

# Title of Papers Presented at the 143rd Meeting of The JAPANESE SOCIETY OF BREEDING

## Oral Presentations

**101** The extreme deep-rooted allele of *qSOR1* in rice contributes to deep-rooting in dicotyledonous plants

☆Kuroda, R., Y. Kitomi, K. Sugimoto, Y. Uga (Inst. Crop. Sci., NARO)

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**102** Genetic analysis of short grain rice mutants, *srs2* and *srs6*.

☆Ogawa, G.<sup>1</sup>, G. Chaya<sup>1,2</sup>, S. Segami<sup>3</sup>, Y. Iwasaki<sup>1</sup>, K. Miura<sup>1</sup> (1.Dep. Biosci., Fukui Pref. Univ., 2.Fukui Agri. Exp. Stn., 3.Res. Inst. Env. Agr. Fish., Osaka Pref.)

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**103** Analysis of the dominant large-grained rice mutant Lgg

○Tsugane, K.<sup>1</sup>, M. Maekawa<sup>2</sup> (1.IBBP Center, Nat. Inst. Bas. Bio., 2.Inst. Plant Sci. Res., Okayama University)

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**104** Effect of fractured starch granules mutation (*fra*) on grain quality of non-waxy and waxy barley

☆Aoki, H.<sup>1</sup>, N. Yuki<sup>1</sup>, M. Seki<sup>2</sup>, T. Nagamine<sup>1</sup> (1.NARO/Central Japan Agricultural Research Center, 2.NARO/Strategic Planning Headquarters)

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**105** Regulatory mechanism of secondary aerenchyma formation via peptide hormone signaling in soybean

☆Hasegawa, F.<sup>1</sup>, Y. Baba<sup>1</sup>, M. Takahashi<sup>2</sup>, Y. Sato<sup>2</sup>, M. Nakazono<sup>1</sup>, H. Takahashi<sup>1</sup> (1.Grad. Sch. Bioagric. Sci., Univ.Nagoya, 2.Nat. Ins. Genetics.)

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**106** Identification and use of genes related to the synthesis of furan fatty acid in soybean oil

Omagari, A.<sup>1</sup>, R. Yamada<sup>1</sup>, A. Egashira<sup>1</sup>, N. Umiguchi<sup>1</sup>, H. Takahama<sup>1</sup>, H. Motomaru<sup>1</sup>, A. Matsumoto<sup>1</sup>, N. Suruga<sup>1</sup>, Y. Kimura<sup>1</sup>, N. Makita<sup>2</sup>, H. Okamoto<sup>2</sup>, R. Okabe<sup>2</sup>, T. Sano<sup>2</sup>, T.

Sato<sup>2</sup>, M. Suzuki<sup>2</sup>, S. Saito<sup>2</sup>, T. Anai<sup>3</sup>, ☆S. Watanabe<sup>1</sup> (1.Fac. Agri., Univ. Saga, 2.J-Oil Mills, Inc., 3.Fac. Agri., Univ. Kyusyu)

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**107** Functional analysis of Fe-S biogenesis gene in the endosperm development of rice

☆Yaguchi, A.<sup>1,2</sup>, H. Maruoka<sup>1,2</sup>, A. Ono<sup>1</sup>, K. Tonosaki<sup>1,2</sup>, M. Endo<sup>1,2,3,4</sup>, T. Kinoshita<sup>1,2</sup> (1.KIBR, Yokohama City University, 2.Grad. Sch. Nanobiol., Yokohama City University, 3.NARO, Inst. Agro. Biol. Sci., 4.NARO, Res. Cent. Agri. Info. Tech.)

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**108** Comparing two methods of WGBS and EM-seq ~ DNA methylation analysis in rice endosperm ~

☆Uechi, M., K. Asai, K. Tonosaki, A. Ono, T. Kinoshita (KIBR,Yokohama City University)

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**109** The effect of varying gene dosage of *R-1* gene on grain color in wheat

○Himi, E.<sup>1</sup>, T. Matsuura<sup>2</sup>, H. Miura<sup>3</sup>, N. Yoshihara<sup>1</sup>, M. Maekawa<sup>2</sup> (1.Sch. Agri., Kibi International Univ., 2.IPSR, Okayama Univ., 3.Agro-Environmental Sci., Obihiro Univ. of Agri. and Vet. Med.)

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**110** Identification of a candidate gene encoding for the breaking factor of the gametocidal gene *Gc2* in wheat

Yoshioka, M.<sup>1</sup>, N. Mizuno<sup>1</sup>, B. Friebel<sup>2</sup>, K. Murata<sup>1</sup>, N. Sakai<sup>1</sup>, T. Uchino<sup>3</sup>, H. Yamada<sup>1</sup>, A. Hashimoto<sup>1</sup>, F. Abe<sup>4</sup>, K. Sato<sup>5</sup>, Y. Sato<sup>6</sup>, B. Gill<sup>2</sup>, ○S. Nasuda<sup>1</sup> (1.Grad. Sch. Agric., Kyoto Univ., 2.Dept. Plant Pathol., Kansas State Univ., 3.Fac. Agric., Kyoto Univ., 4.Inst. Crop Sci., NARO, 5.IPSR, Okayama Univ., 6.Natl. Inst. Genet.)

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**111** Fine mapping of the gametocidal gene *Gc2* in wheat by *de novo* genome assembly of the donor species *Aegilops sharonensis*

☆Murata, K.<sup>1</sup>, M. Yoshioka<sup>1</sup>, B. Friebel<sup>2</sup>, B. Gill<sup>2</sup>, S. Nasuda<sup>1</sup> (1.Grad. Sch. Agric., Kyoto Univ., 2.Dept. Plant Pathol., Kansas State Univ.)

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**112** Live-cell imaging revealed function of the *Gc2* gametocidal system in wheat

○Kakui, H.<sup>1,2</sup>, K. Murata<sup>1</sup>, T. Uchino<sup>3</sup>, Y. Sato<sup>4</sup>, Y. Mizuta<sup>4</sup>, S. Nasuda<sup>1</sup> (1.Grad. Sch. Agric., Kyoto Univ., 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.Fac. Agric., Kyoto Univ., 4.ITbM, Nagoya Univ.)

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**113** CRISPR/Cas3-mediated gene knock-out in rice

○Saika, H.<sup>1</sup>, S. Yasumoto<sup>2</sup>, T. Muranaka<sup>2</sup>, K. Yoshimi<sup>3</sup>, T. Mashimo<sup>3</sup>, S. Toki<sup>1,4,5,6</sup>  
(1.Institute of Agrobiological Sciences, NARO, 2.Graduate School of Engineering, Osaka University, 3.Institute of Medical Science, University of Tokyo, 4.Graduate School of Nanobioscience, Yokohama City University, 5.KIBR, Yokohama City University, 6.Faculty of Agriculture, Ryukoku University)

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**114** Effect of targeted base substitution in miR172 binding site on *TaAP2* on anther extrusion in wheat.

○Ogawa, T.<sup>1</sup>, K. Negishi<sup>2</sup>, F. Abe<sup>3</sup>, S. Toki<sup>1,4,5</sup> (1.NIAS, 2.NIFTS, 3.NICS, 4.Fac. Agr., Ryukoku Univ., 5.Grad.Sch.Nonobio., Yokohama City Univ.)

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**115** Evaluation of seed dormancy of the wheat with *TaQsd1* triple mutations, which were generated by genome editing, in field cultivation.

☆Kishi-Kaboshi, M.<sup>1</sup>, F. Abe<sup>1</sup>, M. Chono<sup>1</sup>, H. Hisano<sup>2</sup>, K. Sato<sup>2</sup> (1.NICS, NARO, 2.IPSR, Okayama U.)

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**116** Highly efficient targeted mutagenesis by CRISPR/Cas9 method using proximal guide RNAs in barley.

○Hisano, H.<sup>1</sup>, M. Kishi-Kaboshi<sup>2</sup>, F. Abe<sup>2</sup>, M. Hamaoka<sup>1</sup>, H. Munemori<sup>1</sup>, T. Yaeno<sup>3</sup>, J. Kumlehn<sup>4</sup>, K. Sato<sup>1</sup> (1.IPSR, Okayama U., 2.NARO, NICS, 3.Dep. Agr, Ehime U., 4.Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany)

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**117** Genome-editing by iPB-RNP in soybean

○Kuwabara, C.<sup>1</sup>, R. Miki<sup>2</sup>, N. Maruyama<sup>3</sup>, H. Hamada<sup>2</sup>, Y. Nagira<sup>2</sup>, R. Imai<sup>4</sup>, N. Taoka<sup>2</sup>, T. Yamada<sup>1</sup> (1.Grad. Sch. Agric., Hokkaido Univ., 2.Agro-Bio Research Center, Kaneka corp., 3.Grad. Sch. Agric., Kyoto Univ., 4.Inst. Agrobiological Sci., NARO)

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**118** Application of iPB-RNP method to mutagenesis of duplicated *GmBAS* genes in soybean with a single guide RNA

☆Asa, H.<sup>1</sup>, C. Kuwabara<sup>1</sup>, I. Tanaka<sup>2</sup>, T. Yamamoto<sup>3</sup>, T. Yamada<sup>1</sup> (1.Grad. Sch. Agric., Hokkaido Univ., 2.Fac. Agric., Hokkaido Univ., 3.Kanematsu Corp.)

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**119** Production of hypoallergenic soybean by iPB-RNP method

☆Chatani, S.<sup>1</sup>, C. Kuwabara<sup>2</sup>, M. Hibara<sup>2</sup>, N. Maruyama<sup>3</sup>, T. Yamada<sup>2</sup>  
(1.Fac.Agric.,Hokkaido Univ., 2.Grad.Sch.Agric.,Hokkaido Univ., 3.Grad.Sch.Agric.,Kyoto

**120** Functional analysis of clover FCL1 involved in the formation of compound leaves

Nakata, Y., H. Waizumi, ○Y. Saitoh (Fac.agri., Univ.Iwate)

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**121** *Agrobacterium*-mediated targeted deletion of grape retrotransposon associated with fruit skin color via CRISPR/Cas9.

Nakajima, I.<sup>1</sup>, ○H. Kawahigahshi<sup>1</sup>, C. Nishitani<sup>1</sup>, A. Azuma<sup>1</sup>, T. Haji<sup>1</sup>, S. Toki<sup>2,3,4</sup>, M. Endo<sup>2,4,5</sup> (1.Institute of Fruit Tree and Tea Science, NARO, 2.Institute of Agrobiological Sciences, NARO, 3.Ryukoku University, 4.Yokohama City University, 5.Research Center for Agricultural Information Technology, NARO)

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**122** Gene-disruption of *Fv.LigIV* involved in non-homologous end joining of Enokitake mushroom *Flammulina velutipes*

☆Fujino, Y.<sup>1</sup>, K. Tsuji<sup>2</sup>, T. Tsukiyama<sup>1</sup>, E. Tanesaka<sup>1</sup> (1.Grad. Sch. Agr., Kindai Univ, 2.Grad. Sch. Agr., Kyoto Univ)

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**123** Effects of the insertion position of a rice transposable element *mPing* on alternative splicing

☆Yoshida, R., E. Tanesaka, T. Tsukiyama (Fac. Agr., Kindai Univ.)

