saga U., 4.KONARC/NARO)

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**318** Analysis of Defense-related redox protein OsCSP2 in rice.

○Morino, K., M. Kimizu, K. Saito (NARO Agricultural Research Center)

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**401** Complete sequence of mitochondrial genome of an alloplasmic line of common wheat with *Aegilops geniculata* cytoplasm

☆Gyawali, Y., T. Terachi (Fac. Life Sci., Kyoto Sangyo U.)

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**402** Analysis of Msh1 function for mitochondrial genome in Brassica napus

☆Terao, Y., M. Oonishi, S. Oziro, J. Imamura (Fac. Agr. Tamagawa U.)

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**403** Mapping of mitochondrial mRNA termini and recombinant breakpoint in Raphanus sativus

☆Torizuka, y., J. Imamura, N. Koizuka (Fac.Agr.Tamagawa U.)

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**404** Structural analysis of the *Rft* gene locus associated with fertility restoration in Ogura male-sterile radish

Yasumoto, K.<sup>1</sup>, H. Takagi<sup>2</sup>, R. Terauchi<sup>2</sup>, T. Terachi<sup>1</sup>, ○H. Yamagishi<sup>1</sup> (1.Fac. Life Sci., Kyoto Sangyo U., 2.Iwate Biotechnology Research Center)

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**405** Analysis of genes located in QTL regions for intergeneric hybrid formation ability in *Brassica rapa*

☆Tonosaki, K.<sup>1</sup>, H. Kitashiba<sup>1</sup>, Y. Kaneko<sup>2</sup>, T. Nishio<sup>1</sup> (1.Grad. Sch. Agric. Sci., Tohoku Univ., 2.Fac. Agric., Utsunomiya U.)

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**406** Search for the pollen S factor by transcriptome and proteome analyses in a wild self-incompatible species of barley, *Hordeum bulbosum*

☆Hashimoto, S.<sup>1</sup>, L. Yamada<sup>2</sup>, H. Sawada<sup>2</sup>, K. Kakeda<sup>1</sup> (1.Grad. Sch. Biores., Mie Univ., 2.Sugashima Marine Biol. Lab., Grad. Sch. Sci., Nagoya Univ.)

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**407** Diversity of Rf1 allele for ancestral varieties of Japanese sugar beet (*Beta vulgaris*) breeding population

○Taguchi, K.<sup>1</sup>, T. Kubo<sup>2</sup> (1.NARO Hokkaido Agr. Res. Cent., 2.Hokkaido Univ.)

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**408** Development of a New Giant Embryo Rice Variety "Tohoku-hai 202" with Low Amylose Content.

☆Saeki, K.<sup>1</sup>, T. Endo<sup>1</sup>, K. Nagano<sup>2</sup>, K. Sasaki<sup>3</sup>, B. Chiba<sup>2</sup>, K. Wagatsuma<sup>4</sup>, H. Hayasaka<sup>5</sup>, M. Sakai<sup>1</sup> (1.Miyagi Prefectural Furukawa Agricultural Experiment Station, 2.Miyagi Prefectural Hokubu Regional Promotion Office, 3.Miyagi Prefectural Plant Protection Office, 4.Miyagi Prefectural Agriculture Promotion Division, 5.Miyagi Prefectural Institute of Agriculture and Horticulture)

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**409** Breeding of new winter wheat variety "Tsurukichi" with good Chinese alkali noodle quality

☆Kobayashi, S.<sup>1</sup>, Y. Yoshimura<sup>1</sup>, H. Jinno<sup>1</sup>, M. Sato<sup>1</sup>, M. Kurushima<sup>1</sup>, N. Ashikaga<sup>1</sup>, T. Nishimura<sup>2</sup>, M. Ikenaga<sup>2</sup>, K. Nakamichi<sup>3</sup>, A. Yanagisawa<sup>4</sup>, K. Araki<sup>3</sup>, K. Tanifuji<sup>3</sup> (1.Kitami Agri. Exp. Stn.,HRO, 2.Central Agri. Exp. Stn.,HRO, 3.Tokachi Agri. Exp. Stn.,HRO, 4.Donan Agri. Exp. Stn.,HRO)

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**410** Genetic studies on Bambuseae species in Japan XXXIII. Studies on the aspect of growth and the characteristics of the F1 plants.

○Muramatsu, M. (\*)

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**411** Analysis of the incompatibility factor in sweet potato by cross-breeding

☆Hasegawa, K., E. Tanesaka, M. Yoshida (Grad. Sch. Agr., Univ. Kinki)

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**412** Exploitation of Job's tears genetic resources for edible Job's tears breeding in cold region.

○Honda, Y. (NARO Tohoku ARC)

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**413** Characteristics about lower gelatinized line selected from rice suited for sake brewing

○Okamoto, K.<sup>1</sup>, M. Tabata<sup>1</sup>, K. Kawamata<sup>1</sup>, N. Aoki<sup>2</sup>, T. Umemoto<sup>3</sup> (1.Ibaraki Agricultural Center PBI, 2.NARO, Institute of Crop Science, 3.NARO, Hokkaido Agricultural Research Center)

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**414** Evaluation of diversity in wild rice 1. Detection of retro-transposon insertion using WGS and application to phylogenetic study in Australian wild rice

☆Sotowa, M.<sup>1</sup>, K. Otsuka<sup>1</sup>, R. Terauchi<sup>2</sup>, R. Ishikawa<sup>1</sup> (1.Fac. Agri and Life Sci, Hirosaki U., 2.Iwate Biotech. Res. Ctr.)

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**415** Evaluation of diversity in wild rice 2. Detection of polymorphism using WGS in cytoplasmic genomes and application to phylogenetic study of Australian wild rice

Ootsuka, K.<sup>1</sup>, R. Terauchi<sup>2</sup>, ○R. Ishikawa<sup>1</sup> (1.Fac. of Agri. and Life Sci., Hirosaki Univ., 2.Iwate Biotech. Res. Ctr.)

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**416** Development and Utilization for large scale mutant lines in japonica rice cultivar "Hitomebore"

☆Utsushi, H., A. Abe, H. Takagi, Y. Ochiai, H. Yaegashi, F. Rym, R. Terauchi (Iwate Biotechnology Research Center)

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**417** Inheritance of the dimorphism of grain size in a spikelet and the seed dormancy in wild emmer wheat

Uenomachi, N., R. Kariyasu, A. Yamauchi, M. Watanabe, ○S. Ohta (Dep. Biosci., Fukui Pref. Univ.)

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**418** Phylogenetic relationships and chromosome evolution of ten *Torenia* species.

☆Kanno, K., S. Kikuchi, H. Sassa, T. Koba (Grad. Sch. Hor., Univ. Chiba)

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**419** Development of colored lipoxygenase deficit soybean lines

○Kono, Y., M. Takahashi, N. Oki, M. Takahashi (Kyushu Okinawa Agricultural Research Center)

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**501** Meristem maintenance in the vegetative phase in rice.

Ohmori, Y.<sup>1,3</sup>, W. Tanaka<sup>1</sup>, M. Kojima<sup>2</sup>, H. Sakakibara<sup>2</sup>, ☆H. Hirano<sup>1</sup> (1.Sch. Sci., Univ. Tokyo, 2.Plant Sci. centr., Riken, 3.Sch. Agric. Life Sci., Univ. Tokyo)

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**502** Analysis of *QHB/OsWOX5* gene involved in organization of root apical meristem in rice

☆Shibata, K.<sup>1</sup>, T. Sazuka<sup>2</sup>, J. Itoh<sup>3</sup>, Y. Inukai<sup>1</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Grad. Sch. Agric. Life Sci., U. Tokyo)

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**503** Genetic analysis of a malformed spikelet gene located on the chromosome 7 in rice.

Oshima, K., K. Fukuroi, Y. Nara, A. Nakada, Y. Kishima, ○I. Takamure (Grad. Sch. Agr., Hokkaido U.)

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**504** Exploration and usage of marker genes that show cell type specific expression during early rice embryogenesis.

☆Omae, M.<sup>1</sup>, H. Yagi<sup>1</sup>, K. Ishimoto<sup>1</sup>, Y. Noda<sup>1</sup>, Y. Sato<sup>2</sup>, K. Hibara<sup>3</sup>, J. Ito<sup>3</sup>, Y. Sato<sup>1</sup> (1.Grad.Sch.Bioagri.Sci.,Nagoya U., 2.NIAS, 3.Grad.Sch.Agric.Life Sci.,U.Tokyo)

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**505** The growth phase modification by heading time genes pleiotropically affects yield related traits in rice

☆Saito, H., Y. Imamura, K. Kikuzawa, K. Katsura, Y. Yoshitake, T. Yokoo, M. Kamal, I. Hirose, T. Tanisaka, Y. Okumoto (Grad. Sch. Agri., Univ. Kyoto)

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**506** Effects of ABA-inducible chitinase CHT11 on growth and development in rice.

Uramaru, K., ○T. Tsukiyama, K. Inouye, M. Teraishi, T. Nakazaki, T. Tanisaka, Y. Okumoto (Graduate School of Agriculture, Kyoto University)

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**507** The origin of barley awn length gene *Lks2* and comparative analysis of locations of awn genes among grasses

○Taketa, S., T. Yuo, E. Himi (Inst. Plant Science and Resources)

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**508** What is the function of a novel mitochondrial gene, *orf260*, which induces pistillody in alloplasmic wheat lines?

Kato, H., ○K. Murai (Dep. Biosci., Fukui Pref. Univ.)

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**509** Effect of the photoperiod sensitivity gene *Ppd-1* on expression pattern of the downstream gene *TaCO1* in wheat

Yamashita, M.<sup>1</sup>, ○H. Nishida<sup>2</sup>, K. Kato<sup>2</sup> (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U.)

