Title of Papers Presented at the 144th Meeting of The JAPANESE SOCIETY OF BREEDING

Oral Presentations

101 Genome wide association study for the trichome density on leaf blade using rice core-collection

Hashimoto, A.[1], J. Ito[2], ○T. Yoshikawa[1,3] (1.Grad. Sch. Agri. Kyoto Univ., 2.Grad. Sch. Agric. Life Sci., U. Tokyo, 3.Nat. Inst. Genet.)

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102 Searching for genes involved in the panicle shape of pearl millet using photogrammetry and GWAS.

☆Kambara, K.[1], S. Gupta[2], T. Takano[1], D. Tsugama[1] (1.Grad. Sch. Agr., Univ. Tokyo, 2.ICRISAT)

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103 Construction of a tobacco high-quality reference genome and its application for identifying a natural mutation relating to low nicotine phenotype

○Hisashi, U.[1], T. Takeuchi[1], H. Magome[1], M. Arai[1], Y. Kotoge[1], T. Komatsu[1], S. Sato[1], H. Iwata[2], Y. Takakura[1] (1.JAPAN TOBACCO INC. Leaf Tobacco Research Center, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

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104 Heat stress reduces the betalain content of *Amaranthus tricolor*

○Lin, Y.[1], A. Nashiki[2], H. Okubo[2], Y. Yoshioka[2], S. Isobe[3], K. Shirasawa[3], K. Hoshikawa[1,4] (1.World Vegetable Center, Taiwan, 2.Faculty of Life and Environmental Sciences, University of Tsukuba, 3.Kazusa DNA Research Institute, 4.Biological Resources and Post-harvest Division, Japan International Research Center for Agricultural Sciences)

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105 Can Armchair Detective do molecular genetics?

○Matsuoka, M.[1], M. Suganami[1], S. Kojima[2], W. Fanmiao[3], H. Yoshida[1], M. Watanabe[4], T. Matsuda[1], E. Yamamoto[5] (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Graduate School of Agricultural Science, Tohoku University, 3.National Agriculture and Food Research Organization (NARO),

4.Graduate School of Life Sciences, Tohoku University, 5.Graduate School of Agriculture, Meiji University)

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106 Using Legacy Data to Detect QTLs Regulating Flowering time in Soybean

☆Suganami, M.[1], H. Takahashi[1,2], N. Nihei[1,2], H. Yoshida[1], S. Kojima[3], I. Sato[4], E. Yamamoto[5], S. Yoshida[1], M. Watanabe[6], T. Matsuda[1,2], M. Matsuoka[1] (1.Faculty of Food and Agricultural Sciences, Institute of Fermentation Sciences, Fukushima University, 2.Faculty of Food and Agricultural Sciences, Fukushima University, 3.Graduate School of Agricultural Science, Tohoku University, 4.Fukushima Agricultural Technology Centre, 5.Graduate School of Agriculture, Meiji University, 6.Graduate School of Life Sciences, Tohoku University)

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107 How have rice breeders in Fukui utilized genes related to heading?

○Kobayashi, A.[1], M. Suganami[2], H. Yoshida[2], S. Watanabe[1], Y. Machida[1], G. Chaya[1], F. Nakaoka[1], Y. Morinaka[3], K. Miura[3], N. Sato[1], M. Matsuoka[2] (1.Fukui Agri. Exp.Stn., 2.Fukushima Univ., 3.Fukui Pref. Univ.)

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108 Characterization of the African rice genome based on a comprehensive orthology analysis.

☆Furuta, T.[1], Y. Sato[2], A. Yoshimura[3], M. Ashikari[4] (1.Inst. Plant Sci. & Res., Okayama Univ., 2.Nat. Inst. Genet., 3.Fac. Agri., Kyusyu Univ., 4.Biosci. & Biotech. center, Nagoya Univ.)

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109 Genome structure and expression profile of an allotetraploid potato.

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

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110 Genome analysis of tomato 'Micro-Tom' by a long-read technology

○Shirasawa, K.[1], T. Ariizumi[2] (1.Kazusa DNA Res Inst, 2.U Tsukuba)

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113 Buckwheat genome project -outline and perspectives -

○Ota, T.[1], J. Fawcett[2], R. Takeshima[3], S. Kikuchi[4], T. Ohsako[5], K. Shirasawa[6], M. Norizuki[4], K. Matsui[3], E. Yazaki[2], E. Ogiso[7], K. Fujii[3], T. Hara[8], M. Jones[9], H. Hirakawa[6], C. Li[10], Y. Yasui[11] (1.RCIES, SOKENDAI, 2.iTHEMS, RIKEN, 3.Inst. Crop. Sci., NARO,

4.Grad. Sch. Hort., Chiba Univ., 5.Grad. Sch. Life Env. Sci, Kyoto Oref. Univ., 6.Kazusa DNA Res. Inst., 7.CMBR, NMNS, 8.Hokkaido Agr. Res. Cent., NARO, 9.Univ. Cambridge, 10.Yunnan Agr. Univ, 11.Grad. Sch. Agr., Kyoto Univ.)

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114 Development of waxy common buckwheat using NGS-TILLING

○Yasui, Y.[1], F. Jeffrey[2], T. Tanaka[1], K. Nishimura[1,3], T. Nakazaki[1], Y. Iwahashi[1], H. Saito[4], N. Takeuchi[1], M. Ueno[1,5], K. Shirasawa[6], H. Hirakawa[6], T. Ota[7] (1.Grad. Sch. Agr., Kyoto U., 2.iTHEMS, RIKEN, 3.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama U., 4.Trop. Agr. Res Front, JIRCAS, 5.Inst. Agr., TUAT, 6.Kazusa DNA Res. Inst., 7.RCIES, SOKENDAI)

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115 Flavonoid biosynthesis and regulatory system revealed by genome sequencing in buckwheat

○Matsui, K.[1], Y. Oshima[2], N. Mitsuda[2], S. Sakamoto[2], J. Fawcett[3], H. Hirakawa[4], T. Ota[5], Y. Yasui[6] (1.Inst. Crop Sci., NARO, 2.Bio. Res. Inst., AIST, 3.iTHEMS, RIKEN, 4.Kazusa DNA Res. Inst., 5.RCIES, SOKENDAI, 6.Grad. Sch. Agr., Kyoto U.)