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**124** Interactions between mRNAs dirived from a rice transposon *mPing* and SR proteins

☆Toma, H., E. Tanesaka, T. Tsukiyama (Fac. Agr., Kindai Univ.)

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**125** Analysis of high-frequency T-DNA cleavage during transformation process in Prinsettia (*Euphorbia pulcherrima* × *Euphorbia cornastrum*).

☆Ito, K.<sup>1</sup>, R. Kogishi<sup>1</sup>, S. Shindo<sup>1</sup>, R. Shimo<sup>1</sup>, Y. Shinbo<sup>1</sup>, M. Ohtsubo<sup>1</sup>, K. Matsui<sup>2</sup>, K. Suzuki<sup>2</sup>, K. Tomomatsu<sup>2</sup>, N. Ohtsubo<sup>1</sup> (1.Grad. Sch. Life Environ. Sci., Kyoto Pref. Univ., 2.Suntory Flowers, Ltd.)

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**126** Development of a highly efficient genome editing technique in melon via *in planta* particle bombardment (iPB) and creation of a long shelf-life plants

Sasaki, K.<sup>1</sup>, N. Mimida<sup>2</sup>, S. Nonaka<sup>3</sup>, H. Ezura<sup>3</sup>, ○R. Imai<sup>1,3</sup> (1.NIAS, NARO, 2.Sanatech Seed Co., 3.Fa. Life Environ. Sci.)

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**127** Phytoene desaturase gene knockout as a model genome editing technique and culture conditions in tea plant (*Camellia sinensis*)

☆Aoshima, C.<sup>1</sup>, H. Mochiduki<sup>2</sup>, K. Furukawa<sup>3</sup> (1.NIT, Numazu College, advanced course, 2.Graduate School of Agricultural and Life Sciences, The University of Tokyo, 3.NIT, Numazu College, Department of Chemistry and Biochemistry)

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**128** Development of non-destructive, high-throughput metabolite measurement technology for Micro-Tom mutant populations

☆Suzuki, S.<sup>1</sup>, N. Suzuki<sup>1</sup>, K. Sugimoto<sup>1</sup>, A. Imakura<sup>1</sup>, K. Yano<sup>2</sup>, M. Asari<sup>2</sup>, Y. Date<sup>3</sup>, R. Yano<sup>3</sup>, H. Ezura<sup>1</sup>, T. Ariizumi<sup>1</sup> (1.Univ.Tsukuba, 2.Univ.Meiji, 3.NARO)

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**129** Improvement of a plant genome information portal site, Plant GARDEN (2022, Q4 ver)

☆Ichihara, H.<sup>1</sup>, H. Hirakawa<sup>1</sup>, M. Yamada<sup>1</sup>, M. Kohara<sup>1</sup>, S. Yamashita<sup>1</sup>, S. Shirasawa<sup>1</sup>, T. Yosuke<sup>1</sup>, T. Shimizu<sup>1</sup>, Y. Nakamura<sup>1,2</sup>, T. Tanabata<sup>1</sup>, S. Tabata<sup>1</sup>, S. Isobe<sup>1</sup> (1.Kazusa DNA Research Institute, 2.National Institute of Genetics)

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**130** Development and release of an online screening system for rice mutants

○Kubo, T.<sup>1</sup>, Y. Yamagata<sup>1</sup>, H. Matsusaka<sup>1</sup>, Y. Sato<sup>2</sup>, T. Kumamaru<sup>1</sup> (1.Fac. Agr. Kyushu Univ., 2.National Institute of Genetics)

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**131** A transcriptome analysis for understanding mechanisms underlying mugifumi signaling

Kambara, K., T. Takano, ○D. Tsugama (Grad. Sch. Agric. Life Sci., Univ. Tokyo)

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**132** Identification of QTLs for internode elongation in African wild rice *Oryza longistaminata*

☆HA Thi, Q.<sup>1</sup>, Y. Yamagata<sup>2</sup>, H. Yasui<sup>2</sup>, A. Yoshimura<sup>2</sup>, K. Nagai<sup>3</sup>, M. Ashikari<sup>3</sup> (1.Graduate School of Bioagricultural Sciences, Nagoya University, 2.Faculty of Agriculture, Kyushu University, 3.Bioscience and Biotechnology Center, Nagoya University)

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**201** Investigation of genotyping method for QTL analysis of rice using iSeq 100 sequencer

☆Chigira, K.<sup>1</sup>, C. Nomura<sup>2</sup>, A. Abe<sup>2</sup>, T. Ookawa<sup>1</sup> (1.Graduate School of Agriculture, Tokyo University of Agriculture and Technology, 2.Iwate Biotechnology Research Center)

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**202** Field trial test of *Gn1a*-knockout rice line with enlarged sink capacity by genome-editing

○Komatsu, A.<sup>1</sup>, M. Otake<sup>1</sup>, M. Nagata<sup>1</sup>, M. Kondo<sup>2</sup> (1.Institute of Agrobiological Sciences, NARO, 2.Graduate School of Bioagricultural Sciences, Nagoya University)

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**203** Effect of pyramiding root QTLs on root morphological traits in hydroponic and root distribution in field condition

☆Iba, M.<sup>1</sup>, A. Henry<sup>3</sup>, Y. Kitomi<sup>2</sup>, M. Quintana<sup>3</sup>, M. Natividad<sup>3</sup>, A. Centeno<sup>3</sup>, K. Irie<sup>1</sup>, Y. Uga<sup>2</sup> (1.Grad. Sch. Tokyo Univ. Agri., 2.NICS, 3.IRRI)

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**204** *qDTH3*, heading gene for rice stable production in northern-most region in Japan.

☆Ikegaya, T.<sup>1</sup>, K. Fujino<sup>1,2</sup> (1.HARC., NARO, 2.NARO)

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**205** Composition and expression of the rDNA units in wheat NORs

☆Hyuga, Y.<sup>1</sup>, H. Handa<sup>2</sup> (1.Fac. Life Envi. Sci., Kyoto Pref. Univ., 2.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ.)

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**206** Identification of causal mutation in gamma-irradiated short-culm bread wheat mutant

☆Komura, S.<sup>1</sup>, M. Chono<sup>2</sup>, H. Matsunaka<sup>3,4</sup>, K. Nakamura<sup>3</sup>, G. Ishikawa<sup>2</sup>, F. Kobayashi<sup>2</sup>, K. Yoshida<sup>1</sup> (1.Grad. Sch. Agr., Kyoto Univ., 2.NICS, 3.KARC, 4.HARC)

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**207** Verification of the QTL for root architecture in the recombinant inbred lines from a cross between Japanese and modern US soybean varieties

○Fukuda, A., A. Kaga (Inst. Crop. Sci., NARO)

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**208** Identification of the recombination region between A and C genome in *Brassica napus* cv. HANNA

☆Segawa, T., R. Kumazawa, M. Hara, N. Makita, M. Nishikawa, S. Saiga, H. Takagi (Ishikawa Prefectural University)

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**209** GRAS-Di analysis of genomic diversity of Japanese Moso bamboo

☆Nishiyama, N., T. Izawa (Grad.Sch.Agric.Life Sci., U.Tokyo)

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**210** Fine mapping of gene associated with fruit juiciness in Mizunasu (*Solanum melongena* L.)

☆Segami, S. (Res. Inst. Env. Agr. Fish., Osaka Pref.)

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**211** Selection of cross combinations based on predicted breeding value of later generation: application to mating scheme using multiple F<sub>3</sub> populations of red perilla

☆Kinoshita, S.<sup>1</sup>, K. Sakurai<sup>2</sup>, K. Hamazaki<sup>2</sup>, T. Chen<sup>2</sup>, T. Tsusaka<sup>3</sup>, M. Sakurai<sup>3</sup>, T. Kurosawa<sup>3</sup>, K. Shirasawa<sup>4</sup>, S. Isobe<sup>4</sup>, H. Iwata<sup>2</sup> (1.Fac. Agr., Univ. Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.TSUMURA & CO., 4.Kazusa DNA Res. Inst.)

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**212** Identification of candidate genes for *Rf* and presumption of functions for each haplotype of the region in which the candidate genes is present in CMS of citrus

○Goto, S.<sup>1</sup>, H. Fujii<sup>1</sup>, H. Hamada<sup>1</sup>, S. Ohta<sup>2</sup>, T. Endo<sup>1</sup>, T. Shimada<sup>1</sup> (1.Inst. Fruit & Tea Sci., NARO, 2.Facu. Agri. Prod. Mana., Shizuoka Pro. Univ. Agri.)

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**213** Whole genome sequencing of plants, bacteria and others by Oxford Nanopore.

○Naito, K., C. Muto, T. Seiko, F. Wang (Res Cntr Genet Resour, NARO)

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**214** Origin of intra-individual polymorphisms in Next Generation Sequencing of sugar beet mitochondrial genome

☆Taniguchi, E.<sup>1</sup>, K. Sato<sup>1</sup>, M. Okubo<sup>1</sup>, H. Matsuhira<sup>2</sup>, Y. Kuroda<sup>2</sup>, K. Kitazaki<sup>1</sup>, T. Kubo<sup>1</sup> (1.Research Faculty of Agriculture, Hokkaido University, 2.Hokkaido Agricultural Research Center, National Agriculture and Food Research Organization)

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**215** Identification fo the genes conrolling flowerirng time in *Brassica rapa* cv. 'CHOY SUM EX CHINA 3'

☆Nishikawa, M., T. Segawa, R. Kumazawa, M. Hara, N. Makita, S. Saiga, H. Takagi (Ishikawa Prefectural University)

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**216** De novo assemblies of wild potatoes toward understanding the dynamics of ploidy evolution

○Hosaka, A.<sup>1,2</sup>, R. Sanetomo<sup>3</sup>, K. Hosaka<sup>3</sup> (1.Nihon BioData Corporation, 2.KIBR., Univ. Yokohama-City, 3.Potato Germplasm Enhancement Laboratory, Obihiro University of Agriculture and Veterinary)

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**217** Haplod-resolved and chromosome-scale genome assembly in hexa-autoploid sweetpotato (*Ipomoea batatas* (L.) Lam)

○Isobe, S.<sup>1</sup>, U. Yoon<sup>2</sup>, H. Hirakawa<sup>1</sup>, K. Shirasawa<sup>1</sup>, Q. Cao<sup>3</sup>, M. Tanaka<sup>4</sup>, S. Kwak<sup>5</sup>, Q. Liu<sup>6</sup>, T. Genome Sequencing Consortium<sup>1,2,3,4,5,6</sup> (1.Kazusa DNA Res. Inst., 2.National Institute of Agricultural Sciences, RDA, 3.Sweetpotato Res. Inst., CAAS, 4.Kyusyu Okinawa Agric. Res. Cent., NARO, 5.Korea Res. Inst. Biosci. Biotech., 6.China Agric. Univ.)