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**510** Analysis on sequence variation in 5' upstream region and first intron of *Vrn-D1* in winter wheat



Takahashi, H.<sup>1</sup>, H. Nishida<sup>2</sup>, O.K. Kato<sup>2</sup> (1.Fac. Agr., Okayama U., 2.Grad. Sch. Environ. Life Sci., Okayama U.)

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**511** Effect of seed maturation regulators on seed dormancy in wheat

○Rikiishi, K., M. Maekawa (Inst. Plant Sci. Res., Okayama U.)

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**512** The early-flowering mutant of einkorn wheat lacks a wheat homolog of *PHYTOCLOCK 1* gene

☆Mizuno, N.<sup>1,2</sup>, M. Nitta<sup>1</sup>, K. Sato<sup>3</sup>, S. Nasuda<sup>1</sup> (1.Grad.Sch.Agric.Sci., Kyoto U., 2.JSPS Research Fellow, 3.IPSR, Okayama U.)

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**513** Research about breakage and cracks of brown rice kernels induced by heat pulse

☆Ohnishi, T., D. Sekine, T. Kinoshita (NAIST)

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**514** QTL analysis for photoperiod-insensitivity in a Chinese early-maturing cultivar.

☆Takeshima, R.<sup>1</sup>, T. Hayashi<sup>1</sup>, M. Xu<sup>1</sup>, B. Liu<sup>2</sup>, T. Yamada<sup>1</sup>, J. Abe<sup>1</sup> (1.Research Faculty of Agriculture, Hokkaido University, 2.North-east Institute of Geography and Agroecology, CASA, China)

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**515** Analysis of juvenile-adult phase change in soybean

☆Yoshikawa, T.<sup>1</sup>, S. Ozawa<sup>2</sup>, T. Sayama<sup>3</sup>, H. Sasama<sup>3</sup>, K. Hibara<sup>1</sup>, J. Ito<sup>1</sup>, M. Ishimoto<sup>3</sup>, S. Yokoi<sup>2</sup>, Y. Nagato<sup>1</sup> (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Fac. Agric., Iwate U., 3.NIAS)

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**516** Functional analysis of *MOR11* gene regulating juvenile-adult phase change in rice.

☆Kitomi, Y.<sup>1</sup>, N. Tanaka<sup>1</sup>, M. Kojima<sup>2</sup>, H. Sakakibara<sup>2</sup>, K. Hibara<sup>1</sup>, J. Ito<sup>1</sup>, Y. Nagato<sup>1</sup> (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.RIKEN, PSC)

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**517** Flower-bud-appearing in tea cuttings and expression levels of florigen gene, *CsFT1*

☆Yamada, M., K. Kato, S. Kitagawa, K. Murai (Dep. Biosci., Fukui Pref. Univ.)

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**518** Functional analysis of gibberellin 2-oxidase genes in Satsuma mandarin

○Kotoda, N.<sup>1</sup>, K. Yano<sup>1</sup>, S. Matsuo<sup>2</sup>, I. Honda<sup>3</sup>, H. Fujii<sup>1</sup>, T. Shimada<sup>1</sup>, T. Endo<sup>1</sup>, T. Shimizu<sup>1</sup> (1.NARO Inst. Fruit Tree Sci., 2.NARO Inst. Vegetable and Tea Sci., 3.Maebashi Inst. Tech.)

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**519** Functional analysis of an Arabidopsis nuclear-cytoplasmic shuttling protein, VIP1

☆Tsugama, D., T. Takano (ANESC., Univ. Tokyo)

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**601** Mapping a quantitative trait locus for resistance to bacterial grain rot in rice.

○Mizobuchi, R.<sup>1</sup>, H. Sato<sup>2</sup>, S. Fukuoka<sup>1</sup>, T. Tanabata<sup>3</sup>, S. Tsushima<sup>4</sup>, T. Imbe<sup>5</sup>, M. Yano<sup>1</sup> (1.NIAS, 2.NICS, 3.RIKEN, 4.NIAES, 5.NARO)

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**602** Resistance of mutant line, XM6 resistant to bacterial blight in rice. 1. Chromosomal location of resistant mutant gene, *xa20* .

○Taura, S.<sup>1</sup>, A. Tsuneyoshi<sup>2</sup>, K. Ichitani<sup>2</sup>, K. Kawabe<sup>1</sup>, M. Sato<sup>2</sup> (1.Inst. Gene Res., Kagoshima U., 2.Fac. Agri., Kagoshima U.)

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**603** Approach to cyanamide biosynthetic pathway in hairy vetch (*Vicia villosa* Roth) using cDNA subtraction

☆Yamaguchi, C.<sup>1</sup>, N. Wasano<sup>1</sup>, T. Kamo<sup>2</sup>, Y. Fujii<sup>1</sup> (1.Grad.Sch.Agric, Tokyo University of Agriculture and Technology, 2.National Institute for Agro-Environmental Sciences)

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**604** QTL analysis of resistance to common cutworm (*Spodoptera litura* Fabricius) in soybean by visual classification of feeding damage under field conditions.

☆Oki, N.<sup>1</sup>, K. Komatsu<sup>2</sup>, T. Sayama<sup>3</sup>, M. Ishimoto<sup>3</sup>, M. Takahashi<sup>1</sup>, M. Takahashi<sup>1</sup>, Y. Kono<sup>1</sup> (1.Kyushu Okinawa Agr. Res. Ctr., 2.Hokkaido Agr. Res. Ctr., 3.Natl. Inst. Agrobiol. Sci.)

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**605** Identification of a candidate gene for hard seededness in soybean.

☆Jang, S.<sup>1</sup>, M. Sato<sup>1</sup>, K. Sato<sup>1</sup>, R. Takahashi<sup>2</sup>, B. Liu<sup>3</sup>, T. Yamada<sup>1</sup>, J. Abe<sup>1</sup> (1.Research Faculty of Agriculture, Hokkaido Univ, 2.National Institute of Crop Science, 3.Northeast Institute of Geography and Agroecology, China)

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**606** QTL analysis for flooding tolerance at germination in soybean

Sato, M.<sup>1</sup>, K. Sato<sup>1</sup>, S. Jang<sup>1</sup>, K. Seki<sup>2</sup>, B. Liu<sup>3</sup>, T. Yamada<sup>1</sup>, ○J. Abe<sup>1</sup> (1.Res. Fac. Agr., Hokkaido Univ., 2.Nagano Vegetable and Ornamental Crops Experimental Station, 3.Northeast Institute of Geography and Agroecology, China)

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**607** Analysis of the field resistance gene NRKc2 with high homology to the true resistance gene Xa26 against bacterial blight disease.

○Aoki, H., K. Saito, O. Yatou (NARC)

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**608** QTL analysis using the Nipponbare/ Kasalath CSSL lines on the tolerance to the high-temperature stress during seed development

Matsubara, K.<sup>1</sup>, K. She<sup>1</sup>, H. Kusano<sup>1</sup>, ☆H. Shimada<sup>1,2</sup> (1.Dept. Biol. Sci. & Technol., Tokyo Univ. of Science, 2.Res. Center for RNA Sci., Tokyo Univ. of Science)

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**609** Decline in the extent of SMV mottling in yellow soybean cultivar Toyoharuka being tolerant for cold-induced seed coat discoloration.

○Senda, M.<sup>1</sup>, H. Okubo<sup>1</sup>, T. Matsumoto<sup>1</sup>, T. Sano<sup>1</sup>, S. Ohnishi<sup>2</sup> (1.Fac. Agric. Life Sci., Hirosaki U., 2.Central Agr. Exp. Sta., HRO)

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**610** Effect of tolerance of low temperature-induced seed coat discoloration to seed mottling by SMV in soybean

○Saruta, M.<sup>1</sup>, Y. Takada<sup>1</sup>, H. Funatsuki<sup>1</sup>, S. Ohnishi<sup>2</sup>, T. Miyoshi<sup>3</sup> (1.WARC/NARO, 2.Central Agr.Exp.Stn., 3.Tokachi Agr.Exp.Stn.)

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**611** Two NBS-LRR genes are required for resistance to green rice leafhopper governed by GRH2

☆Suesada, T., Y. Yamagata, A. Yoshimura, H. Yasui (Fac. Agr., Grad. Sch., Kyushu Univ.)

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**612** Salinity responses of germination, growth, photosynthesis, and ion accumulation in *Miscanthus sinensis*  
Andersson

○Sun, Q.<sup>1</sup>, T. Takano<sup>1</sup>, T. Yamada<sup>2</sup> (1.ANESC U. TOKYO, 2.Field Science Center for Northern Biosphere, Hokkaido University)

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**613** Comparison of aerenchyma formation in rice roots grown under nitrogen deficient or anaerobic conditions

☆Abiko, T., M. Obara (JIRCAS)

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**614** Identification of *CYP86* and *GPAT* involved in suberin lamella formation in rice root

☆Watanabe, K., S. Nishiuchi, M. Nakazono (Grad. Sch. Bioagric Sci., Nagoya U)

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**615** Involvement of auxin in the lysigenous aerenchyma formation in rice

☆Yamauchi, T., H. Inahashi, Y. Inukai, M. Nakazono (Grad.Sch.Bioagric.Sci., Nagoya U.)

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**616** Analysis of the expression of triterpene biosynthetic genes in secondary aerenchyma of soybean

☆Takahashi, H.<sup>1</sup>, A. Yanagawa<sup>1</sup>, Y. Shimizu<sup>2</sup>, E. Fukushima<sup>2</sup>, S. Hiraga<sup>3</sup>, S. Shimamura<sup>4</sup>, H. Seki<sup>2</sup>, T. Muranaka<sup>2</sup>, M. Nakazono<sup>1</sup> (1.Grad. Sch. Agric. Sci., Nagoya U., 2.Grad. Sch. Eng., Osaka U., 3.NARO Nat. Inst. Crop. Sci., 4.NARO Tohoku Agric. Res. Cent.)