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116 Genetic architecture of heteromorphic self-incompatibility in common buckwheat

☆Takeshima, R.[1], J. Fawcett[2], K. Matsui[1], N. Mizuno[1], D. Matsumoto[3], H. Hirakawa[4], T. Ota[5], Y. Yasui[6] (1.Inst. Crop. Sci., NARO, 2.iTHEMS, RIKEN, 3.Department of Bioscience and Biotechnology, Fukui Pref. Univ., 4.Kazusa DNA Res. Inst., 5.RCIES, SOKENDAI, 6.Grad. Sch. Agr., Kyoto Univ.)

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117 Gene of salt tolerance indentified by multiple genome and transcriptome sequencing

Itoh, M.[1], C. Muto[2], M. Takemoto[3], Y. Monden[4], ○K. Naito[2] (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.NGRC, NARO, 3.Dpt. Agr., Okayama Univ., 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ.)

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118 Identification of a candidate gene for sex determination in *Dioscorea tokoro*

☆Kudoh, A.[1], Y. Sugihara[2], A. Abe[3], K. Oikawa[3], S. Natsume[3], M. Shimizu[3], K. Itoh[3], M. Tsujimura[4], T. Terachi[5], A. Ohta[1], R. Terauchi[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.IBRC, 4.Fac. Agr., Ryukoku Univ, 5.Fac. Life Sci., Kyoto Sangyo Univ.)

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119 MSH1 might be involved in mitochondrial genome repairment by cutting the mismatch base pair.

☆zhou, c., N. Tsutsumi, S. Arimura (Grad. Agri., Univ. Tokyo)

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120 Exploration of Cytosine Methylation in Plant Mitochondrial DNA

☆Zhong, Y.[1], M. Okuno[2], N. Tsutsumi[1], S. Arimura[1] (1.Grad. Sch. of Agri., Univ. Tokyo, 2.Kurume Univ. Sch. of Med.)

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121 Discovery of Potential QTL Regions for Sex Ratio Genes in Monoecious Bitter Gourd

☆Ismail, S.[1], H. Karube[1], N. Miyagi[2], N. Taniai[2], K. Tarora[2], N. Urasaki[2], H. Matsumura[3] (1.Grad. Sch. Sci. Tech., Shinshu Univ., 2.Okinawa Pref. Agri. Res. Ctr., 3.Gene Res. Ctr., Shinshu Univ.)

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122 QTL analysis using segregation population of autotetraploid rice

☆Okada, S.[1], I. Kamachi[1], Z. Myint[1], Y. Kishima[2], Y. Koide[2] (1.Graduate School of Agriculture, Hokkaido University, 2.Research Faculty of Agriculture, Hokkaido University)

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123 Effects of QTL involved in traits associated with good eating quality on rice cultivar "Tsuyahime"

○ishizuka, Y.[1], K. Watanabe[1,2], R. Saito[1], N. Saito[1], T. Sato[3], N. Adachi[4,5], K. Hori[6], M. Wakayama[7,8] (1.Yamagata Pref. Integrated Agric. Res. Cen., Rice. Breed. Crop. Sci. Res. Inst., 2.Yamagata Pref. Shonai Agric. Tech. Extens. Div., 3.Former Yamagata Pref. Integrated Agric. Res. Cen., Rice. Breed. Crop. Sci. Res. Inst., 4.Yamagata Pref. Integrated Agric. Res. Cen., 5.Yamagata Pref. Gover. Office, 6.Inst. Crop. Sci.,NARO, 7.Former Inst. for Advanced Biosciences, Keio Unv., 8.Integrated Medical and Agricultral School of Public Health, Ehime Unv.)

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124 Isolation of QTLs associated with glume length, glume hardness, and 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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201 Allelic frequency of recessive *rf1* alleles in garden beet

☆Taniguchi, E.[1], R. Hayakawa[1], Y. Kanomata[1], H. Tanaka[1], H. Matsuhira[2], Y. Kuroda[2], K. Kitazaki[1], T. Kubo[1] (1.Research Faculty of Agriculture, Hokkaido University, 2.Hokkaido Agricultural Research Center, National Agriculture and Food Research Organization)

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202 High-sugar yield breeding of high-biomass lines pyramided dominant alleles for culm length in Sorghum

☆Kikuchi, T.[1], S. Okada[2], S. Araki-Nakamura[2], K. Ohmae—Shinohara[2], C. Ogino[3], S. Kasuga[4], T. Sazuka[2] (1.Grad. Sch. Bioagri., Nagoya Univ., 2.Biosci. and Biotech. Center, Nagoya Univ., 3.Grad. Sch. Eng., Kobe Univ., 4.AFC, Fac. of Agri. Shinshu Univ.)

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203 Amino acid modification of rice HSL1 by gene targeting creates new herbicide resistance genes.

○Hirose, S.[1], A. Yokoi[1], Y. Tozawa[2], M. Ohshima[1], H. Yoshida[1] (1.Inst. Agrobiol. Sci., NARO, 2.Grad. Sch. Sci. and Eng. , Saitama Univ.)

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204 Evaluation of three novel loci involved in non-seed-shattering behaviour of a rice cultivar ‘Kasalath’

☆Yamaguchi, Y., N. Shionari, N. Takama, Y. Oka, Y. Takenaka, T. Htun, C. Inoue, K. Numaguchi, T. Ishii, R. Ishikawa (Grad. Sch., Agr. Sci., Kobe Univ.)

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205 Estimating suitable regions for growing robust and late flowering isogenic Koshihikari sp using data analysis

○Tomita, M.[1], H. Honda[2] (1.Res. Inst. Green Sci. & Technol., Shizuoka Univ., 2.Honda Biotech. Labo.)

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206 Development of a simple and rapid variety identification system for domestically bred citrus varieties.