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**218** Elucidation of the causal mutation in the *SSII* gene that confers low pasting temperature in starch of sweetpotato cultivar "Quick Sweet"

☆Kataoka, I.<sup>1</sup>, K. Shimo<sup>1</sup>, K. Tada<sup>2</sup>, M. Tanaka<sup>3</sup>, A. Kobayashi<sup>3</sup>, M. Izumitani<sup>2</sup>, H. Nishida<sup>2</sup>, K. Kato<sup>2</sup>, Y. Monden<sup>2</sup> (1.Fac. Agri., Okayama Univ., 2.Grad. Sch. Env. & Life Sci., Okayama Univ., 3.KARC/NARO)

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**219** Accurate detections of spontaneous mutations transferred from a parent to progenies in rice varieties

☆Balinponya, E.<sup>1</sup>, M. Dwiyanti<sup>1</sup>, K. Yamamori<sup>1,2</sup>, Y. Koide<sup>1</sup>, Y. Kishima<sup>1</sup> (1.Hokkaido University, Graduate School of Agriculture, 2.Kyoto University, Graduate School of Agriculture)

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**220** High-yielding genotypes developed by using short-stem tillering gene in the genetic background of rice variety Koshihikari

☆Fujita, K., M. Tomita, M. Yoshida (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

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**221** Pyramiding genes for large grain, short culm, and late flowering in the genetic background of rice variety Koshihikari.

☆Nakayama, K., M. Tomita, Y. Asano (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

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**222** Genome analysis of the old 'Somei-Yoshino' trees in Koishikawa Botanical Garden

○Shirasawa, K., S. Isobe (Kazusa DNA Res Inst)

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**223** Identification of genetic loci affecting spike morphology of *Aegilops bicornis*, a wild relative of wheat

☆Atsushi, O.<sup>1</sup>, M. Nishihara<sup>1</sup>, R. Terauchi<sup>1,2</sup> (1.Grad. Sch. Agri., Kyoto Univ., 2.Iwate Biotechnology Research Center)

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**224** Identification of an awn inhibitor locus in a wild wheat relative, *Aegilops caudata*

☆Tsutsumi, H.<sup>1</sup>, A. Ohta<sup>1</sup>, R. Terauchi<sup>1,2</sup> (1.Grad. Sch. Agri., Kyoto Univ., 2.Iwate Biotechnology Research Center)

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**225** Detection of the Quantitative Trait Loci associated with reduced grain number per spike in barley under warming conditions

○Saisho, D.<sup>1</sup>, Y. Okada<sup>2</sup> (1.IPSR, Okayama Univ., 2.Kyushu Okinawa Agricultural Research Center, NARO)

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**226** Isolation of QTLs associated with cleistogamy in sorghum

☆MAKINO, A., M. Ishimori, K. Yamazaki, T. Fujiwara, H. Iwata, N. Tsutsumi, H. Takanashi (Graduate School of Agricultural and Life Sciences, The University of Tokyo)

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**227** The sixth gene important for hybrid vigor in the sorghum F1 variety "Tentaka".

☆Kikuchi, T.<sup>1</sup>, S. Okada<sup>2</sup>, s. hashimoto<sup>2</sup>, S. Nakamura-Araki<sup>2</sup>, K. Ohmae-Shinohara<sup>2</sup>, K. Miura<sup>3</sup>, H. Kawaguchi<sup>4</sup>, C. Ogino<sup>5</sup>, S. Kasuga<sup>6</sup>, T. Sazuka<sup>2</sup> (1.Grad. Sch. Bioagri., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Fact. Biosci. Fukui Pref. Univ., 4.Engineering Biology Research Center, Kobe Univ., 5.Grad. Sch. Eng., Kobe Univ., 6.AFC, Fac. of Agri. Shinshu Univ.)

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**228** A possibility to explain a part of the hybrid vigor by an overdominance effect of the auxin transport-related gene *Dw3* of sorghum

☆Hashimoto, S.<sup>1</sup>, S. Okada<sup>1</sup>, S. Nakamura-Araki<sup>1</sup>, K. Shinohara-Ohmae<sup>1</sup>, K. Miura<sup>2</sup>, H. Kawaguchi<sup>3</sup>, C. Ogino<sup>4</sup>, S. Kasuga<sup>5</sup>, T. Sazuka<sup>1</sup> (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Fac. Biosci. Fukui Pref. Univ., 3.Engineering Biology Research Center, Kobe Univ., 4.Grad. Sch. Eng., Kobe Univ., 5.Fac. of Agri., Shinshu Univ.)

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**229** Construction of linkage maps and genetic analysis using Japanese rice crossed populations by GRAS-Di technology

○Yamasaki, M.<sup>1,2</sup>, R. Ono<sup>2</sup>, R. Fekih<sup>2</sup>, S. Okada<sup>2,3</sup>, M. Maeda<sup>2</sup>, K. Hori<sup>4</sup>, R. Miyagi<sup>5</sup>, T. Obata<sup>5</sup>, H. Enoki<sup>6</sup> (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Food Res. Edu. Res. Cent., Grad. Sch. Agri. Sci., Kobe Univ., 3.Biosci. Biotech. Ctr., Nagoya Univ., 4.Inst. Crop. Sci., NARO, 5.Eurofins Genomics K.K., 6.Toyota Motor Corp.)

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**230** QTL analysis for eating quality related traits in Dadachamame

☆Shioya, N.<sup>1</sup>, T. Fujimura<sup>2</sup>, N. Koshika<sup>1</sup>, E. Ogiso-Tanaka<sup>3</sup>, T. Hoshino<sup>1,2</sup> (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ., 3.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci.)

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**231** Two major QTLs for epicotyl length *qECL7* and *qECL10* identified in adzuki bean (*Vigna angularis*) using QTL-seq analysis.

☆Kachapila, M.<sup>1</sup>, Y. Horiuchi<sup>2</sup>, H. Nagasawa<sup>2</sup>, N. Michihata<sup>1</sup>, T. Yoshida<sup>1</sup>, Y. Kato<sup>1</sup>, P. Bethke<sup>3</sup>, K. Kato<sup>1</sup>, M. Mori<sup>1</sup> (1.Obihiro Univ. Agri. Vet. Med., 2.Tokachi Agric. Expt. Stn., HRO, 3.Univ. Wisconsin Madison)

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**232** Identification of QTL for seed coat color and polyphenolic content in adzuki bean

☆Morita, K.<sup>1</sup>, Y. Horiuchi<sup>2</sup>, S. Murayama<sup>1</sup>, K. Kato<sup>1</sup> (1.Obihiro Univ. Agr. & Vet. Med., 2.Tokachi Agr. Exp. Sta., HRO)

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**301** Characteristics of Lao rice genetic resources cultivated in Fukui.

○Kobayashi, A.<sup>1</sup>, H. Asai<sup>2</sup>, K. Maruyama<sup>2</sup>, F. Nakaoka<sup>1</sup>, S. Watanabe<sup>1</sup>, G. Chaya<sup>1</sup> (1.Fukui Agri.Exp. Stn., 2.JIRCAS)

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**302** Variations in grain traits among local rice varieties collected more than half-century ago in Indo-China countries

☆Lim, S.<sup>1</sup>, A. Onoda<sup>1</sup>, C. Orn<sup>1,2</sup>, H. Iwamoto<sup>1</sup>, R. Ishikawa<sup>1</sup>, H. Saito<sup>3</sup>, Y. Sato<sup>4</sup>, T. Ishii<sup>1</sup> (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodian Agr. Res. Dev. Inst., 3.Trop. Agr. Res. Front, JIRCAS, 4.Natl. Inst. Genet.)

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**303** A Report of B chromosome in *B. juncea* populations collected in southern Shan State in Myanmar.

☆Nohara, T.<sup>1</sup>, S. Yoshida<sup>2</sup>, K. Tanaka<sup>3</sup>, O. Aung<sup>4</sup>, H. Kikuno<sup>5</sup>, K. Irie<sup>5</sup>, K. Wakui<sup>2</sup> (1.Agr. Science, Grad Agri, Tokyo Univ of Agri, 2.Dept of Bio Res Dev, Grad Agri, Tokyo Univ of

Agri, 3.NODAI Genome Res Ctr, Tokyo Univ of Agri, 4.Dept of Agri Res, Min of Agri, Livest and Irrig, Myanmar, 5.Fac of Intl Agri and Food Stud, Tokyo Univ of Agri)

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**304** Evaluating the earliness of new shoots in the genetic resources of tea (*Camellia sinensis*) using UAV time-series data

☆Furuya, S.<sup>1,2</sup>, T. Suzuki<sup>1</sup>, K. Hasegawa<sup>1</sup>, C. Yonezawa<sup>2</sup> (1.Shizuoka Tea Res. Cent., 2.Grad. Agri., Univ. Tohoku)

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**305** Genome and transcriptome wide association studies for root traits in world rice core collection

☆Wei, S.<sup>1</sup>, R. Tanaka<sup>1</sup>, S. Yabe<sup>1</sup>, T. Kawakatsu<sup>2</sup>, N. Tanaka<sup>1</sup>, S. Matthew<sup>1</sup>, Y. Uga<sup>1</sup> (1.Inst. Crop Sci., NARO, 2.Inst. Agro Sci., NARO)

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**306** Genome-wide association analysis detected a gene region correlated with rice crown root number

☆Teramoto, S.<sup>1</sup>, M. Yamasaki<sup>2,3</sup>, Y. Uga<sup>1</sup> (1.NICS, 2.Grad. Sch. Agri. Sci., Kobe Univ., 3.Grad. Sch. Sci. Tech., Niigata Univ.)

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**307** Development of a novel GWAS method for the detection of causal genes with population specific allelic effects

☆Hamazaki, K.<sup>1</sup>, H. Iwata<sup>1</sup>, T. Mary-Huard<sup>2</sup> (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Département MMIP, AgroParisTech)

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**308** Phenotyping and GWAS with pearl millet elite lines

☆Kambara, K.<sup>1</sup>, D. Tsugama<sup>1</sup>, G. Shashi K<sup>2</sup>, T. Takano<sup>1</sup> (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.ICRISAT)

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**309** Genome wide association study of yield-related traits in common bean breeding programs

○Yamaguchi, N.<sup>1</sup>, K. Tanaka<sup>2</sup>, K. Nakagawa<sup>3</sup>, H. Sato<sup>3</sup>, Y. Nakazawa<sup>4</sup> (1.Central Agr. Exp. Sta., HRO, 2.Genome Research Center, Tokyo Univ. of Agri., 3.Tokachi Agr. Exp. Sta., HRO, 4.Faculty of Bioindustry, Tokyo Univ. of Agri.)

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**310** Genome-wide association study (GWAS) of agronomic traits using genomic information of Japanese sugar beet breeding lines.

○Kitazaki, K.<sup>1</sup>, K. Hiroki<sup>1</sup>, T. Narihiro<sup>2</sup>, H. Matsuhira<sup>2</sup>, T. Kubo<sup>1</sup>, Y. Kuroda<sup>2</sup> (1.Res. Fac. Agri., Hokkaido Univ., 2.HARC, NARO)

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**311** Identification and comparative analysis of QTLs related to sweetpotato yield using multiple reference genome sequences

☆Horita, N.<sup>1</sup>, Y. Okada<sup>2</sup>, M. Kurihara<sup>3</sup>, H. Nishida<sup>3</sup>, K. Kato<sup>3</sup>, Y. Monden<sup>3</sup> (1.Fac. Agri., Okayama Univ., 2.KARC/NARO, 3.Grad. Sch. Env. & Life Sci., Okayama Univ.)