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**617** The Arabidopsis Adaptor Protein AP-3 $\mu$  interacts with the G protein  $\beta$  subunit AGB1 and is involved in seed germination and early seedling development

☆Kansup, J., D. Tsugama, T. Takano (ANESC, U.Tokyo)

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**618** Identification of plant hormone that controls a barrier to radial oxygen loss in rice roots

○Shiono, K.<sup>1</sup>, M. Yoshikawa<sup>1</sup>, Y. Yamashita<sup>2</sup>, Y. Matsuura<sup>2</sup>, T. Hirayama<sup>2</sup>, T. Yoshioka<sup>1</sup>, I. Mori<sup>2</sup> (1.Dept. Biosci., Fukui Pref. Univ., 2.IPSR, Okayama Univ.)

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**619** QTL analysis of ABA responsiveness in seedlings of synthetic hexaploid wheat lines

☆Iehisa, M., S. Takumi (Grad. Sch. Agri. Sci., Kobe Univ.)

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**620** Functional analysis of salt response gene TaSAMT in wheat

☆Masui, Y., K. Kawaura, K. Sekine, T. Naruse, Y. Ogihara (KIBR, Yokohama City U.)

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**701** Research on flour milling evaluation in Japanese common wheats. 16. Effect of median particle size, mean particle size, grain microstructure on flour yield

○Nakamura, H. (National Institute of Crop Science, N.A.R.O.)

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**702** Cryopreservation and genetic transformation of embryogenic callus of switchgrass.

○Ogawa, Y.<sup>1</sup>, M. Honda<sup>1</sup>, Y. Kondo<sup>1</sup>, I. Hara-Nishimura<sup>2</sup> (1.Kazusa U., HRI-JP, 2.Grad. Sch. Sci., Kyoto Univ.)

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**703** The relation between dynamics of centromere specific histon H3 <CENH3> and chromosome elimination in subfamily cross of Triticeae or oat and pearl millet

☆Ishii, T.<sup>1</sup>, N. Sunamura<sup>2</sup>, T. Ueda<sup>2</sup>, A. Eltayeb<sup>3</sup>, H. Tsujimoto<sup>3</sup> (1.Uni.Grad.Sch.Agr.Sci., Univ.Tottori, 2.Faculty of Agri., Univ.Tottori, 3.Arid Land Research Center, Univ.Tottori)

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**704** Canceled

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**705** Gene targeting system via induced excision of donor molecule from plant genome.

☆Endo, M.<sup>1</sup>, S. Gelvin<sup>2</sup>, S. Toki<sup>1</sup> (1.Natl. Inst. Agrobiol. Sci., 2.Purdue Univ.)

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**706** A knockout of an allergen gene via gene targeting in rice

☆Saika, H.<sup>1</sup>, A. Yokoi<sup>1</sup>, K. Osakabe<sup>1,2</sup>, S. Toki<sup>1,3</sup> (1.Agrogenomics Res. Center, Natl. Inst. Agrobiol. Sci., 2.Inst. Env. Sci. Tech., Saitama Univ., 3.Kihara Inst. Biol. Res., Yokohama City Univ.)

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**707** Generation of transgenic rice lines with OsIRE1 missense alleles by gene targeting.

☆Wakasa, Y., S. Hayashi, K. Ozawa, F. Takaiwa (NIAS)

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**708** Activation of a retrotransposon in recombinant inbred populations derived from interspecific crosses of *Lotus*

☆Fukai, E.<sup>1</sup>, N. Sandal<sup>2</sup>, M. Yoshikawa<sup>1</sup>, H. Hirakawa<sup>3</sup>, Y. Umehara<sup>1</sup>, H. Kouchi<sup>1</sup>, S. Sato<sup>3</sup>, J. Stougaard<sup>2</sup>, H. Hirochika<sup>1</sup>, M. Hayashi<sup>1</sup> (1.NIAS, 2.Aarhus Univ., 3.Kazusa DNA Res. Inst.)

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**709** Verification of pyramiding effect of QTLs for heat-induced quality decline using near isogenic lines.

○Kobayashi, A.<sup>1</sup>, K. Sugimoto<sup>2</sup>, N. Iwasawa<sup>3</sup>, M. Kondo<sup>3</sup>, J. Sonoda<sup>4</sup>, T. Tsukaguchi<sup>5</sup>, K. Tomita<sup>1</sup> (1.Fukui Agr. Exp. Stn., 2.NIAS, 3.NICS, 4.Kagoshima Pref. Inst. Agr. Dev., 5.Ishikawa Pref. Univ.)

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**710** QTL analysis for occurrence of ring-type milky-white grains of brown rice caused by shading treatment during ripening period

Miyahara, K., M. Miyazaki, ○T. Wada, M. Tsubone (Fukuoka Agric. Res. Cent.)

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**711** α-amylase genes are involved in grain chalkiness through degradation of starch once accumulated in the developing grains under high temperature

☆Hakata, M.<sup>1</sup>, M. Kuroda<sup>1</sup>, T. Miyashita<sup>1</sup>, T. Yamaguchi<sup>1</sup>, M. Kojima<sup>2</sup>, H. Sakakibara<sup>2</sup>, T. Mitsui<sup>3</sup>, H. Yamakawa<sup>1</sup> (1.National Agricultural Research Center, 2.RIKEN Plant Science Center, 3.Niigata University)

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**712** Structure and Properties of Starch synthase SS4b Deficient Mutant with low amylose in riping temperature

☆Kodama, I.<sup>1</sup>, T. Kawamoto<sup>1</sup>, K. Kato<sup>1</sup>, K. Sato<sup>1</sup>, N. Kurofutsu<sup>2</sup>, N. Oitome<sup>2</sup>, M. Matsunami<sup>2</sup>, N. Fujita<sup>2</sup> (1.Akita Prefectural Agricultural Experiment Station, 2.Department of Biological Production, Akita Prefectural University)

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**713** Genotypic and environmental variations of wheat flour color.

○Sato, M.<sup>1</sup>, H. Jinno<sup>1</sup>, Y. Yoshimura<sup>1</sup>, T. Nishimura<sup>1,2</sup>, H. Maijima<sup>3</sup>, G. Ishikawa<sup>4</sup>, K. Nakamura<sup>4,5</sup>, H. Ito<sup>4</sup>, M. Saito<sup>4</sup>, Y. Uehara<sup>3</sup>, T. Nakamura<sup>4</sup> (1.HRO/Kitami Agri.Exp.Sta., 2.HRO/Central Agri.Exp.Sta., 3.Nagano

**714** Genotypic and environmental variations in endosperm brightness of wheat seeds

○Maejima, H.<sup>1</sup>, G. Ishikawa<sup>2</sup>, K. Nakamura<sup>2,4</sup>, H. Ito<sup>2</sup>, M. Saito<sup>2</sup>, T. Nakamura<sup>2</sup>, Y. Uehara<sup>1</sup>, M. Sato<sup>3</sup>, T. Nishimura<sup>3,5</sup>, H. Jinno<sup>3</sup>, Y. Yoshimura<sup>3</sup> (1.Nagano Pref.Agr.Exp.Sta., 2.NARO/TARC, 3.HRO/Kitami Agri.Exp.Sta., 4.NARO/KARC, 5.HRO/Central Agri.Exp.Sta.)

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**715** Genome-wide association study of wheat flour color and its related traits

○Ishikawa, G.<sup>1</sup>, K. Nakamura<sup>1,2</sup>, H. Ito<sup>1</sup>, M. Saito<sup>1</sup>, T. Nakamura<sup>1</sup>, M. Sato<sup>3</sup>, H. Jinno<sup>3</sup>, Y. Yoshimura<sup>3</sup>, T. Nishimura<sup>3,4</sup>, H. Maejima<sup>5</sup>, Y. Uehara<sup>5</sup> (1.NARO/TARC, 2.NARO/KARC, 3.HRO/Kitami Agri. Exp. Sta., 4.HRO/Central Agri. Exp. Sta., 5.Nagano Pref. Agri. Exp. Sta.)

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**716** Effect of puroindoline and glutenin alleles on milling and bread-making quality of wheat.

☆Ashikaga, N.<sup>1</sup>, T. Abe<sup>2</sup>, T. Suzuki<sup>2</sup>, M. Kurushima<sup>1</sup>, H. Jinno<sup>1</sup>, Y. Yoshimura<sup>1</sup> (1.Kitami Agr.Exp.Stn.,HRO, 2.Central Agr.Exp.Stn.,HRO)

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**717** A mutated maize line that haploids produce fertile pollen grains was induced by sodium azide mutagenesis

Sugihara, N., T. Higashigawa, D. Aramoto, ○A. Kato (Kyoto Prefectural University)

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**718** Improvement of dough strength in a wheat-barley translocation line with a barley 1HS chromosome segment

○Ikeda, T.<sup>1</sup>, K. Takata<sup>1</sup>, Y. Kurimoto<sup>2</sup>, Y. Terasawa<sup>1</sup>, M. Yanaka<sup>1</sup>, S. Taketa<sup>3</sup> (1.NARO/WARC, 2.Nippon Flour Mills Co., Ltd., 3.Inst. Plant Sci. Res. Okayama U.)

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**719** Characterization and Genetic Mapping of Micro-Tom mutants exhibiting elongated fruit shape

☆Chusreeaeom, K., E. Asamizu, T. Ariizumi, Y. Okabe, H. Ezura (Grad. Sch. Life & Environ. Sci., Univ. Tsukuba)

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**720** Characterization of a novel *MYB* gene involved in splatter development in Asiatic hybrid lily

○Yamagishi, M., S. Toda, K. Tasaki (Res. Fac. Agr., Hokkaido U.)

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## Poster presentations

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**P001** Evaluation of winter hardiness of gentian cultivars using *W14/15* gene markers

○Hikage, T.<sup>1,2</sup>, K. Kume<sup>2</sup>, Y. Saitoh<sup>2</sup>, K. Tsutsumi<sup>2</sup> (1.Hachimantai City Floricultural R & D Center, 2.Cryobiofrontier Res. Center, Iwate Univ.)