○Okamoto, M.[1], Y. Monden[2], A. Shindo[2], T. Takeuchi[3], T. Endo[4], Y. Shigematsu[5], K. Takasaki[3], H. Fujii[6], T. Shimada[4] (1.Res. Inst. Agr., pref. Ehime, 2.Grad. Sch. Environ. Life Sci., Okayama Univ, 3.FASMAC Co., Ltd., 4.Inst. Fruit Tree and Tea Sci., NARO, 5.Res. Inst. Citrus Fruits., pref.Ehime, 6.Fac. Agr., Shizuoka Univ.)

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207 Comparative Analysis of reference genome and Linkage map developed using F2 population from "Sekizaiso" x "Kokuso21"

☆Suzuki, M.[1], A. Koyama[2], M. Uemoto[1], S. Kajita[2], H. Matsumura[1] (1.Grad. Sch. Sci. Tech., Shinshu Univ, 2.Tokyo U Agr. Tech)

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208 Development of a DNA maker related to anthocyanin less in broccoli florets

☆Adachi, T.[1], H. Okamoto[2], Y. Shiroto[2], K. Tonosaki[3], M. Shimizu[4], K. Hatakeyama[1] (1.Faculty of Agriculture, Iwate Univ., 2.Nippon Norin Seed Co., 3.Kihara Inst. Biol. Res., Yokohama City Univ., 4.IBRC)

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209 Genome-wide DNA marker designning tool, "ngs-mkdesigner", which is useful for PCR-based genotyping

☆Chigira, K., M. Iwasa, S. Honda, S. Adachi, T. Ookawa (Graduate School of Agriculture, Tokyo University of Agriculture and Technology)

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210 Development of DNA marker of *Vat* gene in melon, by comparative analysis of genomic sequence of *Vat* and nearby region

☆Sogo, N.[1], M. Okuma[1], O. IMOH[1], T. Nagai[1], G. Shigita[2,7], K. Tanaka[3], K. Nishimura[4], T. Seiko[5], C. Muto[5], K. Naito[5], Y. Monden[4], M. Sugiyama[6], H. Nishida[4], Y. Kawazu[6], N. Tomooka[5], K. Kato[4] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.TUM, 3.Fac. Agr. Life Sci., Hirosaki U., 4.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 5.Genetic ResourcesCenter, NARO, 6.Inst. Vegetable & Floriculture Sci., NARO, 7.Fac. Life Environ. Sci., U. Tsukuba)

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211 High-dense genetic linkage map using multiple-dose markers and random-effect multiple QTL mapping of root-knot nematode resistance in hexaploid sweetpotato

☆Kurihara, M.[1], H. Tabuchi[2], K. Kato[3], H. Nishida[3], Y. Monden[3] (1.Grad. Sch. Env. & Life Sci., Okayama U., 2.KARC/NARO, 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

---

212 DNA markers to identify *Fusarium oxysporum* resistance derived from inbred line Ohkawa No.1

○Kawakatsu, K.[1], T. Yasunaga[2], M. Satou[1], M. Kawabe[1], T. Kawakatsu[3], K. Sato[4], Y. Fuji[4], A. Iriya[5], M. Suzuki[5] (1.NIVFS, NARO, 2.Fukuoka Agric Forest. Res.Cen.,, 3.Inst Agrobiollgical Sci, NARO, 4.Nagano Veg. Orn. Crop Ex. Sta., 5.Shizuoka Res. Inst. Agric. and For.)

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213 Exploring genomic regions involved in hybrid vigor of *Arabidopsis thaliana*.

☆Fujiwara, K.[1], N. Miyaji[2], T. Yasuda[1], R. Fujimoto[1] (1.Grad. Sch. Agr. Sci., Kobe U., 2.Iwate Biotech. Res. Ctr)

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214 Relationship between salt tolerance and biomass heterosis in *Arabidopsis thaliana*.

☆Kamiya, Y., M. Hasan, T. Yasuda, R. Fujimoto (Graduate School of Agricultural Science Faculty of Agriculture Kobe University)

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215 Development of a measuring method using digital 3D model of rice (*Oryza sativa*)

☆Pongpiyapaiboon, S.[1], H. Tanaka[2], S. Hirano[3], Y. Kishima[3], R. Akashi[4] (1.Interdiscip. Grad. Sch. Agr. Engi., Univ. Miyazaki, 2.Fac. Agr., Univ. Miyazaki, 3.Grad. Sch. Agr., Hokkaido Univ., 4.Univ. Miyazaki)

---

216 Comparison of growth patterns in diploids and tetraploids of the same cultivars using digital 3D models

☆Hirano, S.[1], S. Pongpiyapaiboon[2], S. Sasagawa[1], I. Takamure[1], H. Tanaka[3], R. Akashi[4], Y. Kishima[1] (1.Agr., Hokkaido Univ., 2.Interdiscip. Grad Sch. of Agr. and Engi., Univ. Miyazaki, 3.Fac. of Agr., Univ. Miyazaki, 4.Univ. Miyazaki)

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217 Comparison of QTLs of elemental content in rice grain and straw estimated by GWAS of two multi-parental populations

☆ZHANG, Q.[1], T. Furuta[1], K. Kashihara[1], D. Ogawa[2], J. Yonemaru[3], J. Ma[1], T. Yamamoto[1] (1.IPSR, Grad. Sch. Environ. Life Sci., Okayama Univ., 2.NICS, NARO, 3.RCAIT, NARO)

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218 The identification of gene controlling super high genistein isoflavones in soybean seeds.