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**312** Web system to visualize seed production information of major crops in Hokkaido

○Tanaka, Y., H. Satou, T. Yoshimura, A. Sawaguchi (Central Agri. Exp. Sta., HRO)

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**313** Targeted A-to-G base editing in chloroplast and mitochondrial genomes in *Arabidopsis thaliana*

☆ZHOU, C., I. Nakazato, Y. Tamura, R. Masuda, N. Tsutsumi, S. Arimura (Grad. Agri., Uni. Tokyo)

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**314** Targeted C-to-T base editing in the *Arabidopsis* plastid genome by a highly active type of ptptALECD

☆Nakazato, I.<sup>1</sup>, M. Okuno<sup>2</sup>, T. Itoh<sup>3</sup>, N. Tsutsumi<sup>1</sup>, S. Arimura<sup>1</sup> (1.Grad. Sch. of Agr. and Life Sci., Univ. of Tokyo, 2.Sch. of Med., Kurume Univ., 3.Sch. of Life Sci. and Tech., Tokyo Institute of Technology)

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**315** Genetic analysis on differentiation at *S21* for *F<sub>1</sub>* pollen sterility in AA genomic species of genus *Oryza*

Murakami, R.<sup>1</sup>, M. Sakata<sup>1,2</sup>, H. Yasui<sup>1</sup>, ○Y. Yamagata<sup>1</sup> (1.Fac. Agr., Kyushu Univ., 2.Fac. Agr. Mar. Sci., Kochi Univ.)

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**316** Breeding and properties of glutinous foxtail millet cultivar with short culm and high yield, 'Awa Iwatemochi 11'

☆Yoshitsu, Y.<sup>1</sup>, M. Takakusagi<sup>1,2</sup>, H. Kan<sup>1,2</sup>, T. Osato<sup>1</sup>, A. Abe<sup>3</sup>, M. Shimizu<sup>3</sup>, K. Ito<sup>3</sup>, R. Terauchi<sup>3,4</sup> (1.Iwate Agric. Res. Ctr. Kenpoku Agr. Inst, 2.Iwate Pref. Govt., 3.Iwate Biotechnol. Res. Ctr., 4.Grad. Sch. Agric., Kyoto Univ.)

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**317** Variety identification of Enokitake mushroom *Flammulina velutipes* using InDel markers and changes of heterozygosity under breeding process

☆Yamaguchi, S.<sup>1</sup>, H. Shimizu<sup>2</sup>, E. Tanesaka<sup>1</sup> (1.Grad. Sch. Agr., Kindai Univ.,  
2.Agricultural Technology Institute of Nagano Farmers Federation)

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**318** The current status of Wasabi (*E. japonicum*) genome project

○Tanaka, H.<sup>1</sup>, T. Hori<sup>1</sup>, S. Yamamoto<sup>2</sup>, A. Toyoda<sup>3</sup>, K. Yano<sup>4</sup>, K. Yamane<sup>2</sup>, T. Itoh<sup>1</sup>  
(1.Tokyo Inst. Tech. LST., 2.Gifu U. App. Bio. Sci., 3.Nat. Inst. of Gen. Comp. Genome.,  
4.Meiji U. Agri.)

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**319** Allyl isothiocyanate and 6-(methylsulfinyl) hexyl isothiocyanate contents vary among wild and cultivated wasabi (*Eutrema japonicum*)

○Yamane, K.<sup>1</sup>, T. Kato<sup>2</sup>, N. Haga<sup>1</sup>, K. Ishida<sup>2</sup>, S. Murayama<sup>3</sup>, K. Kobayashi<sup>1</sup>, I. Okunishi<sup>2</sup>  
(1.Fac. Appl. Biol. Sch., Univ. Gifu., 2.Kinjirushi Co., 3.Rebun Bot. Gard.)

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**320** Glucosinolate profiling wasabi

☆Tsunekawa, R.<sup>1</sup>, N. Haga<sup>1</sup>, M. Hiraumi<sup>1</sup>, M. Morita<sup>1</sup>, K. Kobayashi<sup>1</sup>, S. Takashima<sup>2</sup>, K. Yamane<sup>1</sup> (1.Fac. Appl. Biol. Sch., Univ. Gifu, 2.Ins. Glyco-core Res., Univ. Nagoya, Gifu, Tokai National High. Edu. Res. Sys.)

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**321** Molecular polymorphisms reveals genetic diversity among African melon germplasms with emphasis on Sudan melon

☆Imoh, O.<sup>1</sup>, G. Shigita<sup>2</sup>, T. Dung<sup>1</sup>, K. Tanaka<sup>3</sup>, P. Nhi<sup>4</sup>, Y. Monden<sup>1</sup>, H. Nishida<sup>1</sup>, K. Kato<sup>1</sup>  
(1.Grad. Sch. Environ. Life Sci., Okayama Uni., 2.TUM, 3.Fac. Agric. Life Sci., Hirosaki Uni., 4.Fac. Agric., Hue Uni.)

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**322** A new rice cultivar "Shiga 83" with good eating quality and good grain appearance

○Yamaguchi, K.<sup>1</sup>, T. Yoshida<sup>1</sup>, T. Nishimura<sup>1</sup>, T. Yokoi<sup>1</sup>, K. Hino<sup>1</sup>, J. Nakagawa<sup>1</sup>, S. Mori<sup>2</sup>, S. Shiigi<sup>2</sup>, H. Miyamura<sup>3</sup> (1.Shiga Pref. Agric. Tech. Prom. Cent., 2.Shiga Pref. Higashiomari Agric.Rural.Develop.Prom., 3.Shiga Pref. Northern Shiga Agric.Rural.Develop.Prom.)

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**323** Isogenic lines of rice variety Koshihikari integrated with biomass-increasing gene

☆Sugihara, H., M. Tomita, T. Kuboi (Res. Inst. Green Sci. & Technol., Shizuoka Univ.)

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**324** Genetic studies on Bambuseae species in Japan. XLIV. Japan is a hot spot of bambuseae speciation as studied on crosscompatibility and shown by endemic species.

○Muramatsu, M. (Professor emeritus, Okayama U.)

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**325** Photoperiod response of Myanmar rice varieties based on seasonal changes

☆Moe Moe, H.<sup>1</sup>, W. Khin Thanda<sup>1</sup>, S. Ohm Mar<sup>2</sup>, Y. Yamagata<sup>1</sup>, H. Yasui<sup>1</sup>, A. Yoshimura<sup>1</sup>  
(1.Fac. Agr., Grad. Sch., Kyushu Univ., 2.シードバンク・農業研究局・ミャンマー)

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**326** Two NILs of low Cd absorption in the genetic background of 'Hanaechizen' and 'Akisakari'.

○Watanabe, S.<sup>1</sup>, A. Kobayashi<sup>1</sup>, Y. Morozumi<sup>1</sup>, K. Tomita<sup>1</sup>, F. Nakaoka<sup>1</sup>, G. Chaya<sup>1</sup>, Y. Machida<sup>1</sup>, S. Ishikawa<sup>2</sup>, T. Abe<sup>2</sup>, Y. Sato<sup>1</sup>, N. Sato<sup>1</sup> (1.Fukui Agr. Exp. Stn., 2.NARO)

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**327** 'Megumitsukushi', a New Rice Cultivar with Blast Field Resistance, High Temperature Tolerance and Fine Palatability.

○Okubo, Y.<sup>1</sup>, O. Yamaguchi<sup>1</sup>, K. Miyahara<sup>1</sup>, M. Ishibashi<sup>1</sup>, T. Wada<sup>1,2</sup>, M. Miyazaki<sup>1,3</sup>, T. Inoue<sup>1,4</sup>, T. Ishimaru<sup>1,5</sup>, M. Tsubone<sup>1,3</sup>, M. Takata<sup>1</sup> (1.Fukuoka Agric. Forest. Res. Cent., 2.Takii&Co., Ltd., 3.Fukuoka Pref. Gover. Office, 4.Fukuoka Pref. Kitakyusyu Cent. for the Dissemination of Improved Agric. Meth., 5.Fukuoka Pref. Iizuka Cent. for the Dissemination of Improved Agric. Meth.)

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**328** Genetic dissection of non-seed-shattering behaviour of *japonica* rice cultivar, 'Asahi'

☆Karino, M., Y. Tsujimura, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

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**329** Identification of the causal genes for awnlessness in African rice domestication I

○Ashikari, M.<sup>1</sup>, K. Masuda<sup>2</sup>, D. Wang<sup>4,5</sup>, R. Angeles-Shim<sup>6</sup>, K. Obara<sup>7</sup>, K. Nagai<sup>1</sup>, R. Murase<sup>2</sup>, S. Aoki<sup>2</sup>, T. Furuta<sup>1,8</sup>, K. Miura<sup>9</sup>, J. Wu<sup>10</sup>, Y. Yamagata<sup>11</sup>, H. Yasui<sup>11</sup>, K. Michael<sup>12</sup>, A. Yoshimura<sup>11</sup>, T. Kamura<sup>7</sup>, S. McCouch<sup>4</sup>, K. Bessho-Uehara<sup>3</sup> (1.Bioscience Center, Nagoya Univ., 2.Grad. Sch. Bioagri. Sci. Nagoya Univ., 3.Grad. Sch. Life Sci. Tohoku Univ., 4.Grad. Sch. Genetics. Cornell Univ., 5.Dep. Agronomy. Purdue Univ., 6.Dep. Plant and Soil Sci. Texas Tech Univ., 7.Grad. Sch. Sci. Nagoya Univ., 8.Inst. Plant Sci. and Resources, Okayama Univ., 9.Facul. Biotech., Fukui Prefectural Univ., 10.Inst. Crop Science, NARO, 11.Facul. Agri. Kyushu Univ., 12.Dep. Tropical Plant and Soil Sci. Univ. Hawai)

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**330** Identification of the causal genes for awnlessness in African rice domestication I

☆Bessho-Uehara, K.<sup>1,2</sup>, K. Masuda<sup>3</sup>, D. Wang<sup>4,5</sup>, R. Angeles-Shim<sup>6</sup>, K. Obara<sup>7</sup>, K. Nagai<sup>1</sup>, R. Murase<sup>3</sup>, S. Aoki<sup>3</sup>, T. Furuta<sup>1,8</sup>, K. Miura<sup>9</sup>, J. Wu<sup>10</sup>, Y. Yamagata<sup>11</sup>, H. Yasui<sup>11</sup>, M. Kantar<sup>12</sup>, A. Yoshimura<sup>11</sup>, T. Kamura<sup>7</sup>, S. McCouch<sup>4</sup>, M. Ashikari<sup>1</sup> (1.Bioscience Center, Nagoya Univ., 2.Grad. Sch. Life Sci. Tohoku Univ., 3.Grad. Sch. Bioagri. Sci. Nagoya Univ., 4.Grad. Sch. Genetics. Cornell Univ., 5.Dep. Agronomy. Purdue Univ., 6.Dep. Plant and Soil Sci. Texas Tech Univ., 7.Grad. Sch. Sci. Nagoya Univ., 8.Inst. Plant Sci. and Resources, Okayama Univ., 9.Facul. Biotech., Fukui Prefectural Univ., 10.Inst. Crop Science, NARO, 11.Facul. Agri. Kyushu Univ., 12.Dep. Tropical Plant and Soil Sci. Univ. Hawaii)

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**331** Phylogenetic analysis of foxtail millet landraces by ddRAD-seq and geographical distribution of transposon-insertion type in the *PRR37* gene

○Fukunaga, K.<sup>1</sup>, A. Abe<sup>2</sup>, K. Tanaka<sup>3</sup>, M. Tsuji<sup>1</sup>, M. Kawase<sup>4</sup> (1.Grad. Sch. Comprehensive Sci. Res., Pref.U.Hiroshima, 2.Iwate Biotech.Res.Center, 3.NODAI Genome Res. Center, Tokyo U. Agr., 4.Fac. Agr., Tokyo U.Agr.)