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**P002** Highly efficient phenotyping of rice heading date in the system "FieldBook".

☆Okada, S.<sup>1</sup>, A. Garcia<sup>2</sup>, T. Goda<sup>1</sup>, M. Maeda<sup>1</sup>, T. Kataoka<sup>3</sup>, M. Suehiro<sup>1</sup>, M. Yamasaki<sup>1</sup> (1.Food Resources Education and Research Ctr, Grad. Sch. Agric. Sci., Kobe U., 2.United States Department of Agriculture-Agricultural Research Service, 3.NARO Kyushu Okinawa Agric. Res. Ctr.)

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**P003** SNP detection and genome annotation on the basis of large-scale sequence data

☆Tsuchida, H.<sup>1</sup>, T. Kuchiki<sup>1</sup>, K. Harada<sup>1</sup>, Y. Sasaki<sup>1</sup>, T. Suzuki<sup>1</sup>, K. Yokoyama<sup>1</sup>, E. Asamizu<sup>2</sup>, K. Shirasawa<sup>3</sup>, H. Hirakawa<sup>3</sup>, K. Aoki<sup>4</sup>, K. Yano<sup>1</sup> (1.Bioinf., Sch. of Agri., Meiji Univ., 2.Fac. Life Environ. Sci., Univ. Tsukuba, 3.Kazusa DNA Res., 4.Grad. School of Life Environ. Sci., Osaka Pref. Univ.)

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**P004** Genome Information Database System for Innovation of Crop and Livestock Production. 3 Common infrastructure for the system development

☆Solovieva, E., Y. Teramoto, Y. Nagamura, T. Itoh, A. Miyao (Agrogenomics Res. Cent., NIAS)

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**P005** Blast converter: The program converting the class value into the severity of rice blast disease

○Hideki, K., K. Zenbayashi (NARO Tohoku Agricultural Research Center)

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**P006** Breeding of a new black soybean cultivar "Kurosayaka" with three lipoxygenase isozyme deletions

○Takahashi, M.<sup>1</sup>, M. Takahashi<sup>1</sup>, Y. Kono<sup>1</sup>, N. Oki<sup>1</sup>, K. Komatsu<sup>2</sup>, Y. Nakazawa<sup>1</sup>, R. Matsunaga<sup>3</sup> (1.KONARC/NARO, 2.NARCH/NARO, 3.JIRCAS)

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**P007** Breeding of a new sweetpotato cultivar "Aikomachi" with good confectionery quality.

○Takada, A.<sup>1</sup>, T. Kumagai<sup>1,2</sup>, T. Kuranouchi<sup>1</sup>, Y. Nakamura<sup>1</sup>, T. Fujita<sup>1</sup>, M. Nakatani<sup>1,3</sup>, S. Tamiya<sup>1,4</sup>, K. Katayama<sup>1</sup> (1.NARO Inst. of Crop Sci., 2.Headquarters, NARO, 3.MAFF, 4.NARO Hokkaido Agric. Res. Cent.)

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**P008** Genetic variation of tolerant for iron toxicity using agar nutrient solution in rice

Tomita, A., ○Y. Fukuta, M. Wissuwa (JIRCAS)

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**P009** Phenotypic expression of semidwarfing multiple alleles at the *sd1* locus in rice

○Irie, K., R. Matsushita, K. Koshio, H. Shiwachi, H. Toyohara (Tokyo Univ. of Agri.)

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**P010** Characterization of rice near-isogenic lines with the cleistogamy mutation, *spw1-cl*s.

☆Ohmori, S.<sup>1</sup>, T. Akiyama<sup>2</sup>, H. Tabuchi<sup>1</sup>, H. Yoshida<sup>2</sup> (1.Hokuriku Research Center, NARC, 2.NICS)

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**P011** Genotyping of *Aegilops tauschii* collected in North Caucasia

○Sasanuma, T.<sup>1</sup>, A. Kakizaki<sup>1</sup>, T. Abe<sup>1</sup>, T. Kawahara<sup>2</sup>, T. Smekalova<sup>3</sup>, K. Sato<sup>4</sup> (1.Fac. Agr., Yamagata U., 2.Grad. Sch. Agr., Kyoto U., 3.VIR, 4.IPSR, Okayama U.)

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**P012** Characterization of sorghum varieties for cadmium accumulation in shoots

☆Satoh-Nagasawa, N.<sup>1</sup>, J. Yoneda<sup>2</sup>, K. Okuno<sup>3</sup>, S. Uruguchi<sup>2</sup>, T. Fujiwara<sup>2</sup>, S. Lin<sup>2</sup>, T. Tokunaga<sup>4</sup>, Y. Ito<sup>4</sup>, M. Itou<sup>5</sup>, H. Hattori<sup>1</sup>, N. Nagasawa<sup>1</sup>, R. Itoh<sup>1</sup>, H. Akagi<sup>1</sup>, H. Takahashi<sup>1</sup>, K. Sakurai<sup>1</sup>, A. Watanabe<sup>1</sup>, N. Tsutsumi<sup>2</sup> (1.Fac. Biores. Sci., Akita Pref. U., 2.Grad. Sch. Agric. Life Sci., U. Tokyo, 3.Grad. Sch. Life & Env. Sci., U. Tsukuba, 4.Earth Note Co., Ltd., 5.Akita Agric. Exp. Stn.)

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**P013** Splicing variants of rice *HD1* ( *HEADING DATE 1* ) homolog in foxtail millet and their geographical distribution

○Fukunaga, K.<sup>1</sup>, N. Izuka<sup>1</sup>, K. Ichitani<sup>2</sup> (1.Fac. Life Environ. Sci., Pref. Univ. Hiroshima, 2.Fac.Agr., Kagoshima Univ.)

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**P014** Phylogenetic relationship among three genetically differentiated groups in Timopheevi wheat based on molecular markers

☆Kudo, E., S. Otani, T. Abe, T. Sasanuma (Fac. Agr., Yamagata U.)

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**P015** Relationship between fruit color and *Psy* gene in *Capsicum chinense*

☆Inaba, Y., Y. Aizawa, R. Akaike, T. Abe, T. Sasanuma (Fac. Agr., Yamagata U.)

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**P016** Morphological difference between native *Gentiana triflora* var. *japonica* and its variant and their geographical divergence

○Takahashi, Y.<sup>1</sup>, T. Hikage<sup>2</sup>, K. Wakameda<sup>1</sup>, Y. Saitoh<sup>1</sup>, K. Tsutsumi<sup>1</sup> (1.Cryobiofronteer Research Center, Iwate University, 2.Floricultural Research and Development Center)

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**P017** Analysis of genetic structure in populations of *Oryza rufipogon* with rice retroposon *p-SINE1* members.

Usami, J.<sup>1</sup>, ○R. Shishido<sup>1</sup>, S. Tsuchimoto<sup>2</sup>, M. Akimoto<sup>3</sup>, T. Ishii<sup>4</sup>, S. Minn<sup>5</sup>, S. Than<sup>5</sup>, H. Tin<sup>5</sup>, S. Men<sup>6</sup>, T. Nguyen<sup>7</sup> (1.Coll. Bioresource Sci., Nihon U., 2.Grad.Sch.Engineering, Osaka Univ., 3.Obihiro U. Agr. Vet. Med., 4.Grad.Sch.Agric.Sci., Kobe U., 5.Dept. Agr. Res., Min. Agr. & Irri., Myanmar, 6.Agr. Res. & Devel. Inst., Cambodia, 7.Cuu Long Delta Rice Res. Inst., Vietnam)

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**P018** Cytogenetic and breeding studies among three species of *Pogonia* and their artificial cross-hybrids (Orchidaceae)

○Takahashi, C.<sup>1</sup>, K. Kondo<sup>2</sup> (1.Onomichi-City Office, 2.Pl. Genet.Breed.Sci.Lab., Dept. Agri., Fac. Agri., Tokyo Univ. Agri.)

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**P019** Breeding of a new sweetpotato variety "Hoshikogane" suitable for hoshi-imo steamed and cured slices with high yield and high quality.

○Kuranouchi, T.<sup>1</sup>, A. Takada<sup>1</sup>, Y. Nakamura<sup>1</sup>, T. Fujita<sup>1</sup>, t. kumagai<sup>2</sup>, M. Nakatani<sup>3</sup>, K. Katayama<sup>1</sup> (1.NARO Inst. of Crop Sci., 2.NARO Headquarters, 3.MAFF)

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**P020** Analysis of easily gelatinize mutant line in rice

☆Ikegaya, T.<sup>1</sup>, S. Matsuba<sup>1</sup>, T. Ishii<sup>2</sup>, T. Noda<sup>1</sup>, Y. Nakaura<sup>3</sup>, N. Inouchi<sup>3</sup>, K. Ashida<sup>1</sup>, H. Shimizu<sup>1</sup>, T. Umemoto<sup>1</sup> (1.NARO Hokkaido. Agr. Res. Cent, 2.NARO Western. Agr. Res. Cent, 3.Life Sci and Biotech., Univ. Fukuyama)

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**P021** Development of the multi-disease resistant transgenic rice I. Procedure for field trial

○Yamazaki, M., S. Goto, H. Takatsuji (Natl. Inst. of Agrobiol. Sci.)

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**P022** Production of transplastomic plants with high concentrations of glutathione

☆Fukunaga, A.<sup>1</sup>, T. Tsujimura<sup>1</sup>, K. Uemura<sup>2</sup>, T. Terachi<sup>2</sup> (1.Grad.Sch.Fac.Eng.,Kyoto Sangyo U., 2.Fac.Life Sci.,Kyoto Sangyo U.)