○Watanabe, S.[1], J. Irie[1], R. Yamada[1], T. Anai[2] (1.Fac. Agri., Univ. Saga, 2.Fac. Agri., Univ. Kyusyu)

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219 Effect of stay-green mutation accumulation on chlorophyll content in soybean seeds

☆Hase, A.[1], H. Nakano[2], J. Abe[3], T. Yamada[3] (1.Grad. Sch. Agri., Univ. Hokkaido, 2.Sch. Agri., Univ. Hokkaido, 3.Res. Fac. Agri., Univ. Hokkaido)

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220 Genetic insight into adzuki seed coat color via component analysis

☆Sasada, H.[1], Y. Sato[2], N. Tomooka[3], Y. Takahasi[3], T. Yamada[2] (1.Faculty of Agriculture, Hokkaido University, Sapporo, Japan, 2.Graduate School of Agriculture, Hokkaido University, Sapporo, Japan, 3.Institute of Crop Science, National Agriculture and Food Research Organization, Tsukuba, Japan)

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221 Wild emmer and durum wheats took different strategies to produce more grains per plant

☆Kojima, H.[1], S. Yoshioka[1], K. Taniyoshi[1], T. Yoshikawa[1,2], Y. Tanaka[1,3], S. Nasuda[1] (1.Grad. Sch. Agric., Kyoto Univ., 2.Nat. Inst. Genet., 3.Grad. Sch. Env. Life Nat. Sci. and Tech., Okayama Univ.)

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222 Genomic prediction accuracy of yield-related traits in soybean breeding programs.

○Yamaguchi, N.[1], H. Igarashi[2], H. Takahashi[2], S. Hagihara[2], C. Suzuki[2], S. Kobayashi[2] (1.Central Agr. Exp. Sta., HRO, 2.Tokachi Agr. Exp. Sta., HRO)

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223 Effect of short-term storage and storage temperature on quality of sweetpotato variety "Amahazuki".

○Nishinaka, M., K. Taguchi (Central Reg. Agri. Res. Cent., NARO)

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224 Unique dough characteristics of the bread wheat cultivar "Natsukogane"

○Ikenaga, S., T. Nakamura, A. Nakamaru, H. Ito (Tohoku Agric.Res.Cent.,NARO)

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301 Improvement of efficiency somatic embryogenesis on cotyledon explants induced by high-concentration sugar treatment in carotto (*Daucus carota*).

☆Kubota, R.[1], Y. Takahara[2] (1.Grad. Sch. Mta. And Bio., Nagaoka Univ. tech., 2.Mta. And Bio., Nagaoka Univ. tech.)

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302 Development of a whole-mount immunostaining method for rice shoot apical meristem

☆MORISHITA, Y.[1], R. Takata[2], A. Yoshida[2], A. Higo[2], H. Tsuji[2,3] (1.Sch Agri, Nagoya Univ., 2.KIBR, Yokohama City Univ., 3.BBC, Nagoya Univ.)

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303 The impact of carbohydrates on coleoptile elongation in germinating rice (Oryza sativa L.) under low oxygen.

☆Hirano, H., M. Fukuda, T. Fukao (Grad. Sch. Biosci., Fukui Pref. Univ.)

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304 A significant relationship between salt tolerance and ABA-induced seed-germination delay of seedling in *Brassica napus*

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

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305 Plastic developmental mechanisms of latral root primordium in rice

☆Kushida, S.[1], R. Akahoshi[1], T. Kawai[2], M. Inari-Ikeda[3], Y. Inukai[4] (1.Grad. Sch. Bioagr., Nagoya U., 2.Inst. Crop Sci., NARO, 3.Sch. Hel. Nut., U. Tokaigakuen, 4.ICREA, Nagoya U.)

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306 Analysis of strigolactone biosynthetic pathway that associates with root development

☆Morishita, H.[1], K. Sumi[1], R. Sugita[2], T. Suzuki[3], K. Yoneyama[4], T. Yamauchi[5] (1.Grad. Sch. Bioagr. Sci., Nagoya Univ., 2.Radioisotope Res. Center, Nagoya Univ., 3.Coll. Biosci. Biotech., Chubu Univ., 4.Res. Dev. Bureau, Saitama Univ., 5.Biosci. Biotech. Center, Nagoya Univ.)

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307 Molecular mechanisms on promoted lateral root development by rice *our1* mutation focusing on *OsWOX10* regulation

☆Dong, Y.[1], C. Wainaina[2], Y. Inukai[3] (1.Grad. Sch. Bioagr., Nagoya U., 2.Dept. Hort. Food Sec., JKUAT, 3.ICREA, Nagoya U.)

---

308 Genetic basis of the stem node and internode patterning in rice II.

○Tsuda, K.[1,2], A. Maeno[1], K. Hibara[3], W. Tanaka[4], K. Nonomura[1,2] (1.National Institute of Genetics, 2.SOKENDAI, 3.Kibi International University, 4.Hiroshima University)

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309 Fine mapping and identification of genes responsible for tuberous stem formation in kohlrabi (*Brassica oleracea* var. *gongylodes* L.)

☆Nuruzzaman, M.[1], M. Sato[1], M. Shimizu[2], E. Fukai[1], K. Okazaki[1] (1.Grad. Sch. Sci. & Tech., Niigata Univ., 2.Iwate Biotech. Inst.)

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310 Identification of the causal gene in bread wheat early flowering strain obtained from gamma-ray irradiated population

☆Komura, S.[1], F. Kobayashi[2], Y. Oono[2], H. Handa[3], K. Yoshida[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.NICS, 3.Grad. Sch. Life Envi. Sci., Kyoto Pref. Univ.)

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311 Flowering-related QTLs of KU-195, a unique line with early flowering characteristics detected in the wild emmer wheat accessions

☆Chang, Y.[1], K. Nishimura[2], M. Kakusaka[3], T. Chen[1], Y. Iwahashi[1], K. Motoki[2], K. Nagasaka[1], K. Murata[1], T. Maki[1], Y. Kinoshita[1], R. Nakano[1], H. Inoue[1], K. Kawaura[3], N.

Mori[4], T. Nakazaki[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.Grad. Sch. Environ. Life Nat. Tech., Okayama Univ., 3.KIBR, Yokohama City Univ., 4.Grad. Sch. Agr. Sci., Kobe Univ.)