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**332** Breeding of Miyazaki prefetural original [Itomaki Daikon] using mass selection method - A new line of [MR-T] -

○Chen, L., S. Mandai, S. Yagi, Y. Kimura, F. Abe, O. Sarugaku (Fac. Environ. Hirt., Minami Kyusyu U.)

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**401** QTL analysis of the stigma exsertion rate in the F2 population between 'Koshihikari' and *Oryza rufipogon* W1944

○Takase, Y., T. Kuboyama (Col. Agr., Ibaraki U.)

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**402** Production of hybrids and amphidiploids between cultivated rice and closely and distantly related wild *Oryza* to cultivated species by in vitro fertilization

☆Ono, S.<sup>1</sup>, E. Toda<sup>2</sup>, T. Tezuka<sup>3</sup>, A. Agata<sup>3,4</sup>, A. Kinoshita<sup>1</sup>, Y. Sato<sup>3</sup>, T. Okamoto<sup>1</sup> (1.Dept. Biol., Tokyo Met. Univ., 2.Dept. Biol., Univ. Tokyo, 3.Dept. Gen. Evol., NIG, 4.Bioagric. Sci., Nagoya Univ.)

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**403** Genome composition of wheat-rice hybrid (Oryzawheat) produced by in vitro fertilization system

Maryanti, T.<sup>1</sup>, S. Koshimizu<sup>2</sup>, T. Ishii<sup>3</sup>, K. Yano<sup>4</sup>, ○T. Okamoto<sup>1</sup> (1.Dept. Biol. Sci., Tokyo Met. Univ., 2.Dept. Informatics, NIG, 3.Tottori Univ., ALRC, 4.Dept. Biol. Sci., Meiji Univ.)

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**404** Production of maize-wheat (Zeawheat) and pearl millet-wheat (Cenchruswheat) hybrid plants by in vitro fertilization system

☆Onda, N.<sup>1</sup>, M. Tety<sup>1</sup>, T. Ishii<sup>2</sup>, T. Okamoto<sup>1</sup> (1.Dept. Biol., Tokyo Met. Univ., 2.ALRC., Tottori Univ.)

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**405** Effect of callose on symplastic connections and apoplastic space-maintenance in meiotic anther locules in rice

☆Somashekar, H.<sup>1,2</sup>, K. Takanami<sup>3</sup>, R. Hiratsuka<sup>4</sup>, K. Nonomura<sup>1,2</sup> (1.Plant Cytogenetics, Natl. Inst. Genet., 2.Sch. Life Sci., SOKENDAI, 3.Dept. Environ. Health, Nara Women's Univ., 4.Fac. Medicine Sch. Medicine, Jikei Univ. Sch. Medicine)

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**406** Expression analysis of mitochondrial gene *orf288* in *Oryza glaberrima* with cytoplasm replaced by Nipponbare.

☆Takeda, S., K. Igarashi, Y. Iwai, K. Toriyama (Grad. Sch. Agri. Sci., Tohoku Univ.)

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**407** Genetic variation and breeding effect of seed retention in Italian ryegrass (*Lolium multiflorum* Lam.)

○Tamura, K., T. Kiyoshi (NILGS, NARO)

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**408** Development of a NAM population construction method utilizing the genome doubling ability of triploid wheat

☆Nishimura, K., R. Nakano, T. Nakazaki (Grad. Sch. Agr., Kyoto Univ.)

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**409** Search for the origin of the *HLA1* gene causing hybrid lethality in interspecific hybrids of tobacco species

☆Nishide, N.<sup>1</sup>, S. Yokoi<sup>1,2</sup>, T. Tezuka<sup>1,2</sup> (1.Grad. Sch. Life Environ. Sci., Osaka Pref. Univ., 2.Grad. Sch. Agr., Osaka Metro. Univ.)

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**410** Genetic analysis of hybrid seed lethality and ovary abscission in interspecific-interploidy crosses in *Nicotiana*

☆Kida, M.<sup>1</sup>, S. Yokoi<sup>1,2</sup>, T. Tezuka<sup>1,2</sup> (1.Grad. Sch. Life Environ. Sci., Osaka Pref. Univ., 2.Grad. Sch. Agr., Osaka Metro. Univ.)

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**411** Deletion of the chromosomal region containing the hybrid lethality gene *HLA1* in spontaneous viable hybrids from the cross *Nicotiana amplexicaulis* × *N. tabacum*

☆Nagai, S.<sup>1</sup>, K. Matsumoto<sup>2</sup>, K. Kawaguchi<sup>3</sup>, S. Yokoi<sup>1,3</sup>, T. Tezuka<sup>1,3</sup> (1.Grad. Sch. Agr., Osaka Metro. Univ., 2.Sch. Life Environ. Sci., Osaka Pref. Univ., 3.Grad. Sch. Life Environ. Sci., Osaka Pref. Univ.)

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**412** Culture condition for rapid differentiation of somatic embryo in tea plant (*Camellia sinensis*)

○Furukawa, K.<sup>1</sup>, H. Segawa<sup>1</sup>, Y. Aoki<sup>1</sup>, W. Hayashi<sup>1</sup>, S. Hirata<sup>2</sup> (1.National Institute of technology(KOSEN),Numazu college, 2.KOSEN,Numazu college AC)

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**413** Production of interspecific hybrid with melon and analysis of its genome structure

☆Nagai, T.<sup>1</sup>, G. Shigita<sup>2</sup>, N. Sogo<sup>1</sup>, I. Odirichi Nnennaya<sup>1</sup>, T. Seiko<sup>3</sup>, C. Muto<sup>3</sup>, K. Naito<sup>3</sup>, Y. Monden<sup>1</sup>, K. Tanaka<sup>4</sup>, H. Nishida<sup>1</sup>, K. Kato<sup>1</sup> (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.TUM, 3.Genetic Resources Center, NARO, 4.Fac. Agr. Life Sci., Hirosaki U.)

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**414** Spatiogenetic analysis of the S allele using a naturalized populations of *Raphanus sativus* L. on the coastal area of the Minami-Kaga region, Ishikawa, Japan.

☆Masuko, E.<sup>1</sup>, K. Fukushima<sup>1</sup>, M. Hayashi<sup>1</sup>, M. Yamamoto<sup>2</sup>, T. Teragishi<sup>3</sup>, S. Takayama<sup>4</sup>, M. Watanabe<sup>1</sup> (1.Grad. Life Sci., Univ. Tohoku, 2.Grad. Sci and Eng., Univ. Toyama, 3.Ishikawa Pref. Board Educ., 4.Grad. Agric. Life Sci., Univ. Tokyo)

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**415** Histological observation and identification of the causal locus of the genic male sterility in the native turnip "Suwa-benikabu".

☆Ozeki, M.<sup>1</sup>, K. Komatsu<sup>1,2</sup>, H. Masuko-Suzuki<sup>3</sup>, Y. Takada<sup>3</sup>, M. Watanabe<sup>3</sup>, Y. Mitsui<sup>1,2</sup>, K. Wakui<sup>1,2</sup> (1.Grad. Agri. Dept. of Human and Animal-Plant Relationships, Tokyo Univ. of Agri., 2.Faculty of Agr. Dept. of Bioresource Dev., Tokyo Univ. of Agri., 3.Grad. Sch. Sci., Tohoku Univ.)

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**416** Characterization of temperature-sensitive restorer lines in Owen cytoplasmic male sterility of sugar beet.

○Matsuhira, H.<sup>1</sup>, K. Kitazaki<sup>2</sup>, K. Matsui<sup>2</sup>, K. Kubota<sup>2</sup>, Y. Kuroda<sup>1</sup>, T. Kubo<sup>2</sup> (1.Hokkaido Agri. Res. Cent., NARO, 2.Grad. Sch. Agri., Hokkaido Univ.)

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**417** Line selection of potential yield using canopy temperature measured by UAV with thermography or hand-held thermometer at a wheat breeding program

○Ohnishi, S.<sup>1</sup>, H. Kiuchi<sup>1</sup>, T. Iijima<sup>2</sup>, T. Uraiike<sup>2</sup>, S. Adegawa<sup>3</sup>, Y. Sato<sup>1</sup>, T. Sonoda<sup>1</sup>, K. Araki<sup>1</sup> (1.HRO Kitami AES, 2.HRO Industrial RI, 3.HRO Central AES)

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**418** Genetic structure of the rice genome shuffling population

○Yamamoto, T.<sup>1,2,3</sup>, T. Furuta<sup>1</sup>, K. Kashihara<sup>1</sup>, Z. Qian<sup>1</sup>, E. Yamamoto<sup>2,4</sup>, T. Ohtani<sup>2</sup>, R. Mizobuchi<sup>2,3</sup>, D. Ogawa<sup>2,3</sup>, J. Yonemaru<sup>2,3</sup>, M. Yano<sup>2,3</sup> (1.IPSR, Okayama Univ., 2.NIAS, 3.NICS, NARO, 4.Meiji Univ.)

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**419** Production and analysis of multiple genome editing rice using an original plasmid set and a method for high-density crop hydroponics in a plant incubator

○Kuroda, M., T. Oikawa (Inst. Agrobiol. Sci., NARO)

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**420** Development of a method for organelle-specific random mutagenesis by a mutation on the exonuclease domain of *A. thaliana* DNA polymerase I.

☆Kosaka, N.<sup>1</sup>, M. Okuno<sup>3</sup>, I. Nakazato<sup>1</sup>, Y. Harada<sup>1</sup>, A. Toyoda<sup>2</sup>, T. Itoh<sup>4</sup>, N. Tsutsumi<sup>1</sup>, S. Arimura<sup>1</sup> (1.Grad. Sch. Agri. and Life Sci., Univ. Tokyo, 2.National Inst. Genetics, 3.Sch. Med., Kurume Univ., 4.Grad. Sch. Life Sci. and Tech., Tokyo Inst. Tech.)

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**421** Development of a model for predicting heading date based on genome information and meteorological data utilizing big data of rice breeding

○Goto, A.<sup>1,2</sup>, S. Taniguchi<sup>2</sup>, T. Hayashi<sup>2</sup>, H. Nakagawa<sup>2</sup>, K. Matsushita<sup>1</sup>, H. Kajiya-Kanegae<sup>2</sup>, M. Yano<sup>2</sup>, J. Yonemaru<sup>2</sup> (1.Inst. Crop Sci., NARO, 2.Res. Cent. Agric. Info. Tech., NARO)

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**422** New phenotyping method usign crop growth model: Apply to rice-yield big data

○Shimono, H.<sup>1</sup>, A. Abe<sup>3</sup>, C. Kim<sup>1</sup>, C. Sato<sup>2</sup>, H. Iwata<sup>4</sup> (1.Fac. Agric., Iwate Univ., 2.Ifuu Rinrin, 3.Iwate Biotechnology Research Center, 4.Fac. Agric., University of Tokyo)

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**423** Development of rice panicle number prediction method using heading detection technology

Isago, K., S. Shibata, Y. Kato, ○S. Nishiuchi (Grad. Sch. Bioagri., Nagoya Univ.)