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**P023** Analysis of temperature-sensitive virescent mutant in rice II

○Morita, R.<sup>1</sup>, M. Nakagawa<sup>2</sup>, S. Kogure<sup>1</sup>, Y. Hayashi<sup>1</sup>, H. Tokairin<sup>1</sup>, H. Takehisa<sup>3</sup>, T. Sato<sup>4,5</sup>, T. Abe<sup>1,5</sup> (1.RIKEN, Nishina Cent., 2.Grad. Sch. Bioagric. Sci., U. Nagoya, 3.NIAS, 4.Grad. Sch. Life. Sci., U. Tohoku,

**P024** Analysis on the *Arabidopsis* mutant, T-32, that exhibits prolonged branch elongation free from growth repression through apical dominance

○Watanabe, A., Y. Domeki, N. Satoh, K. Sakurai, H. Takahashi, H. Akagi (Akita Pref. Univ.)

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**P025** Development of disruptant lines of tandemly arrayed genes using heavy-ion beam in *Arabidopsis thaliana*

☆Kazama, Y.<sup>1</sup>, T. Hirano<sup>1,3</sup>, K. Ishii<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, Innovat. Cent., 2.RIKEN, Nishina Cent., 3.Grad. Sch. Adv. Sci. Technol., Tokyo Denki Univ.)

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**P026** Whole genome analysis of *Arabidopsis* mutants induced by heavy-ion irradiation

☆Hirano, T.<sup>1,2</sup>, Y. Kazama<sup>1</sup>, K. Ishii<sup>3</sup>, S. Ohbu<sup>3</sup>, Y. Shirakawa<sup>3</sup>, Y. Hayashi<sup>3</sup>, T. Abe<sup>1,3</sup> (1.RIKEN Innovat. Cent., 2.Grad. Sch. Adv. Sci. Technol., Tokyo Denki Univ., 3.RIKEN Nishina Cent.)

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**P027** Cyclopedic analysis of rice genes induced by heavy-ionbeam irradiation

☆Ishii, K.<sup>1</sup>, R. Morita<sup>1</sup>, S. Kogure<sup>1</sup>, Y. Hayashi<sup>1</sup>, T. Hirano<sup>2,3</sup>, T. Shibukawa<sup>4</sup>, Y. Nagamura<sup>4</sup>, T. Abe<sup>1,2</sup> (1.RIKEN Nishina Cent., 2.RIKEN Innovat. Cent., 3.Grad. Sch. Adv. Sci. Technol., Tokyo Denki U., 4.NIAS)

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**P028** Precision marker gene excision system using transposon in plants

☆Nishizawa-Yokoi, A.<sup>1</sup>, S. Toki<sup>1,2</sup> (1.NIAS, 2.Kihara Inst. Biol. Res, Yokohama City Univ.)

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**P029** Analysis of rice dwarf mutants induced by ion beam irradiation.

☆Kogure, S.<sup>1</sup>, R. Morita<sup>1</sup>, Y. Hayashi<sup>1</sup>, K. Ichinose<sup>1</sup>, T. Wakana<sup>1</sup>, H. Toukairin<sup>1</sup>, K. Ishii<sup>1</sup>, L. Ma<sup>1,2</sup>, S. Hatakeyama<sup>2</sup>, S. Tanaka<sup>2</sup>, T. Sato<sup>3,4</sup>, T. Abe<sup>1,3</sup> (1.RIKEN, Nishina Cent., 2.Grad. Sch. Sci. Tec., U. Saitama, 3.RIKEN, Innovat. Cent., 4.Grad. Sch. Life. Sci., U. Tohoku)

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**P030** Function of low nitrogen responsive *MYB101* in roots of legume.

Kushibiki, H.<sup>1</sup>, T. Anai<sup>2</sup>, ○S. Akada<sup>1</sup> (1.Fac. Agri. and Life Sci., Hirosaki Univ., 2.Fac. Agri., Saga Univ.)

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**P031** Variation of nut characteristics in the interspecific hybrids between Japanese chestnut and Seguin chestnut

Okabe, S.<sup>1</sup>, ○E. Inoue<sup>1</sup>, S. Tsunoda<sup>1</sup>, Y. Takatsu<sup>2</sup>, H. Higashio<sup>1</sup> (1.Coll. Agr., Ibaraki Univ., 2.Plant Biotech. Inst., Ibaraki Agr. Center)

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**P032** The functional analysis of apomixis-specific gene - observation of reproduction mode of *Arabidopsis* using embryo sac analysis method-

○Chen, L.<sup>1</sup>, Y. Nishimura<sup>1</sup>, T. Tetumura<sup>2</sup>, T. Sugita<sup>3</sup>, R. Nagata<sup>3</sup>, K. Yoshida<sup>4</sup>, H. Ichikawa<sup>5</sup> (1.Fac. Envir. Hort. Minami Kyushu University, 2.Fac. Agri. U. Miyazaki, 3.Miyazaki Pref. Agri. Experi. Sta., 4.Fac. Agri. U. Tokyo, 5.NIAR)

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**P033** The functional analysis of apomixis specific gene - fluorescent expression of ASG1::GFP in transgenic *Arabidopsis* -



○Nishimura, Y.<sup>1</sup>, T. Tetsumura<sup>2</sup>, T. Sugita<sup>3</sup>, R. Nagata<sup>3</sup>, K. Yoshida<sup>4</sup>, D. Kurihara<sup>5</sup>, T. Higashiyama<sup>5</sup>, L. Chen<sup>1</sup> (1.Fac. Envir. Hort. Minamikyushu U., 2.Fac. Agri. U. Miyazaki, 3.Miyazaki Pref. Agri. Experi. Sta., 4.Fac. Agri. U. Tokyo, 5.Fac. Sci. Nagaya U.)

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**P034** Production of a transplastomic lettuce containing a ferritin gene from soybean.

○Inoue, R.<sup>1</sup>, K. Uemura<sup>2</sup>, T. Terachi<sup>2</sup> (1.Grad.Fac.Eng.,Kyoto Sangyo U., 2.Fac.Life.Sci.,Kyoto Sangyo U.)

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**P035** Establishment of *Agrobacterium* -mediated transformation of *Begonia Semperflorens*

☆Shimomae, K., S. Hirutani, A. Yaguti, D. Chin, M. Mii (Grad. Sch. Hort., Chiba U.)

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**P036** Production of a transplastomic tobacco plant containing a glutamate dehydrogenase gene (gdh1) in the chloroplast genome.

☆Ohya, Y.<sup>1</sup>, T. Terachi<sup>2</sup> (1.Gra. Sch. Fac. Eng., Kyoto Sangyo U., 2.Fac. Life. Sci., Kyoto Sangyo U.)

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**P037** The functional analysis of apomixis specific gene - PCR analysis and determination of variants in ASG1::GFP transgenic Arabidopsis-

☆Naito, T.<sup>1</sup>, Y. Nishimura<sup>1</sup>, T. Tetsumura<sup>2</sup>, T. Sugita<sup>3</sup>, R. Nagata<sup>3</sup>, K. Yoshida<sup>4</sup>, D. Kurihara<sup>5</sup>, T. Higashiyama<sup>5</sup>, L. Chen<sup>1</sup> (1.Minamikyushu u., 2.Fac. Agri. U. Miyazaki, 3.Miyazaki Pref. Agri. Experi. Sta., 4.Fac. Agri. U. Tokyo, 5.Fac. Sci. Nagaya U.)

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**P038** The functional analysis of apomixis specific gene - Efficient plant regeneration from matured seed-derived calli of Guinea grass-

☆Umeki, K., Y. Nishimura, L. Chen (Fac. Envir. Hort. Mianmikyushu U.)

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**P039** Development of a new method for assessment of resistance to rice karnel cracking.

☆Hayashi, T., A. Kobayashi, K. Tomita (Fukui Agr. Exp. Sta.)

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**P040** Analysis of a root-to-shoot signaling under phosphate deficiency

☆Yoshida, A.<sup>1,2</sup>, Z. Zhang<sup>2</sup>, J. Kyojuka<sup>1</sup>, W. Lucas<sup>2</sup> (1.University of Tokyo, Grad Sch Agric Life Sci, 2.University of California, Davis)

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**P041** Transgenic tomato plants expressing two antifungal protein genes driven by a root-specific AtNRT2.1 promoter confer tolerance against root pathogen

☆kong, k., s. makabe, V. ntui, R. khan, i. nakamura (Graduate School of Horticulture, Chiba University)

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**P042** Crubroot resistance in F<sub>1</sub> between *Brassica napus* and synthetic *B. napus* having resistance gene from *B. rapa*.

○Ohara, T., T. Kakizaki, N. Fukino, K. Hatakeyama, S. Matsumoto, M. Ishida (NARO Inst. Veg. Tea Sci.)

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**P043** Relationships between resistance of SCN race1 and newly reported *Rhg4* gene.

○Suzuki, C., Y. Yamashita, R. Ogura (Central Agri.Exp.Stn., HRO)

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**P044** Evaluation of sweet potato resistance to West Indian Sweetpotato Weevil (*Euscepes postfasciatus*). I. Preference of adult to tubers and larva growth on tuber.

☆Okada, Y.<sup>1</sup>, K. Ichinose<sup>2</sup>, T. Sakai<sup>3</sup>, M. Yoshida<sup>1</sup>, M. Yoshinaga<sup>3</sup> (1.KONARC, 2.KONARC, 3.KONARC)

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**P045** Genetic diversity in response to salt stress among durum wheat germplasm

☆Turki, N.<sup>1</sup>, T. Shehzad<sup>1</sup>, H. Moncef<sup>2</sup>, K. Okuno<sup>1</sup> (1.Grad. Sch. Life & Envi. Sci., U.Tsukuba, 2.National Institute of Agronomy Tunisia (INAT))

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**P046** The characteristics of rice breeding lines introducing *qCTB8*, a QTL for cold tolerance at the booting stage.

○Kuroki, M.<sup>1</sup>, T. Ikegaya<sup>2</sup>, S. Matsuba<sup>2</sup>, N. Yokogami<sup>2</sup>, H. Shimizu<sup>2</sup>, Y. Sato<sup>2</sup>, K. Saito<sup>3</sup> (1.NARO Inst. Crop Sci., 2.NARO Hokkaido Agric. Res. Ctr., 3.NARO Agric. Res. Ctr.)