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312 Elucidation of the mechanism of tomato fruit set controlling by spatiotemporal dynamics of jasmonate in the ovule

☆Nomura, Y.[1], Y. Lu[2], H. Enomoto[3], K. Harada[1], Y. Shinozaki[2], R. Yano[4], M. Kojima[5], Y. Takebayashi[5], H. Sakakibara[6], H. Ezura[2,7], T. Ariizumi[2,7] (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Dept. Biosci., Univ. Teikyo, 4.Advanced Analysis Center., NARO, 5.CSRS., RIKEN, 6.Grad. Sch. Bioagric Sci., Univ. Nagoya, 7.T-PIRC., Univ. Tsukuba)

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313 Developmental analysis of rice shoot apical meristem by cytoskeleton imaging and depolymerization

☆Takata, R.[1], M. Tanaka[1], H. Takeuchi[2], D. Maruyama[1], J. Ito[1], H. Tsuji[1,3] (1.KIBR, Yokohama City Univ., 2.ITbM, Nagoya Univ., 3.BBC, Nagoya Univ.)

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314 Dissection of developmental state transition in the shoot apical meristem of barley by single meristem RNA-seq

○Ito, J.[1], Y. Nomura[1], K. Takahagi[1], J. Kim[2,3], M. Kashima[4], S. Okada[5], N. Sato[1], M. Shimizu[2], D. Saisho[3], K. Mochida[2], T. Hirayama[3], H. Tsuji[1,5] (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Toho Univ., 5.Bioscience and Biotechnology Center, Nagoya Univ.)

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315 Importance of inflorescence in internode elongation in barley

Tanaka, M.[1], H. Akashi[1], ○H. Tsuji[1,2] (1.Kihara Inst. Biol. Res., Yokohama City Univ., 2.Biosci. Biotechnol. Center, Nagoya Univ.)

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316 Single-cell growth analysis of rice leaf primordium by 3D timelapse scanning

☆Tokuyama, Y.[1], R. Kelly-Bellow[2], R. Smith[2], Y. Koide[3] (1.Graduate School of Agriculture, Hokkaido University, 2.Department of Computational and System Biology, John Innes Centre, 3.Research Faculty of Agriculture, Hokkaido University)

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317 Transcriptome analysis of monoecious spinach lines with different femaleness.

☆Yamano, K.[1], B. Pachakkil[2], K. Tanaka[2,3], H. Hirakawa[4], Y. Onodera[5] (1.Graduate School of Agriculture, Hokkaido University, 2.NODAI Genome Research Center, Tokyo

University of Agriculture, 3.Department of Informatics, Tokyo University of Information Sciences, 4.Kazusa DNA Research Institute, 5.Research Faculty of Agriculture, Hokkaido University)

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318 Dynamic change in transcriptome in leaves at early vegetative stages of hexaploid wheat 'Norin 61' and its relationships to juvenile-adult phase transition

☆Senoo, K.[1], K. Yamamori[2], S. Yoshioka[2], S. Nasuda[2], T. Yoshikawa[3] (1.Fac. Agri., Kyoto Univ., 2.Grad. Sch. Agri., Kyoto Univ., 3.Nat. Inst. Genet.)

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319 Response to mild drought in soybean plants in the field

☆Nagatoshi, Y.[1], K. Ikazaki[2], Y. Kobayashi[1], N. Mizuno[3], R. Sugita[4], Y. Takebayashi[5], M. Kojima[5], H. Sakakibara[5,6], N. Kobayashi[7], K. Tanoi[7], K. Fujii[1], J. Baba[1], E. Ogiso-Tanaka[8], M. Ishimoto[9], Y. Yasui[3], T. Oya[2], Y. Fujita[1,10] (1.Biol. Resources Post-harvest Div., JIRCAS, 2.Crop Livestock Environ. Div., JIRCAS, 3.Grad. Sch. Agri., Kyoto Univ., 4.Radioisotope Research Center, Nagoya Univ., 5.RIKEN CSRS, 6.Grad. Sch. Bioagri. Sci., Nagoya Univ., 7.Grad. Sch. Agri. Life Sci., Univ. Tokyo, 8.CMBR, Natl. Mus. Nat. Sci, 9.Inst. Crop. Sci., NARO, 10.Grad. Sch. Life Environ. Sci., Univ. Tsukuba)

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320 Identification of salt tolerance gene candidates involved in Na and K dynamics in *Vigna luteola*

☆Iki, Y.[1], F. Wang[2], K. Ito[1], Y. Noda[3], T. Wakatake[4], K. Tanoi[5], K. Naito[2] (1.Grad. Sch. Front. Sci., Univ. Tokyo, 2.Res. Cntr. Genet. Resour., NARO, 3.Takasaki Adv. Radiat. Res. Inst., QST, 4.Grad. Sch. Sci. and Technol, NAIST, 5.Grad. Sch. Agri. and Life. sci., Univ. Tokyo)

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322 Mi-Geno: A tool for editing and managing SNP data

○Isobe, S.[1], T. Shimizu[1], T. Hattori[2], M. Yamada[1], T. Tanabata[1] (1.Kazusa DNA Research Institute, 2.IT Contractor)

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323 Improvement of Plant GARDEN, a portal site for plant genome information (2023, Q2 ver)

☆Ichihara, H.[1], M. Kohara[1], S. Yamashita[1], M. Yamada[1], T. Shimizu[1], S. Shirasawa[1], Y. Toda[1], H. Hirakawa[1], Y. Nakamura[1,2], T. Tanabata[1], S. Tabata[1], S. Isobe[1] (1.Kazusa DNA Research Institute, 2.National Institute of Genetics)

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324 Pedigree data analysis using "Pedigree Finder" -Calculation of coefficient of parentage and visualization of phenotype transmission-

○Kajiya-Kanegae, H., T. Hayashi, J. Yonemaru (RCAIT, NARO)

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401 Effect of increased expression of *ACS8* on hybrid vigor in *Arabidopsis thaliana.*

☆Shiraki, S., K. Matsuo, T. Yasuda, R. Fujimoto (Grad. Sch. Agri., Univ. Kobe)

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402 Identification of common genes involved in decreased heterosis level by *DDM1* dysfunction and reduced growth due to shade avoidance syndrome

☆Nishimura, K., K. Matsuo, T. Yasuda, R. Fujimoto (Kobe University, Graduate School of Agricultural Science, Kobe, Japan)

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403 Revealing the competition between sweetpotato and southern root knot nematode by transcriptome analysis

☆Izumitani, M.[1], S. Ohata[1], H. Tabuchi[2], H. Nishida[1], K. Kato[1], Y. Monden[1] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U., 2.KARC/NARO)

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404 Double mutant for PRC2 components induces asexual embryogenesis and/or autonomous endosperm development

○Tonosaki, K., T. Kinoshita (KIBR, Yokohama City Univ.)