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**424** Construction of rice-flour-noodle-suitable "I-J-I"-type haplotype block on short arm of chromosome 6 by sBBS

○Tanaka, J.<sup>1</sup>, T. Umemoto<sup>2</sup> (1.Inst. Crop. Sci., NARO, 2.Inst. Food Res., NARO)

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**425** Study of breeding data visualization, pre-processing, and machine-learning modeling for secure computation AI

○OTA, K.<sup>1</sup>, J. Hashimoto<sup>1</sup>, J. Yonemaru<sup>2</sup>, H. Kajiya-Kanegae<sup>2</sup>, K. Matsushita<sup>2</sup>, T. Hayashi<sup>2</sup> (1.NTT Social Informatics Laboratories, 2.NARO)

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**426** Verification and evaluation of phenotype prediction applying breeding data to secure computation AI

○Hashimoto, J.<sup>1</sup>, K. OTA<sup>1</sup>, J. Yonemaru<sup>2</sup>, H. Kajiya-Kanegae<sup>2</sup>, K. Matsushita<sup>2</sup>, T. Hayashi<sup>2</sup> (1.NTT Social Informatics Laboratories, 2.NARO)

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**427** Bayesian optimisation for breeding schemes.

☆Diot, J., H. Iwata (University of Tokyo, Graduate School of Agricultural and Life Sciences)

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**428** Toward a rapid construction of chromosome segment substitution lines of weedy rice using simplified biotron breeding system and genome-wide genotyping assays

☆Takama, R.<sup>1</sup>, T. Imaizumi<sup>1</sup>, U. Yamanouchi<sup>2</sup>, J. Tanaka<sup>2</sup> (1.Inst. Plant Protection, NARO, 2.Inst. Crop. Sci., NARO)

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**429** Development of an R package for stacking and application to maturity time prediction of soybean

☆Nukui, T.<sup>1</sup>, K. Fujii<sup>2</sup>, A. Kikuchi<sup>3</sup>, K. Komatsu<sup>4</sup>, Y. Kouno<sup>5</sup>, N. Oki<sup>6</sup>, S. Watanabe<sup>7</sup>, A. Kaga<sup>2</sup>, A. Onogi<sup>1</sup> (1.Faculty of Agr., Ryukoku Univ., 2.NICS, NARO, 3.TARC, NARO, 4.WARC, NARO, 5.CARC, NARO, 6.KARC, NARO, 7.Univ. Saga)

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**430** Selection of cross combinations based on genomic-ionomic prediction models: application to the breeding of drought tolerant soybean lines

○IWATA, H.<sup>1</sup>, Y. Toda<sup>1</sup>, K. Sakurai<sup>1</sup>, ユ. フジ<sup>2</sup>, Y. Ohmori<sup>1</sup>, Y. Yamasaki<sup>3</sup>, H. Takahashi<sup>4</sup>, H. Takanashi<sup>1</sup>, M. Tsuda<sup>5</sup>, H. Kanegae<sup>1</sup>, M. Hirai<sup>2</sup>, Y. Ichihashi<sup>6</sup>, H. Tsujimoto<sup>3</sup>, M. Nakazono<sup>4</sup>, T. Fujiwara<sup>1</sup>, A. Kaga<sup>7</sup> (1.Graduate School of Agricultural and Life Sciences., Univ. Tokyo, 2.Center for Sustainable Resource Science, RIKEN, 3.Arid Land Research Center, Tottori Univ., 4.Graduate School of Bioagricultural Sciences, Nagoya Univ.,

5.Faculty of Life Environmental Sciences, Univ. Tsukuba, 6.BioResource Research Center, RIKEN, 7.Institute of Crop Science, NARO)

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**431** Establishment of in vitro fertilization system in sugarcane and creation of interspecific/intergeneric hybrids between sugarcane and sugarcane-related germplasm

☆Rattanawong, K.<sup>1</sup>, Y. Terajima<sup>2</sup>, S. Sakuanrungsirikul<sup>3</sup>, T. Okamoto<sup>1</sup> (1.Dep. Biol. Sci., Tokyo Met. Univ., 2.Jap. Int. Res. Cen. Agri. Sci., JIRCAS, 3.Khon Kaen Field Crop. Res. Cen., Thailand)

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**432** Developing EMS mutant lines in *Fragaria vesca* and identifying the causative mutation in the mutants

☆Makita, N., S. Saiga, T. Segawa, S. Murase, M. Tada, M. Nishikawa, H. Takagi (Ishikawa Prefectural University)

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**501** Effects of QTLs for soil-surface rooting in rice (*Oryza sativa* L.) with respect to salinity and iron-toxicity stresses in paddy fields

○Yoshimichi, F.<sup>1</sup>, A. Tomita<sup>2</sup>, A. Hairmansis<sup>3</sup>, N. Nafisah<sup>4</sup>, R. Hermanasari<sup>4</sup>, H. Saito<sup>1</sup>, T. Kazama<sup>5</sup>, K. Toriyama<sup>6</sup>, T. Sato<sup>6,7</sup> (1.JIRCAS, 2.Faculty of Agriculture, Okayama Univ., 3.Research Center for Food Crops, National Research and Innovation Agency (BRIN), 4.Indonesian Center for Rice Research, 5.Graduate School of Agriculture, Kyushu Univ., 6.Graduate School of Agricultural Science, Tohoku Univ., 7.RIKEN Nishina Center)

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**502** Evaluation of protein aggregation in high-temperature treated seedlings of rice core collection cultivars and its relationship with physiological disorder

☆Sato, T., T. Yamada (Grad. Sch. Agr., Tokyo U. Agr. Tech.)

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**503** Changes in blast disease response along with vegetative phase transition in rice

Koyama, T.<sup>1</sup>, T. Watanabe<sup>2</sup>, J. Murakami<sup>3</sup>, A. Nagano<sup>4,5</sup>, ○T. Yoshikawa<sup>2</sup> (1.Fac. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Kyoto Univ., 3.Fac. Agri., Kibi Int. Univ., 4.Fac. Agr., Ryukoku Univ., 5.IAB, Keio Univ.)

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**504** QTL analysis for cold tolerance of rice focusing on anther-related traits

☆Kuroki, R.<sup>1</sup>, R. V.P.<sup>1</sup>, M. A.D.<sup>1</sup>, S. Nishiuchi<sup>1</sup>, D. Makihara<sup>2</sup>, K. Doi<sup>1</sup> (1.Grad. Sch. Bioagri. Sci., Nagoya U., 2.ICREA, Nagoya U.)

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**505** QTL analysis for the response to water deficit stress in upland rice

☆Matsuyama, E.<sup>1</sup>, M. Nakata<sup>2</sup>, Y. Inukai<sup>2</sup>, R. Kuroki<sup>1</sup>, S. Nishiuchi<sup>1</sup>, D. Makihara<sup>2</sup>, K. Doi<sup>1</sup> (1.Grad. Sch. Bioagri. Sci., Nagoya U., 2.ICREA, Nagoya U.)

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**506** Ionomic analysis of rice leaf blade in low-fertilized paddy field

☆Mori, T.<sup>1</sup>, K. Hasegawa<sup>1</sup>, M. Amano<sup>1</sup>, H. Ito<sup>1</sup>, H. Yoshida<sup>3</sup>, M. Saiki<sup>2</sup>, S. Nishiuchi<sup>1</sup>, J. Murase<sup>1</sup>, T. Kamiya<sup>2</sup>, T. Fujiwara<sup>2</sup>, M. Matsuoka<sup>3</sup>, H. Takahashi<sup>1</sup>, M. Nakazono<sup>1</sup> (1.Grad. Sch. Bioagric. Sci., Nagoya Univ, 2.Grad. Sch. Agri. Life. Sci., Univ. Tokyo, 3.IFeS, Fukushima Univ.)

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**507** Screening of rice genes with haplotypes adapted in global latitude differences

☆Lubba, K.<sup>1</sup>, K. Yamamori<sup>2</sup>, Y. Kishima<sup>1</sup> (1.Graduate School of Agriculture, Hokkaido University, 2.Graduate School of Agriculture, Kyoto University)

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**508** Comprehensive analysis of genes for hydrotropism in agravitropic rice root tip

☆Kuya, N.<sup>1</sup>, R. Nishijima<sup>2,3</sup>, T. Kawakatsu<sup>2</sup>, Y. Uga<sup>1</sup> (1.Inst. Crop. Sci., NARO, 2.Inst. Agrobiological Sci., NARO, 3.Fac. Biosci. Biotech., Fukui Pref. Univ.)

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**509** Development of the imaging system for rhizosphere oxidation using planar optode for elucidating mechanisms behind lower methane emission from rice

☆Kawai, T.<sup>1</sup>, T. Tokida<sup>2</sup>, K. Sugimoto<sup>1</sup>, Y. Uga<sup>1</sup> (1.NICS, 2.NIAES)

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**510** UV irradiation on *Arabidopsis hy5* mutants drastically alters the elongation pattern of the root system

○Watanabe, A., S. Domon, D. Odashima, K. Ueda, K. Sakurai, H. Akagi (Fac. Bioresource Sci., Akita Prefectural Univ.)

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**511** Analysis of the strigolactone-dependent root anatomical response to the phosphate starvation

☆Morishita, H.<sup>1</sup>, K. Sumi<sup>1</sup>, R. Sugita<sup>2</sup>, K. Yoneyama<sup>3</sup>, T. Yamauchi<sup>4</sup> (1.Sch. Agric., Nagoya Univ., 2.Radioisotope Res. Center, Nagoya Univ., 3.Grad. Sch. Agric., Ehime Univ., 4.Biosci. Biotech. Center, Nagoya Univ.)

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**512** Identification of a causative gene for the high sensitivity to herbicide bentazon in soybean

○Kato, S.<sup>1</sup>, Y. Yokota<sup>1</sup>, R. Suzuki<sup>2</sup>, Y. Fujisawa<sup>1</sup>, T. Sayama<sup>3</sup>, A. Kaga<sup>1</sup>, T. Anai<sup>4</sup>, K. Komatsu<sup>3</sup>, N. Oki<sup>5</sup>, A. Kikuchi<sup>6</sup>, M. Ishimoto<sup>1</sup> (1.Institute of Crop Science, NARO, 2.Research Center for Advanced Analysis, NARO, 3.Western Region Agricultural Research Center, NARO, 4.Kyushu University, Faculty of Agriculture, 5.Kyushu Okinawa Agricultural Research Center, NARO, 6.Tohoku Agricultural Research Center, NARO)

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**513** Is the rice Receptor-Like Cytoplasmic Kinase (*OsRLCK19*) involved in budding from soil at low temperature?

☆Okane, F.<sup>1</sup>, A. Watanabe<sup>2</sup>, K. Sakurai<sup>2</sup>, K. Ueda<sup>2</sup>, H. Shimada<sup>3</sup>, H. Akagi<sup>2</sup> (1.Grad. Sch. Biores. Sci., Akita Pref. Univ., 2.Fac. Biores. Sci., Akita Pref. Univ., 3.Dept. Bio. Sci. and Tech., Tokyo Univ. Sci.)