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**P047** Exploring QTLs for high temperature tolerance during ripening by using Introgression lines of *O. meridionalis*.

○Hirabayashi, H., H. Sato, Y. Takemoto-Kuno, Y. Takeuchi (NARO, Natl. Inst. Crop Sci.)

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**P048** Development of "Hoshinoyume" near isogenic lines by pyramiding of QTLs for cold tolerance at the booting stage in rice.

○Matsuba, S.<sup>1</sup>, M. Kuroki<sup>2</sup>, T. Ikegaya<sup>1</sup>, N. Yokogami<sup>1</sup>, H. Shimizu<sup>1</sup>, K. Saito<sup>3</sup> (1.NARO Hokkaido Agric. Res. Ctr., 2.NARO Inst. Crop Sci., 3.NARO Agric. Res. Ctr.)

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**P049** Development of whole crop silage rice line with high salinity tolerance

○Takeuchi, Y., N. Kobayashi, Y. Arai-Sanoh, Y. Takemoto-Kuno, H. Kato, M. Kondo, H. Nemoto (NARO Natl. Inst. Crop Sci.)

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**P050** Genetic analysis of cold tolerance at booting stage of rice cultivar Hitomebore

☆Yamamura, K.<sup>1</sup>, S. Sakazono<sup>1</sup>, S. Maeda<sup>1</sup>, T. Fujioka<sup>2</sup>, H. Masuko-Suzuki<sup>1</sup>, K. Nagano<sup>3</sup>, T. Endo<sup>4</sup>, K. Saeki<sup>4</sup>, R. Terauchi<sup>5</sup>, K. Yano<sup>6</sup>, G. Suzuki<sup>7</sup>, K. Suwabe<sup>2</sup>, M. Watanabe<sup>1</sup> (1.Grad. Sch. Life Sci., Univ. Tohoku, 2.Grad. Sch. Biores., Univ. Mie, 3.Miyagi Pref. Hokubu Regional Promotion Office, 4.Miyagi Pref. Furukawa Agri. Exp. Stn, 5.Iwate Biotech. Res. Center, 6.Fac. Agri., Univ. Meiji, 7.Div. Nat. Sci., Univ. Osaka Kyoiku)

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**P051** The effects of carbonate stress on higher plants.

☆Kobayashi, S., T. Takano (ANESC., Univ. Tokyo)

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**P052** Enhancement of wheat tolerance to aluminum by adding chromosomes from the wild wheat-relative *Leymus racemosus*

Mohammed, Y.<sup>1</sup>, A. Elayeb<sup>2</sup>, ○H. Tsujimoto<sup>3</sup> (1.United Graduate School of Agricultural Sciences, Tottori University, 2.Arid Land Research Center, Tottori University, 3.Arid Land Research Center, Tottori University)

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**P053** Diversity and Evolution of OSHMA3 gene and root-to-shoot cadmium translocation in A-genome species of the genus *Oryza*

☆Kumagai, S.<sup>1</sup>, Y. Horikawa<sup>2</sup>, M. Nakazima-Soma<sup>2</sup>, N. Satoh-Nagasawa<sup>2</sup>, K. Sakurai<sup>2</sup>, H. Takahashi<sup>2</sup>, A. Watanabe<sup>2</sup>, H. Akagi<sup>2</sup> (1.Grad. Sch. Biores. Sci. Akita Pref. Univ. , 2.Akita Pref. Univ. )

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**P054** A Ca metabolism in relation to the Cd resistance in *Athyrium yokoscense* -the ACA genes and the Ca and Cd responsive expression-

☆Ukai, Y.<sup>1,2</sup>, K. Kitazaki<sup>2</sup>, M. Kitazaki<sup>1,2</sup>, S. Hashida<sup>2</sup>, k. Shoji<sup>2</sup>, F. Goto<sup>2</sup>, H. Shimada<sup>1</sup>, T. Yoshihara<sup>1,2</sup> (1.Tokyo Univ. of Sci., Fac. of Ind. Sci. and Technol., 2.CRIEPI)

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**P055** Functional analysis of two putative Major Facilitator Superfamily proteins, AtSIM1 and AtSIM2 in Arabidopsis

☆Li, X., t. takano (Asian Natural Environmental Science Center (ANESC), the University of Tokyo)

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**P056** Regulation of seed germination responding to temperatures and light in radish

☆Nakamura, J., Y. Yoshino, M. Saito, T. Sada, T. Ito, A. Tateishi, S. Kubota, K. Nomura (Coll. Bioresource Sci., Nihon U.)

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**P057** Comparison of miRNA expression profile in anther between two rice cultivars having different cold tolerance at booting stage.

☆Maeda, S.<sup>1</sup>, S. Sakazono<sup>1</sup>, K. Yano<sup>2</sup>, K. Yamamura<sup>1</sup>, H. Suzuki-Masuko<sup>1</sup>, T. Fujioka<sup>3</sup>, K. Nagano<sup>4</sup>, T. Endo<sup>5</sup>, K. Saeki<sup>5</sup>, A. Makino<sup>6</sup>, R. Terauchi<sup>7</sup>, G. Suzuki<sup>8</sup>, K. Suwabe<sup>3</sup>, M. Watanabe<sup>1</sup> (1.Grad. Shc. Life Sci., Univ. Tohoku, 2.Fac. Agr, Univ. Meiji, 3.Grad. Sch. Biores, Univ. Mie, 4.Miyagi Pref. Hokubu Reg. Prom. Office, 5.Miyagi Pref. Furukawa Agr. Exp. Stn, 6.Fac. Agr, Univ. Tohoku, 7.Iwate Bio. Res. Center, 8.Div. Nat. Sci, Univ. Osaka Kyoiku)

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**P058** Genetic analysis of suppressors of brown spots in rice chromosomal segment substitution lines

○Fukuda, A., K. Sugimoto, T. Yamamoto, M. Yano (National Institute of Agrobiological Sciences)

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**P059** Variation of bolting in sugar beet based on expression level of vernalization-related genes (BvFL1 and BvFT1)

☆Kuroda, Y., K. Taguchi, K. Okazaki, H. Takahashi (HARC)

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**P060** QTL analysis of proanthocyanidin content in black seed coated soybean

○Teraishi, M., S. Phommalth, R. Ishii, T. Tsukiyama, Y. Okumoto (Graduate School of Agriculture, Kyoto University)

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**P061** Development of rice quality evaluation technique for gene isolation and identification on good eating quality of Koshihikari

○Suzuki, K.<sup>1</sup>, Y. Okazaki<sup>2</sup>, K. Hori<sup>3</sup>, Y. Takeuchi<sup>1</sup> (1.NARO NICS, 2.RIKEN, 3.NIAS)

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**P062** Metabolomic analysis of rice grain metabolites related to the good taste of Koshihikari

○Okazaki, Y.<sup>1</sup>, K. Suzuki<sup>2</sup>, K. Hori<sup>3</sup>, F. Matsuda<sup>1</sup>, M. Kusano<sup>1</sup>, R. Nakabayashi<sup>1</sup>, A. Oikawa<sup>1</sup>, K. Saito<sup>1,4</sup>, Y. Takeuchi<sup>2</sup> (1.RIKEN PSC, 2.NARO NICS, 3.NIAS, 4.Grad. Sch. Pharm. Sci., Chiba Univ.)

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**P063** Fine mapping of the QTL for low amylose content of Kuiku162 on the short arm of rice chromosome 2.

○Takemoto-Kuno, Y.<sup>1</sup>, Y. Takeuchi<sup>1</sup>, H. Hirabayashi<sup>1</sup>, I. Ando<sup>2</sup> (1.NARO NICS, 2.NARO TARC)

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**P064** Fine mapping of the QTL for eating quality of Koshihikari on the short arm of rice chromosome 3.

☆Hori, K.<sup>1</sup>, Y. Takeuchi<sup>2</sup>, Y. Takemoto-Kuno<sup>2</sup>, H. Sato<sup>2</sup>, H. Hirabayashi<sup>2</sup>, H. Ohta<sup>3</sup>, I. Ando<sup>4</sup>, H. Kato<sup>2</sup>, H. Nemoto<sup>2</sup>, T. Imbe<sup>5</sup>, M. Yano<sup>1</sup> (1.NIAS, 2.NARO NICS, 3.NARO TARC, 4.NARO KOARC, 5.NARO)

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**P065** Efficient assessment of cooked rice whiteness by polished rice ,using a scanner and new software

☆Kogi, Y.<sup>1</sup>, T. Tanabata<sup>2</sup>, K. Tomita<sup>1</sup>, A. Kobayashi<sup>1</sup> (1.Fukui Agr. Exp. Stn, 2.RIKEN PSC)

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**P066** Development of ultra-low-linolenic acid soybean line

○Anai, T., S. Watanabe, Y. Takagi (Faculty of Agriculture, Saga University)

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**P067** Selection for high beta-glucan content barley lines by rapid measurement method of calcofluor solution

○Ichinose, Y., S. Kaneko, K. Komae (NARO Institute of Crop Science (NICS))

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**P068** Structure and expression of caffeine synthase genes from caffeine-less tea plants.

Yamada, T.<sup>1</sup>, M. Kanai<sup>2</sup>, ○M. P. Yamamoto<sup>1</sup>, T. Wakasugi<sup>1</sup>, A. Ogino<sup>3</sup>, K. Yamada<sup>1</sup> (1.Grad. Sch. Sci. Eng., Univ. Toyama, 2.Fac. Sci., Univ. Toyama, 3.Natl. Inst. Veg. Tea Sci.)

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**P069** Mineral contents of brown rice in wild rice introgression lines.