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405 The epigenetic basis of awn formation in barley.

☆Nakamura, K.[1], Y. Kikuchi[1], M. Shiraga[2], T. Kotake[3], S. Taketa[1,2], Y. Ikeda[1,2] (1.Grad. Sch. Environ. and Life Sci., Okayama Univ., 2.IPSR, Okayama Univ., 3.Grad. Sch. Sci. and Eng., Saitama Univ.)

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406 Phased siRNA production of *CHS-A* cosuppression in petunia expands with a preferential increase of specific siRNAs during flower development

☆Yuhazu, M., S. Kaneko, M. Kasai, M. DWIYANTI, A. Kanazawa (Research Faculty of Agriculture, Hokkaido University)

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407 Isolation and characterization of *PH5*-like genes in *Phalaenopsis* and *Doritaenopsis* species.

☆Onoda, I., Y. Takahara (Grad. Sch. Materials Science and Bioengineering, Nagaoka University of Technology)

408 Analysis on difference in P-type H^+ ATPase gene expression among organs and analysis of *NHX1* gene in *Phalaenopsis* orchid.

☆Sugisaki, R.[1], Y. Takahara[2] (1.Materials Science and Bioengineering, Nagaoka University of Technology, 2.Materials Science & Bioengineering, Nagaoka University of Technology)

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409 Fruit body formation on FDS gene transformants of non-fruiting stock of *Flammulina velutipes*

○Tateishi, H., Y. Fujino, T. Tsukiyama, E. Tanesaka (Fac. of Agricultural Sci., Kindai Univ.)

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410 Utilization of none synthesizing glycoalkaloid deficient lines from the wild potato species *Solanum marinasense.*

☆SANETOMO, R.[1], I. Habe[2], N. Nishitani[1], N. Umemoto[3] (1.Obihiro Univ. PGEL, 2.Nagasaki Agri and Forestry Tech. DC, 3.RIKEN, CSRS)

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411 Loss of function mutant of a novel PPR gene inserted by a transposable element in rice landrace, Akage

○Ishikawa, R., T. Dinh (Hirosaki Univ. Fac. Agri. Life Sci.)

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412 Study of transposon insertinoal mutant into rice chloroplast RNA editing factor gene, MORF2

☆Yokoi, N., T. Dinh, R. Ishikawa (Hirosaki Univ. Fac. Agri. Life Sci.)

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413 Communication activities for promoting public understanding for genome editing in the fields of agriculture and food

○Takahara, M.[1], Y. Nakano[1,2], R. Moriyama[1,3], M. Ohta[1], I. Akahane[1], K. Sumitomo[1], K. Fujino[1], H. Mizuno[1], M. Kasai[1], S. Nishiyama[4], S. Tachibana[4], K. Nakajima[4], T. Fujii[5] (1.New Tech. Promotion Office, Strategic Planning HQ, NARO, 2.NIVFS, NARO, 3.F-REI, 4.Leave a Nest Co., Ltd., 5.JATAFF)

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414 Production of a cytoplasmic male sterility gene knock out line in eggplant using mitochondrial genome editing.

○Tsujimura, M.[1], T. Shizuka[2], A. Miyata[3], A. Susami[4], S. Arimura[5], T. Terachi[3] (1.Fac. Agr., Ryukoku Univ., 2.Cent. Plant Sci., Kyoto Sangyo Univ., 3.Fac. Life Sci., Kyoto Sangyo

Univ., 4.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 5.Grad. Sch. Agr. Life Sci., Univ. Tokyo)

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415 Evaluation of agronomic traits of genome-edited potato lines (cv. Sayaka) with reduced accumulation of steroidal glycoalkaloids under field conditions.

○YAMAZAKI, M.[1], K. ASANO[2], K. AKAI[2], N. UMEMOTO[3], K. SAITO[3], S. YASUMOTO[4], T. MURANAKA[4,5] (1.Institute of Agrobiological Sciences, NARO, 2.Hokkaido Agricultural Research Center, NARO, 3.RIKEN Center for Sustainable Resource Science, 4.Graduate School of Engineering, Osaka University, 5.Institute for Open and Transdisciplinary Research Initiative, Osaka University)

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416 Developing naked barley for brewing through site-directed mutagenesis

○Hisano, H.[1], H. Sakai[2], M. Hamaoka[1], H. Munemori[1], F. Abe[3], K. Sato[1], P. Hayes[4] (1.IPSR, Okayama U., 2.Research Center for Advanced Analysis, NARO, 3.Institute of Crop Science, NARO, 4.Oregon State U.)

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417 OsbZIP1 regulates phosphorus and nitrogen uptake, contributing to improved yield.

○Tanaka, N.[1], S. Yoshida[2], I. Saiful[2], K. Yamazaki[2], T. Fujiwara[2], Y. Ohmori[3] (1.Institute of Crop Science, National Agriculture and Food Research Organization, 2.Graduate School of Agricultural and Life Sciences, The University of Tokyo, 3.Agricultural Bioinformatics Research Unit, Graduate School of Agricultural and Life Sciences, The University of Tokyo)

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418 Genome editing of the *STAYGREEN* (*SGR*) gene in *Zoysia matrella*

☆Hirata, M.[1], H. Ng[2], T. Gondo[3], R. Akashi[4] (1.Grad. Sch. Agr., Univ. Miyazaki, 2.Interdiscip. Grad. Sch. Agr. & Engr., Univ. Miyazaki, 3.FSRC, Univ. Miyazaki, 4.Univ. Miyazaki)

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419 Genome editing of *CAD* gene involved in lignin biosynthesis in bahiagrass−Production and characterization of homozygous populations of *CAD* mutant loci−

☆Watajima, A.[1], T. Gondo[2], R. Akashi[3] (1.Grad. Sch. Agr., Univ. Miyazaki, 2.Frontier Science Research Center, Univ. Miyazaki, 3.Univ. Miyazaki)

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420 Loss-of-function mutation in rice heterotrimeric G protein γ2 subunit induces seedling lethality

☆CHAYA, G.[1,2], M. Fujita[1], Y. Iwasaki[1], K. Miura[1] (1.Dep.Biosci.,Fukui Pref. Univ., 2.Fukui Agr. Exp. Stn.)