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**514** DNA markers specific to allele-types at *Stvb* locus on rice stripe resistance.

○Hayano-Saito, Y.<sup>1</sup>, Y. Kawahara<sup>2</sup>, H. Maeda<sup>3,4</sup>, K. Hayashi<sup>1</sup> (1.Inst. Agrobiol. Sci., NARO, 2.Res. Cent. Advanced Analysis, NARO, 3.Inst. Crop Sci., NARO, 4.Present address: MAFF)

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**515** Evaluation of panicle blast resistance in rice near-isogenic lines

○Hayashi, K.<sup>1</sup>, M. Nakamura<sup>2</sup>, T. Suzuki<sup>2</sup>, T. Yoshida<sup>3</sup>, Y. Hayano-Saito<sup>1</sup> (1.NARO, 2.Aichi Agricultural Research Center, 3.Mountainous Region Agricultural Institute, Aichi Agricultural Research Center)

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**516** Identification of QTL for brown planthopper resistance from wild rice, *Oryza rufipogon*

☆Nguyen, H.<sup>1</sup>, S. Zheng<sup>2</sup>, T. Ishii<sup>3</sup>, D. Fujita<sup>2</sup> (1.Uni. Grad. Sch. Agr. Sci., Kagoshima Univ., 2.Grad. Sch. Agr., Saga Univ., 3.Grad. Sch. Agr. Sci., Kobe Univ.)

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**517** Genome wide association study on resistance to green rice leafhopper (*Nephotettix cincticeps* Uhler) using Indica type rice cultivars in Myanmar

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

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**518** Race classification of *Pyrenophora tritici-repentis* causing tan spot of wheat and its resistance gene distribution in wheat in Japan

○Kato, K.<sup>1</sup>, Y. Ban<sup>1</sup>, M. Yanaka<sup>2</sup>, S. Kitabayashi<sup>1</sup>, H. Sekiguchi<sup>3</sup>, K. Tomioka<sup>1</sup>, F. Kobayashi<sup>4</sup>, N. Mizuno<sup>4</sup>, M. Ito<sup>1</sup> (1.WARC/ NARO, 2.KARC/NARO, 3.NIPP, 4.NICS)

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**519** Root growth variation of barley accessions responded to oxygen condition in hydroponic culture

○Nakano, Y.<sup>1</sup>, H. Ito<sup>2</sup>, H. Aoki<sup>1</sup>, T. Nagamine<sup>1</sup> (1.CARC, NARO, 2.Grad. Sch. Bioindust., Tokyo Univ. Agr.)

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**520** Identification of quantitative trait loci associated with resistance to *Fusarium solani* in inbred line Ohkawa No.1.

☆Kawakatsu, K.<sup>1</sup>, T. Onozaki<sup>1</sup>, M. Satou<sup>1</sup>, M. Azuma<sup>1</sup>, M. Kawabe<sup>1</sup>, F. Naoko<sup>1</sup>, T. Kawakatsu<sup>2</sup>, T. Yasunaga<sup>3</sup> (1.NIVFS, NARO, 2.Inst Agrobiollgical Sci, NARO, 3.Fukuoka Agric Forest. Res.Cen.)

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**521** Establishment of a method for evaluating herbicide tolerance in Adzuki bean (*Vigna angularis*) and screening for tolerance genetic resources

☆Doman, K.<sup>1</sup>, T. Maruta<sup>1,2</sup>, N. Yamaguchi<sup>1</sup>, M. Okuyama<sup>1</sup>, K. Shirasawa<sup>3</sup>, H. Sato<sup>1</sup>, C. Souma<sup>1</sup>, T. Suzuki<sup>1</sup> (1.Central. Agri. Exp. Stn., HRO, 2.Donan Agri. Exp. Stn., HRO, 3.Kazusa DNA Res. Inst.)

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**522** Selection of herbicide-tolerant adzuki bean plants from organogenic callus

☆Maruta, T.<sup>1</sup>, N. Yamaguchi<sup>2</sup>, K. Douman<sup>2</sup>, C. Souma<sup>2</sup>, M. Okuyama<sup>2</sup>, T. Suzuki<sup>2</sup> (1.Donan AES , HRO, 2.Chuo AES, HRO)

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**523** A brown stem rot resistance gene in adzuki bean derived from "Akamame" is located on chromosome 1

☆Sato, K.<sup>1</sup>, H. Nagasawa<sup>2</sup>, C. Souma<sup>1</sup>, T. Suzuki<sup>1</sup> (1.Central Agr. Exp. Stn., HRO, 2.Tokachi Agr. Exp. Stn., HRO)

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**524** Development of a DNA marker associated with resistance to Phytophthora stem rot of adzuki bean derived from a genetic resource "Acc1142"

☆Horikawa, K.<sup>1</sup>, K. Sato<sup>2</sup>, C. Souma<sup>2</sup>, T. Uchida<sup>1</sup>, M. Nagahama<sup>1</sup>, H. Nagasawa<sup>3</sup>, Y. Horiuchi<sup>3</sup>, T. Suzuki<sup>2</sup> (1.Kamikawa Agri.Exp.Stn.,HRO, 2.Central Agri.Exp.Stn.,HRO, 3.Tokachi Agri.Exp.Stn.,HRO)

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**525** Genetic analysis of resistance to Soybean leaf rugose mosaic virus in soybean cultivar Tsurunotamago 1.

○Saruta, M.<sup>1</sup>, Y. Takada<sup>2</sup> (1.Inst. Crop. Sci., NARO, 2.West. Agri. Res. Cent., NARO)

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**526** Effect of lodging and root necrosis to soybean yield in Hokuriku region

○Kono, Y. (Cent.Reg.Agr.Res.Ctr,NARO)

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**527** Application of *rhg1-b*, a single gene regulating soybean cyst nematode race-3 resistance, into soybean breeding programs in Hokkaido, Japan.

☆Igarashi, H.<sup>1</sup>, S. Kobayashi<sup>1</sup>, S. Hagihara<sup>1</sup>, C. Suzuki<sup>1</sup>, N. Yamaguchi<sup>2</sup> (1.Tokachi Agr. Exp. Stn., HRO, 2.Central Agr. Exp. Stn., HRO)

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**528** Establishment of a method for evaluating strawberry anthracnose resistance for DNA markers development by GWAS analysis

☆Taguchi, M.<sup>1</sup>, Y. Kashiwaya<sup>1</sup>, Y. Nakazawa<sup>1</sup>, R. Yamauchi<sup>1,2</sup> (1.Tochigi Pref. Agric. Exp. Stn, 2.Shioyaminaminasu Agricultural Promotion Office)

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**529** Fine mapping of the Quantitative Trait Locus (*ForRs1*) responsible for Fusarium disease resistance in *Raphanus sativus*

Ezeah, C.<sup>1</sup>, T. Kawanabe<sup>2</sup>, J. Shimazu<sup>3</sup>, S. Kawashima<sup>3</sup>, M. Kaji<sup>4</sup>, M. Shimizu<sup>5</sup>, E. Fukai<sup>1</sup>, ○K. Okazaki<sup>1</sup> (1.Graduate School of Science and Technology, Niigata University,, 2.Faculty of Agriculture, Tokai University, 3.Nanto Seed Co. Ltd., 4.Watanabe Seed Co. Ltd., 5.Iwate Biotechnology Institute)

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**530** Towards development of the clubroot resistant cultivar of cabbage suitable for Iwate Pref. -identification of resistant QTL and development of DNA markers-

Kikuchi, N.<sup>1</sup>, M. Shimizu<sup>2</sup>, M. Katsumata<sup>3</sup>, K. Okazaki<sup>4</sup>, ○K. Hatakeyama<sup>1</sup> (1.Fac. Agric. Iwate Univ., 2.IBRC, 3.Watanabe Seed Co., Ltd., 4.Grad. Sch. Sci. Tech., Niigata Univ.)

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**531** Molecular response in *Vigna* genus under salinity

☆Wang, F.<sup>1</sup>, T. Yamauchi<sup>2</sup>, K. Naito<sup>1</sup> (1.Genetic Resources Center, NARO, 2.Bioscience and Biotechnology Center, Nagoya University)

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**532** Ion dynamics analysis to elucidate the unique salt tolerance mechanism of *Vigna luteola*

☆Iki, Y.<sup>1</sup>, F. Wang<sup>2</sup>, K. Ito<sup>1</sup>, Y. Noda<sup>3</sup>, T. Wakatake<sup>2</sup>, K. Tanoi<sup>4</sup>, K. Naito<sup>2</sup> (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO, 3.Takasaki Adv. Radiat. Res. Inst., QST, 4.Grad. Sch. Agri. and Life. sci., Univ. Tokyo)

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## **601** Genetic analysis of tiller number on local rice varieties

☆Lulie Desalegne, M., N. Munguambe Emilia, S. Zheng, D. Fujita (Grad. Sch. Agr., Saga Univ.)

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## **602** Analysis of *qVBN11* for vascular bundle number at panicle neck in rice

☆Ninomiya, T.<sup>1</sup>, H. Nguyen<sup>1,2</sup>, S. ZHENG<sup>1</sup>, D. Fujita<sup>1</sup> (1.Grad. Sch. Agr., Saga Univ., 2.Grad. Sch. Agr. Sci., Kagoshima Univ.)

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## **603** Development and characterization of early heading mutant lines of glutinous rice variety 'Hiyokumochi'.

☆YA, M.<sup>1</sup>, S. Zheng<sup>1</sup>, T. ANAI<sup>1,2</sup>, D. Fujita<sup>1</sup> (1.Grad. Sch. Agr., Saga Univ., 2.Grad. Sch. Agr., Kyushu Univ.)

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## **604** Study of heterosis in the hybrid-rice seedlings between Taichung 65 and WRC cultivars using GWAS and QTL analyses in BC<sub>1</sub>F<sub>1</sub> population

☆Nakamura, Y.<sup>1</sup>, K. Ichitani<sup>2</sup>, M. Shenton<sup>3</sup>, N. Tanaka<sup>3</sup>, T. Kuboyama<sup>1</sup> (1.Col. Agr. , Ibaraki U., 2.Fac. Agr. , Kagoshima U. , 3.Inst.Crop.Sci, NARO)

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## **605** Comparisons of seed properties between diploid and tetraploid rice varieties

☆Wang, X., S. Sasagawa, S. Hirano, Y. Kishima (Research Faculty of Agriculture, Hokkaido University)

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## **606** Diversity of yield-related traits in tetraploid wheat as revealed by analyses of core collection

☆Kojima, H.<sup>1</sup>, T. Yoshikawa<sup>2</sup>, Y. Tanaka<sup>2</sup>, Z. Su<sup>2</sup>, Y. Liu<sup>2</sup>, K. Taniyoshi<sup>2</sup>, S. Nasuda<sup>2</sup> (1.Fac. Agric., Kyoto Univ., 2.Grad. Sch. Agric., Kyoto Univ.)