☆Ohmori, Y., T. Fujiwara (Grad. Sch. Agri. Life Sci., Univ. Tokyo)

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**P070** QTL analysis of fruit morphological traits in cucumber

○Yoshioka, Y.<sup>1</sup>, N. Fukino<sup>1</sup>, Y. Sakata<sup>2</sup>, M. Sugiyama<sup>1</sup>, K. Shimomura<sup>1</sup> (1.NIVTS, 2.NARO-KARC)

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**P071** Influence of  $\alpha$ -amylase overexpression on grain appearance and starch granule morphology in rice

☆Miyashita, T.<sup>1</sup>, M. Hakata<sup>1</sup>, M. Kuroda<sup>1</sup>, T. Yamaguchi<sup>1</sup>, T. Mitsui<sup>2</sup>, H. Yamakawa<sup>1</sup> (1.Agricultural Research Center, NARO, 2.Niigata University)

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**P072** The effect of pyramiding lines of QTLs affecting the increase of grain number in an extra numerous grain rice cultivar, NP-6 for sink and source organs.

☆Ikeda, M.<sup>1</sup>, Y. Morinaka<sup>1</sup>, T. Hobo<sup>1</sup>, K. Doi<sup>2</sup>, M. Ashikari<sup>1</sup>, M. Matsuoka<sup>1</sup>, H. Kitano<sup>1</sup> (1.Biosci. Biotech. Ctr., Nagoya U., 2.Grad. Sch. Bioagr. Sci., Nagoya U.)

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**P073** Identification of candidate genes of QTL affecting panicle length in rice

☆Hobo, T.<sup>1</sup>, K. Ando<sup>2</sup>, Y. Fujishiro<sup>2</sup>, M. Ikeda<sup>1</sup>, M. Ashikari<sup>1</sup>, M. Matsuoka<sup>1</sup>, K. Doi<sup>2</sup>, H. Kitano<sup>1</sup> (1.Biosci. Biotech. Ctr.,Nagoya U., 2.Grad. Sch. Bioagr. Sci., Nagoya U.)

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**P074** Genetical analysis for morphological traits using NERICA's parent line WAB181-18.

☆Takeda, Y.<sup>1</sup>, T. Hobo<sup>2</sup>, D. Makihara<sup>3</sup>, K. Doi<sup>1</sup>, H. Kitano<sup>2</sup> (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.ICCAE, Nagoya U.)

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**P075** Varietal differences among spinach cultivators in the growth promotion with the supplemental lighting.

☆Kitazaki, K., K. Shoji, F. Goto, S. Hashida, T. Yoshihara (Central Research Institute of Electric Power Industry)

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**P076** Parologue in *Hd1* gene of *Miscanthus sinensis*.

○Nagano, H., N. Uchino, T. Yamada (Field Science Center for Northern Biosphere, Hokkaido University)

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**P077** QTL analysis for some traits in shoot using high biomass rice

☆Kunishima, T.<sup>1</sup>, T. Hobo<sup>2</sup>, H. Kitano<sup>2</sup> (1.Sch. Agric. Sci.,Nagoya U., 2.Biosci. Biotech. Ctr.,Nagoya U.)

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**P078** Analysis of genetic variation competitive ability and allelopathic ability in spelt and common wheat

○Hayashi, K.<sup>1</sup>, S. Yamaguchi<sup>1</sup>, T. Kawahara<sup>2</sup>, H. Miura<sup>1</sup>, K. Onishi<sup>1</sup> (1.Obihiro U. Agr & Vet. Med., 2.Kyoto U.)

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**P079** Analysis of starch properties with null mutation lines of wheat starch synthase IIa homoeologous genes

○Inokuma, T.<sup>1</sup>, M. Fujita<sup>2</sup>, T. Shimbata<sup>1</sup>, Y. Ai<sup>3</sup>, P. Vrinten<sup>4</sup>, A. Sunohara<sup>1</sup>, M. Saito<sup>5</sup>, T. Takiya<sup>1</sup>, J. Jane<sup>3</sup>, T. Nakamura<sup>5</sup> (1.Central Lab. Nippon Flour Mills Co., Ltd., 2.NARO/KARC, 3.Dept. Food Sci. Human Nutr., Iowa State Univ., 4.Bioriginal Food and Science Corp., 5.NARO/TARC)

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**P081** Establish a method measuring whiteness of cooked rice from milled rice.

☆Goto, H.<sup>1</sup>, N. Asanome<sup>2</sup>, K. Suzuki<sup>3</sup>, T. Sano<sup>1</sup>, H. Saito<sup>1</sup>, Y. Abe<sup>1</sup>, M. Chuba<sup>1</sup> (1.Yamagata Integrated Agr. Res. Cent., Rice Breeding and Crop Sci. Exp. Stn., 2.Yamagata Integrated Agr. Res. Cent., 3.NARO Institute of Crop Science)

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**P082** Varietal variation of petal pigment content in *Primula sieboldii* and its seasonal stability.

☆Hashimoto, N.<sup>1</sup>, T. Iwashina<sup>2</sup>, R. Ohsawa<sup>1</sup> (1.Grad. Sch. Life and Envi. Sci., U. Tsukuba, 2.Dept. Botany, Natl. Mus. Nature and Sci.)

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**P084** Comparison of histological morphologies of rice G-protein alpha subunit deficient mutant (*dl*) and BR-related mutants which shows small grain and dwarf phenotype.

☆Segami, S.<sup>1</sup>, Y. Izawa<sup>1</sup>, M. Kono<sup>1</sup>, H. Kitano<sup>2</sup>, K. Miura<sup>1</sup>, Y. Iwasaki<sup>1</sup> (1.Dept. Biosci., Fukui Pref. Univ., 2.Biosci. Biotech. Cent., Nagoya Univ.)

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**P085** Alteration of class D MADS-box gene expression patterns among homoeologous genes in polyploid wheat

☆Tanaka, M., H. Tanaka, K. Kato, S. Kitagawa, K. Murai (Department of Bioscience, Fukui Prefectural University)

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**P086** Compound leaf development in *Trifolium repens* L. increased leaflet mutants

☆Segawa, K., k. Tsutsumi, Y. Saitoh (Cryobiofrontier Research Center, Faculty of Agriculture., Univ. Iwate)

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**P087** Analysis of *leaf lateral symmetry1* mutant showing aberrant leaf development in rice.

☆Honda, E., C. Yew, Y. Nagato, J. Itoh (Grad. Sch. Agric. Life Sci., U. Tokyo)

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**P088** Relationship between *PLASTOCHRON* and *OsSPL* genes in plastochron regulation of rice.

☆Mimura, M., L. Luo, J. Kyojuka, Y. Nagato, J. Itoh (Grad. Sch. Agric. Life Sci., U. Tokyo)

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**P089** Flowering phenotype and expression patterns of flowering-time genes in the einkorn wheat mutant, *extra early-flowering* ( *exe*)

☆Nishiura, A.<sup>1</sup>, Y. Kazama<sup>3</sup>, T. Abe<sup>2</sup>, M. Nitta<sup>4</sup>, S. Nasuda<sup>4</sup>, K. Murai<sup>1</sup> (1.Dep. Biosci., Fukui Pref. Univ, 2.RIKEN, Nishina Cent, 3.RIKEN, Innovat. Cent, 4.Grad. Sch. Agr., Kyoto Univ)

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**P090** Phylogenetic evaluation of morphological variations of starch grains among Poaceae species

☆Matsushima, R., J. Yamashita, M. Maekawa, W. Sakamoto (Institute of Plant Science and Resources, Okayama University)

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**P091** Sequence analysis of the male specific region on spinach Y chromosome

Oda, Y.<sup>1</sup>, Y. Onodera<sup>1</sup>, A. Toyoda<sup>2</sup>, O.M. Ymamoto<sup>3</sup>, T. Mikami<sup>1</sup> (1.Res. Fac. Agri., Hokkaido U., 2.Natl. Inst. Genet., 3.Grad. Sch. Sci. Eng.)

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**P092** Effect of genotype in unfertilized ovule culture of gentian.

☆Doi, H.<sup>1</sup>, N. Hoshi<sup>2</sup>, S. Yokoi<sup>1</sup>, Y. Takahata<sup>1</sup> (1.Fac. Agric., Univ. Iwate, 2.Iwate Agric. Res. Center)

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**P093** The establishment of culture system and histological observation of shoot formation process in HIGOGIKU.

☆Sato, k., Y. Matsuda, T. Murata (School of Agriculture, Tokai University)

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**P094** Analysis of suspension-cultured cells accumulating starch

☆Matsuno, K., T. Fujimura (Grad. Sch. Life. Environ Sci., Univ. Tsukuba)

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**P095** QTL analysis of self-compatibility trait in *Brassica rapa* TSC4

☆Kobushiro, Y.<sup>1</sup>, S. Sakazono<sup>1</sup>, M. Osaka<sup>1</sup>, S. Takayama<sup>2</sup>, L. Yong Pyo<sup>3</sup>, G. Suzuki<sup>4</sup>, K. Suwabe<sup>5</sup>, M. Watanabe<sup>1</sup> (1.Grad. Sch. Life Sci., Tohoku U., 2.Grad. Sch. Biol. Sci., Nara Institute of Science and Technology, 3.Dep. Mol. Gen. Gen., Chungnam U., 4.Div. Nat. Sci., Osaka Kyoiku U., 5.Grad. Sch. Biores., Mie U.)

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**P096** Sequence analysis of BAC clones containing *Rf2*, a novel *restorer-of-fertility* locus for Owen cytoplasmic male sterility in sugar beet.

☆Honma, Y.<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.NARO Hokkaido Agr. Res. Center)

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**P097** Subcellular localization and interaction analysis of F-box proteins specifically expressed in the early phases of rice endosperm development

☆Fujiwara, N., K. Tsutsumi, Y. Saitoh (Cryobiofrontier Research Center, Faculty of Agriculture., Univ. Iwate)

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**P098** High-throughput SuperSAGE for flower bud of bitter melon, *Momordica charantia*.