421 Construction of the ancestral tobacco species *Nicotiana sylvestris* mutant library

○Takakura, Y.[1], H. Udagawa[1], H. Magome[1], T. Takeuchi[1,2], M. Arai[1], T. Tajima[1] (1.JAPAN TOBACCO INC. Leaf Tobacco Research Center, 2.Grad. Sch. Agr., Kyoto U.)

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422 Forward genetics using the *Nicotiana sylvestris* mutant library: Low alkaloid mutants and identification of their responsible genes

○TAKEUCHI, T.[1,2], M. Arai[1], H. Udagawa[1], H. Magome[1], Y. Takakura[1] (1.JAPAN TOBACCO INC. Leaf Tobacco Research Center, 2.Grad. Sch. Agr., Kyoto U.)

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423 Reverse genetics using the *Nicotiana sylvestris* mutant library: *carotenoid cleavage dioxygenase 4* mutants and its characteristics

○Magome, H., M. Arai, K. Oyama, H. Udagawa, Y. Takakura (JT : JAPAN TOBACCO INC. Leaf Tobacco Research Center)

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424 Remarkable differences in chromosomal mutation rates among wild relatives of the genus *Nicotiana*

☆Nakata, K., M. Kanekatsu, T. Yamada (United Grad. Sch. Agr. Tokyo U. Agr. Tech.)

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501 Identification of a post-invasive resistance locus against powdery mildew in the wild relative *Aegilops umbellulata* Zhuk.

☆Kawamura, R.[1], M. Okada[2,3,4], S. Komura[1], K. Shimizu[4,5], K. Nishimura[6], Y. Inoue[1], K. Yoshida[1] (1.Grad. Sch. Agr., Kyoto U., 2.Grad. Sch. Agr., Kobe U., 3.Grad. Sch. Sci. Tech., Niigata U., 4.KIBR, YCU, 5.IEU, UZH, 6.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama U.)

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502 Cloning of *Rmg8*, a gene for resistance to the wheat blast fungus in hexaploid wheat.

☆Asuke, S.[1], K. Morita[1], M. Shimizu[2], F. Abe[3], C. Nago[1], Y. Takahashi[1], M. Shibata[1], M. Yoshioka[1], R. Terauchi[2], Y. Tosa[1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.NICS, NARO, 3.Iwate Biotechnol. Res. Ctr.)

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503 Search for wheat blast resistance genes in Japanese wheat accessions.

☆Sota, K.[1], S. Asuke[2], M. Yoshioka[2], Y. Tosa[2], H. Handa[3] (1.Fac. Life Envi. Sci., Kyoto Pref. Univ., 2.Grad. Sch. Agr. Sci., Kobe Univ ., 3.Grad. Sch. Life Envi. Sci., Kyoto Pref.

Univ.)

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504 Isolation of factors determining host specificity between wheat blast isolate and rice

○Shimizu, M.[1], S. Asuke[2], A. Abe[1], Y. Tosa[2], R. Terauchi[1,3] (1.IBRC, 2.Grad. Sch. Agri. Sci., Univ. Kobe, 3.Grad. Sch. Agri., Univ. Kyoto)

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505 Identification of *OsHIPP20*, a rice susceptibility gene (*S-gene*) against blast fungus

☆Oikawa, K.[1], M. Shimizu[1], N. Miyaji[1], T. Takeda[1], K. Fujisaki[1], R. Terauchi[1,2] (1.IBRC, 2.Grad. Sch. Agri., Univ. Kyoto)

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506 Evaluation of stem resistance to foot rot in genetic resources, cultivars, F_1 and S_1 plants of sweetpotato.

○Tabuchi, H., M. Tanaka, E. Haque, A. Kobayashi, T. Sakaigaichi, K. Suematsu, Y. Kawata, Y. O. Kobayashi (Kyushu Okinawa Agricultural Research Center, NARO)

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507 Development of DNA markers for Fusarium stem rot resistance in sweetpotato developed by polyploid QTL-seq

○Yamakawa, H.[1], T. Mizubayashi[1], M. Tanaka[2], S. Shimada[3], T. Kuranouchi[1], M. Nishinaka[4] (1.NICS, NARO, 2.KARC, NARO, 3.Ibaraki Agric. Center, 4.CARC, NARO)

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508 Refinement of white rust resistance gene loci in *Brassica* vegetables

☆Miyaji, N.[1,2], M. Akter[1], M. Shimizu[2], I. Chuma[3], R. Fujimoto[1] (1.Grad. Sch. Agri., Kobe Univ., 2.IBRC, 3.Obihiro Univ. Agri. Vet. Med.)

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509 Diversity of the secondary aerenchyma formation in the mini-core collections of soybean

☆Suzumura, R.[1], M. Goto[2], A. Kaga[3], H. Iwata[4], A. Agata[1], M. Nakazono[1], H. Takahashi[1] (1.Grad. Sch. Bioagric. Sci. Nagoya Univ., 2.Fac. Agric. Nagoya Univ., 3.NARO, 4.Grad. Sch. Agribio. Sci. Tokyo Univ.)