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## **607** Genetic interaction of starch-related mutations using barley multiple mutants

○Matsushima, R.<sup>1</sup>, H. Hisano<sup>1</sup>, J. Kim<sup>1,2</sup>, I. Ivan<sup>1</sup>, S. Miura<sup>3</sup>, N. Crofts<sup>3</sup>, N. Oitome<sup>3</sup>, N. Fujita<sup>3</sup>, K. Sato<sup>1</sup> (1.Institute of Plant Science and Resources, Okayama University, 2.RIKEN Center for Sustainable Resource Science, 3.Department of Biological Production, Akita Prefectural University)

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## **608** Developing a foundation for mint breeding through genetic analysis

☆Suzuki, H.<sup>1</sup>, H. Ezura<sup>2</sup>, T. Ariizumi<sup>2</sup> (1.Graduate School of Life and Environmental Science, 2.Faculty of Life and Environmental Sciences, University of Tsukuba)

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**609** Estimation of the root thickness gene related to evolution of storage roots in sweetpotato

☆Suematsu, K., M. Tanaka (Kyushu Okinawa Agr. Res. Ctr., NARO)

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**610** New insights into tuberous root development in cassava

☆Utsumi, Y.<sup>1</sup>, C. Utsumi<sup>1</sup>, M. Tanaka<sup>1</sup>, P. Salomé<sup>2</sup>, M. Seki<sup>1</sup> (1.RIEKN CSRS, 2.Centro Nacional de Biotecnología-CSIC)

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**611** Comparative transcriptome and phytohormone profiling of kohlrabi and broccoli in relevant to the tuberous stem initiation in kohlrabi

☆Nuruzzaman, M.<sup>1,2</sup>, M. Kojima<sup>3</sup>, M. Sato<sup>1</sup>, Y. Takebayashi<sup>3</sup>, M. Hoque<sup>4</sup>, S. Okamoto<sup>1</sup>, D. Shea<sup>1</sup>, M. Shimizu<sup>5</sup>, R. Fujimoto<sup>6</sup>, H. Sakakibara<sup>7</sup>, E. Fukai<sup>1</sup>, K. Okazaki<sup>1</sup> (1.Graduate School of Science and Technology, Niigata University,, 2.Department of Genetics and Plant Breeding, Bangladesh Agricultural University, 3.RIKEN Center for Sustainable Resource Science, 4.Faculty of Agriculture, Sylhet Agricultural University, 5.Iwate Biotechnology Institute, Kitakami, Iwate, 6.Graduate School of Agricultural Science, Kobe University, 7.Graduate School of Bioagricultural Sciences, Nagoya University,)

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**612** Identification of the sex-determining gene acting as gynoecium suppression function in a dioecious plant *Silene latifolia*.

○Kazama, Y.<sup>1,2</sup>, M. Kitoh<sup>1</sup>, T. Kobayashi<sup>1</sup>, K. Ishii<sup>2,3</sup>, M. Krasovic<sup>4,5</sup>, Y. Yasui<sup>6</sup>, T. Abe<sup>2</sup>, S. Kawano<sup>7</sup>, D. Filatov<sup>4</sup> (1.Grad. Sch. Biosci. Biotechnol., Fukui Pref. Univ., 2.RIKEN Nishina Cent., 3.NIRS, QST, 4.Dep. Plant Sci., Univ. Oxford, 5.CNRS, Univ. Sorbonne, 6.Grad. Sch. Agr., Univ. Kyoto, 7.Grad. Sch. Front. Sci., Univ. Tokyo)

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**613** Genetic basis of the stem node and internode patterning in rice.

○Tsuda, K.<sup>1</sup>, A. Maeno<sup>1</sup>, W. Tanaka<sup>2</sup>, K. Nonomura<sup>1</sup> (1.National Institute of Genetics, 2.Hiroshima University)

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**614** Analysis of twisting formation principle in rice twisted leaf mutant and its genetic analysis

☆Hikichi, K., S. Okada, Y. Tokuyama, I. Takamure, Y. Kishima, Y. Koide (Grad. Sch. Agr., Univ. Hokkaido)

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**615** Functional analyses of the SAN (*SHORT ANOTHER*) gene in rice

○Kuroha, T., A. Nozaka, M. Kimizu, S. Chechetka, H. Yoshida (Inst. Agrobiological Sci., NARO)

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**616** Screening of the loci associated with the passage cell numbers using the Koshihikari/Takanari CSSLs

☆Sumi, K.<sup>1</sup>, H. Morishita<sup>1</sup>, K. Noshita<sup>2,3</sup>, Y. Tanaka<sup>4</sup>, T. Yamauchi<sup>5</sup> (1.Sch. Agric., Univ. Nagoya, 2.Grad. sch., Univ. Kyushu, 3.Plan. Front. Res. Center, Univ. Kyushu, 4.Grad. Sch. Agric., Univ. Kyoto, 5.Biosci. Biotech. Center, Univ. Nagoya)

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**617** Spatio-temporal oxygen imaging (planar oxygen optode) re-evaluates the germination process of rice under water!

○Shiono, K., H. Shiba, M. Ejiri (Grad. Sch. Biosci. Biotech.)

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**618** Identification of the causal gene for a QTL controlling low-temperature germination in the rice variety Arroz da terra

☆Sugimura, Y.<sup>1</sup>, H. Utsushi<sup>1</sup>, Y. Ogasawara<sup>1</sup>, E. Kanzaki<sup>1</sup>, K. Oikawa<sup>1</sup>, K. Ito<sup>1</sup>, R. Terauchi<sup>1,2</sup>, A. Abe<sup>1</sup> (1.Iwate Biotechnology Research Center, 2.Faculty of Agriculture, Kyoto-University.)

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**619** Effect of red pericarp on seed germination in wild rice, *Oryza rufipogon*

☆Iwamoto, H., A. Onoda, R. Ishikawa, T. Ishii (Grad. Sch. Agri. Sci., Kobe Univ.)

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**620** Identification of the key processes to improve seed longevity in paddy rice by "short-term hydropriming"

☆Murakami, E.<sup>1</sup>, K. Murata<sup>2</sup>, T. Yamada<sup>1</sup>, M. Kanekatsu<sup>1</sup> (1.Grd. Sch. Agr., Tokyo U. Agr. Tec., 2.Toyama Pref. Agr. Forest. Fish. Res. Cent.)

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**621** Variations of catechins content among tea varieties and their response to nutrient deficiencies.

☆Osawa, M.<sup>1</sup>, Y. Ishiguro<sup>1</sup>, J. Kawaki<sup>2</sup>, H. Yamashita<sup>3,4</sup>, T. Ikka<sup>3,4,5</sup> (1.Grad. Agr., Shizuoka Univ., 2.Tea Res. Cent., Shizuoka Pref., 3.Fac. Agr., Shizuoka Univ., 4.Inst. Tea Sci., Shizuoka Univ., 5.Res. Inst. Green Sci. Tech., Shizuoka Univ.)

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**622** Selection of an imperfect black line in soybean

Ohnishi, Y.<sup>1</sup>, E. Negishi<sup>1</sup>, N. Yamaguchi<sup>2</sup>, ○M. Senda<sup>1</sup> (1.Fac. Agric. Life Sci., Univ. Hirosaki, 2.Central Agr. Exp. Sta., HRO)

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**623** Characterization of a low chlorophyll and low tocopherol soybean mutant obtained by ion-beam irradiation

☆Christin, S., A. Kanazawa, M. Dwiyanti (Grad.Sch.Agr., Hokkaido Univ.)

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**624** A novel white-flower mutant of Japanese morning glory obtained by  $\gamma$ -ray irradiation

☆Hasumi, M.<sup>1</sup>, R. Okano<sup>1</sup>, H. Katsuyama<sup>1</sup>, Y. Takahashi<sup>1</sup>, T. Mizuno<sup>2</sup>, A. Hoshino<sup>3,4</sup>, E. Nitashaka<sup>5</sup>, T. Kuboyama<sup>1</sup> (1.Col. Agr., Ibaraki U., 2.Dept. Botany, NMNS, 3.Natl. Inst., Basic Biol., 4.Sch. Life Sci., SOKENDAI, 5.Grad. Sch. Sci., Kyushu U.)

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**625** Development of a wheat mutant lacking the photoperiod response gene *Ppd-D1* by heavy ion-beam irradiation

○Murai, K.<sup>1</sup>, F. Nomura<sup>1</sup>, H. Tada<sup>1</sup>, R. Fueki<sup>1</sup>, S. Arai<sup>1</sup>, T. Abe<sup>2</sup> (1.Fukui Pref. Univ., Fac. Biosc. Biotech., 2.RIKEN, Nishina Cent.)

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**626** Development of an early-flowering mutant in "Fukui-kendai 3 (Fukukomugi)" by heavy ion-beam irradiation

☆Fueki, R.<sup>1</sup>, M. Hatashita<sup>2</sup>, K. Murai<sup>1</sup> (1.Fac. Biosci. Biotech., Fukui Pref. Univ., 2.Wakasa Wan Energy Research Center)

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**627** Exome sequencing identified non-sense mutations in heading-time genes in barley mutants

☆Okuma, M., Y. Monden, K. Kato, H. Nishida (Grad. Sch. Environ. Life Sci., Okayama U.)

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**628** Identification of a set of genes associated with varietal variation in temperature response to heading under short-day conditions in rice

☆Kokaji, H.<sup>1</sup>, K. Nishimura<sup>1</sup>, H. Saito<sup>2</sup>, A. Shimizu<sup>3</sup>, H. Nakagawa<sup>4</sup>, A. Nagano<sup>5,6</sup>, T. Nakazaki<sup>1</sup> (1.Grad. Sch. Agri., Univ. Kyoto, 2.JIRCAS, 3.Sch. Environ. Sci., Univ. Shiga Pref, 4.Res. Ctr. for Agr. Info. Tech., NARO, 5.Sch. Agri., Univ. Ryukoku, 6.IAB., Univ. Keio)

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**629** Exploration of Tea plant (*Camellia sinensis*) secondary embryogenesis factors via transcriptome analysis

☆Hirata, S.<sup>1</sup>, S. Inaba<sup>2</sup>, H. Yamashita<sup>3</sup>, T. Ikka<sup>3</sup>, A. Nagano<sup>4,5</sup>, K. Furukawa<sup>6</sup> (1.National Institute of Technology (KOSEN), Numazu College (advanced course), 2.Tokyo Institute of Technology, Department of Life Science and Technology, 3.Fac. Agi., Shizuoka Univ., 4.Fac. Agi., Ryukoku Univ., 5.Institute for Advanced Biosciences, Keio Univ., 6.KOSEN, Numazu College, Department of Chemistry and Biochemistry)

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**630** Detection for the chromosomal region of the late flowering morning glory, Q63 that alters the number of days to flower in Pekin-Tendan, an early flowering line.

☆Funakawa, N., H. Katsuyama, T. Kuboyama (Col. Agr., Ibaraki U.)

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**631** Analysis of bolting-related genes in extremely early-bolting radish

☆Hayashi, A., H. Mori, A. Tian, M. Yamamoto, H. Kitashiba (Grad. Sch. Agri. Sci., Univ. Tohoku)

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**632** Should *BrFLC5* be considered in the breeding of late-bolting cultivars in Brassica vegetables?

○Fujimoto, R.<sup>1</sup>, K. Kunita<sup>2</sup>, T. Kakizaki<sup>3</sup>, E. Itabashi<sup>3</sup>, K. Okazaki<sup>4</sup> (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Fac. Agric., Kobe Univ., 3.Inst. Veg. Floric. Sci., NARO, 4.Grad. Sch. Sci. Tech., Niigata Univ.)

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