○Urasaki, N.<sup>1</sup>, N. Miyagi<sup>1</sup>, N. Taniai<sup>1</sup>, K. Tarora<sup>1</sup>, A. Shudo<sup>1</sup>, S. Goeku<sup>1</sup>, M. Fukushima<sup>2</sup>, H. Matsumura<sup>2</sup>  
(1.Okinawa pref. agric. res. cent., 2.Gene res. cent., Shinshu univ.)

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**P099** Selection of molecular markers to recognize chromosome identities in important cultivars of cucumber and its close related species

○Hoshi, Y.<sup>1</sup>, H. Kamigomori<sup>2</sup>, M. Kido<sup>2</sup>, N. Tagashira<sup>3</sup>, W. Plader<sup>4</sup>, S. Malepszy<sup>4</sup>, A. Morikawa<sup>1</sup>, Y. Yamamoto<sup>5</sup>  
(1.Sch. Agr., Tokai Univ., 2.Grad. Sch. Agr., Tokai Univ., 3.Fac. Liberal Arts, Hiroshima Jogakuin Univ., 4.Fac. Hort. Landscape Architecture, Warsaw Univ. Life Sci., 5.Sch. Sci., Tokai Univ.)

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**P100** Molecular characterization of double-petaled cyclamen mutant and its application to DNA marker-assisted breeding

☆Aruga, D.<sup>1</sup>, M. Sugiyama<sup>1</sup>, Y. Tanaka<sup>1</sup>, H. Hasegawa<sup>1</sup>, N. Ohtsubo<sup>2</sup>, T. Terakawa<sup>1</sup> (1.Hokko Chemical Industry Co., Ltd., 2.NIFS)

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**P101** Divergent PCR products of Revolver transposon showing cluster-like chromosomal distribution

○Tomita, M., E. Tanaka (Fac. Agr., Tottori Univ.)

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**P102** Comparison of transcriptomes between newly synthesized triploid and its amphidiploidized wheat maintained through long-term self-pollinations

○Jung, Y., K. Kawaura, M. Kishii, S. Sato, Y. Ogihara (KIBR, Yokohama City U.)

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**P103** Structural difference between Papaya Y<sup>h</sup> and Y chromosome

☆Ueno, H.<sup>1</sup>, N. Urasaki<sup>2</sup>, K. Yoshida<sup>3</sup>, S. Natsume<sup>3</sup>, K. Tarora<sup>2</sup>, A. Shudo<sup>2</sup>, R. Terauchi<sup>3</sup>, H. Matsumura<sup>4</sup>  
(1.Dep. Biosci. Tex. Tech., Shinshu U., 2.Okinawa Pref. Agric. Res. Ctr., 3.Iwate Biotech. Res. Center, 4.Gene Res. Ctr., Shinshu U.)

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**P104** QTL Analysis of Spike Morphology, Threshability, and Brittleness in Common Wheat *Triticum aestivum* L.

○Katkout, M.<sup>1</sup>, M. Kishii<sup>1</sup>, K. Kawaura<sup>1</sup>, K. Mishina<sup>1</sup>, K. Umeda<sup>1</sup>, S. Takumi<sup>2</sup>, Y. Ogihara<sup>1</sup> (1.KIBR, Yokohama City U., 2.Grad. Sch. Agric. Sci., Kobe U.)

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**P105** Detection of QTLs for tiller number from low tillering variety 'Kahei'

☆Shimizu, Y., S. Segami, M. Sasaki, M. Nakamura, I. Sugita, M. Matsumura, Y. Iwasaki, k. Miura (Fukui Prefectural University)

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**P106** The refinement and the structural analysis of the QTL region for the paternal inheritance of mitochondrial plasmid on the rapeseed chromosome A05.

○Oshima, M.<sup>1</sup>, H. Handa<sup>2</sup> (1.Grad. sch. Life & Env. Sci., U. Tsukuba, 2.NIAS)

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**P107** Genetic mapping of the triple glume mutant gene in *Aegilops tauschii*

○Amagai, Y., T. Kuboyama, N. Watanabe (Col. Agri., Univ. Ibaraki)

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**P108** Construction of the genetic linkage map of a *GLUP7* gene which participates in the intercellular transport of glutelin in a rice seed

○Kitahara, M., K. Tashiro, T. Kumamaru (Grad. Sch. Agr., Univ. Kyushu)

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**P109** Sequencing BAC clones covering the eggplant *Cop8.1* locus and identifying candidate genes for parthenocarpy.

○Miyatake, K., T. Saito, S. Negoro, H. Yamaguchi, T. Nunome, A. Ohya, H. Fukuoka (NARO Institute of Vegetable and Tea Science)

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**P110** Study of clubroot resistant locus *CRA* in *Brassica rapa*

○Maezawa, M.<sup>1</sup>, H. Ueno<sup>2</sup>, E. Matsumoto<sup>3</sup>, D. Aruga<sup>2</sup>, S. Kitagawa<sup>1</sup>, H. Matsumura<sup>4</sup>, N. Hayashida<sup>5</sup> (1.Dep. of App. Biol., Shinshu Univ., 2.Dep. of Biosci. Tex. Tech., Shinshu Univ., 3.Nagano Veg. and Orn. Crops Exp. Station, 4.Div. of Gene res., Shinshu Univ., 5.Div. of App. Biol., Shinshu Univ.)

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**P111** Construction of a genetic linkage map in Japanese moning glory using EST-SSRs and EST-SNPs

☆Ito, T.<sup>1</sup>, S. Okuno<sup>1</sup>, H. Katsuyama<sup>1</sup>, K. Moriyama<sup>1</sup>, E. Nitasaka<sup>2</sup>, A. Hoshino<sup>3</sup>, S. Iida<sup>4</sup>, H. Fukuoka<sup>5</sup>, S. Isobe<sup>6</sup>, S. Sato<sup>6</sup>, N. Watanabe<sup>1</sup>, T. Kuboyama<sup>1</sup> (1.Col. Agr., Ibaraki U., 2.Grad. Sch. Sci., Kyushu Univ., 3.Natl. Inst. Basic Biol., 4.Grad. Sch. Nutri. and Env. Sci. & Grad. Sch. Pharm. Sci., U. Shizuoka., 5.NIVTS, NARO, 6.Kazusa DNA Res. Inst.)

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**P112** Intra-cultivar identification in *Cymbidium* by 'DNA marking'

○Furukawa, K.<sup>1</sup>, T. Abe<sup>2</sup>, S. Tabata<sup>3</sup>, T. Matsuyama<sup>4</sup> (1.Mukoyama Orchids Co, Ltd., 2.Nishina Center, Riken, 3.Kazusa DNA Inst., 4.Advanced Science Inst., Riken)

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**P113** Development of SSR markers in Octoploid Strawberry (*Fragaria x ananassa* Duch.).

☆Matsumoto, Y.<sup>1</sup>, I. Terakado<sup>1,2</sup>, T. Yamamoto<sup>3</sup>, M. Miyagi<sup>1,4</sup>, R. Ishii<sup>1</sup> (1.Plant Biotec. Inst., Ibaraki Agr. Cent., 2.Ibaraki Agr. Academy, 3.NIFTS, NARO, 4.Dep. Agr. For. Fish., Ibaraki Pref. Gov.)

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**P114** Development of SSR markers based on next-generation genome sequencing data of two cultivars in radish

☆Ajiki, M., T. Kawanabe, A. Fukushima, H. Kitashiba, T. Nishio (Grad. Sch. Agri. Sci., Tohoku Univ.)

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**P115** The expression pattern of ADP-glucose pyrophosphorylase *AgpS1* gene in Tomato plant

☆Goto, Y.<sup>1</sup>, T. Koiwa<sup>1</sup>, Y. Yin<sup>1,2</sup>, S. Nonaka<sup>1</sup>, H. Ezura<sup>1</sup>, C. Matsukura<sup>1</sup> (1.Grad. Sch. Life. Env. Sci., Univ. Tsukuba, 2.Japan Atomic Energy Agency)

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**P116** Functional analysis of rice ESP1/eRF1 for the termination codon.

☆Yamashiro, N., T. Ushijima, T. Kumamaru (Grad. Sch. Agr., Univ. kyushu)

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**P117** Expression analysis of strigolactone-related genes to change in response to nitrogen deficiency

Kikuchi, S., ○M. Umehara (Dept. Appl. Biosci., Fac. Life. Sci., Univ. Toyo)

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**P118** Comparative analysis of *WAP2* homoeogenes function using transformed rice II. Spike morphology alterations in transformants



☆Sakurai, N., K. Kawaura, I. Ishiguro, M. Isshiki, Y. Ogihara (KIBR, Yokohama City U.)

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**P119** Interspecific comparisons of gene expression networks in model plants

☆Kobayashi, M.<sup>1</sup>, T. Kuchiki<sup>1</sup>, K. Harada<sup>1</sup>, H. Tsuchida<sup>1</sup>, K. Kikue<sup>1</sup>, K. Igarashi<sup>1</sup>, T. Suzuki<sup>1</sup>, Y. Sasaki<sup>1</sup>, T. Takano<sup>1</sup>, K. Yokoyama<sup>1</sup>, Y. Yoshida<sup>1</sup>, H. Chiba<sup>2</sup>, Y. Tada<sup>2</sup>, A. Shimizu<sup>3</sup>, K. Aya<sup>4</sup>, M. Matsuoka<sup>4</sup>, M. Watanabe<sup>5</sup>, K. Suwabe<sup>6</sup>, K. Yano<sup>1</sup> (1.Sch. Agri., Meiji Univ., 2.TOHOKU CHEMICAL Co., Ltd., 3.Sch. of Environmental Sci., Univ. of Shiga pref., 4.Bioscience and Biotechnology Center, Nagoya Univ., 5.G. Sch. of Life Sci., Tohoku Univ., 6.G. Sch./Fac. of Bioresources, Mie Univ.)

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**P120** Epimutant generation of tomato *SVirp1* and its characteristics

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

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