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510 Investigation of response of *Brassica napus* to root oxygen deficiency

○Shinozawa, A.[1], H. Takahashi[2], M. Nakazono[2], T. Matsumoto[1], K. Izawa[1], S. Nakamura[1] (1.Dept. Bioscience, Tokyo Univ. Agric., 2.Grad. Sch. Bioagric. Sci., Univ. Nagoya)

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511 Cytokinin is essential for exodermal suberization to form a barrier to radial oxygen loss in rice (*Oryza sativa*)

○Shiono, K.[1], K. Shimizu[1], A. Ishikawa[1,2], M. Ejiri[1], K. Ogata[3], T. Yamamoto[3], S. Tira[4] (1.Dept. Biosci. Biotech., Fukui Pref. Univ., 2.Grad. Sch. Life Sci., Tohoku Univ., 3.Shimadzu Corporation, 4.Fact. Food Agr. Sci., Fukushima Univ.)

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512 Study on requirements for gametophore differentiation from protonemata in *Racomitrium japonicum*

○Yoda, Y.[1], Y. Takahara[2] (1.Grad. Sch. Bio., Nagaoka Univ. Tech., 2.Bio., Nagaoka Univ. Tech.)

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513 Genetic factors causing differences in rice anther culture efficiency between Japonica and Indica cultivars

☆Kudo, N.[1], E. Balimponya[1], Y. Okamoto[2], Y. Kishima[1] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Rakuno Gakuen Univ.)

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514 Development of Agrobacterium-mediated transformation method using matured seeds of pearl millet.

☆Aoki, R.[1], T. Ishii[2], K. Yoshida[1] (1.Grad. Sch. Agr. Sci., Kyoto U., 2.ALRC, Tottori U.)

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515 Linkage analysis of a gene controlling segregation distortion in the cross between Asian cultivated rice and Australian wild rice

☆Shibata, Y.[1], K. Katano[2], R. Takahashi[1], Y. Maeda[1], S. Taura[3], R. Henry[4], R. Ishikawa[5], K. Ichitani[6] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.Takii & Co., LTD., 3.Inst. Gene Res., Kagoshima Univ., 4.Univ. of Queensland, 5.Fac. Agr. and Life Sci., Hirosaki Univ., 6.Fac. Agr., Kagoshima Univ.)

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516 Production of hybrids between bread wheat and 33 lines of *Aegilops umbellulata* Zhuk. for wild wheat prebreeding.

☆Son, I.[1], N. Kasazumi[1], M. Okada[2], K. Yoshida[3], Y. Matsuoka[1] (1.Grad. Sch. Agr. Sci., Kobe U., 2.Grad. Sch. Sci. Tech., Niigata U., 3.Grad. Sch. Agr., Kyoto U.)

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517 Identifying causal loci of the hybrid necrosis between the $A^uA^uBBA^mA^m$ synthetic hexaploids and common wheat.

☆Yoden, Y.[1], S. Noguchi[2], S. Komura[3], K. Murata[3], M. Okada[2,4,5], N. Mizuno[6], F. Kobayashi[6], K. Nishimura[7], Y. Inoue[3], S. Nasuda[3], Y. Matsuoka[2], K. Yoshida[3] (1.Fac. Agr., Kyoto U., 2.Grad. Sch. Agr. Sci., Kobe U., 3.Grad. Sch. Agr., Kyoto U., 4.Grad. Sch. Sci. Tech., Niigata U., 5.KIBR, YCU, 6.NICS, NARO, 7.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama U.)

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518 Alien chromosome fragment introgression to *Triticum aestivum* L. using *Pairing homoeologous 2* deletion lines

☆Tabuchi, M.[1], M. Okada[2,3,4], A. Michikawa[2], Y. Inoue[1], K. Nishimura[5], N. Mizuno[6], K. Shimizu[4,7], F. Kobayashi[6], S. Takumi[2], K. Yoshida[1] (1.Grad. Sch. Agr., Kyoto U., 2.Grad. Sch. Agr., Kobe U., 3.Grad. Sch. Sci. Tech., Niigata U., 4.KIBR, YCU, 5.Grad. Sch. Environ. Life Nat. Sci. and Tech., Okayama U., 6.NICS, 7.IEU, UZH)

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519 How the HS-genes in tetraploid hybrid between Asian and African rice work

☆Kuniyoshi, D.[1,2], M. Ishihara[2], Y. Sato[3], Y. Kishima[2] (1.Tropical Agriculture Research Front, JIRCAS, 2.Grad. Sch. Agr., Univ. Hokkaido, 3.Hokkaido Agricultural Research Center, NARO)

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520 Genomic regions of improvement of seed and pollen fertility in interspecific hybrid tetraploid rice between *O. sativa* and *O. glaberrima*

☆Oka, T.[1], T. Furuta[1], K. Kashihara[1], H. Mu[1], Y. Kishima[2], K. Nagaki[1], T. Yamamoto[1] (1.IPSR, Grad. Sch. Environ. Life Sci., Okayama Univ., 2.Grad. Sch. Agr., Hokkaido Univ.)

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521 Duplication of the *S* locus may be involved in the self-compatibility of *Lycium sandwicense*

☆Ikebe, K., H. Sassa (Grad. Sch. Hort., Chiba Univ.)

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522 Dominance-relationships on pollen-side among six class-II *S* haplotypes in radish self-incompatibility show linearity including two most recessive *S* haplotypes.

☆Yamashita, M., T. Ishii, M. Yamamoto, H. Kitashiba (Grad. Sch. Agric. Sci., Tohoku Univ.)

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523 Most of loss-of-function mutations in the receptor domain of *A. lyrata* SRKb, which functions in self-incompatibility, are caused by conformational instability

○Yamamoto, M.[1], S. Ohtake[1], A. Sinosawa[2], M. Shirota[4], Y. Mitsui[3], H. Kitashiba[1] (1.Grad. Sch. of Agri., Tohoku Univ., 2.NODAI Genome Research Center, Tokyo Univ. of

Agri., 3.Grad. Sch. of Agri., Tokyo Univ. of Agri., 4.Grad. Sch. of Med., Tohoku Univ.)

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524 Breaking down reproductive isolation in *Oryza sativa* × *O. australiensis* hybrid endosperm by H3K27me3 level modification.

☆Kurosaka, E.[1], R. Nakayama[1], H. Furuumi[2], Y. Sato[2], T. Kinoshita[3], K. Hatakeyama[1], K. Tonosaki[3] (1.Fac. Agri., Iwate Univ., 2.Natl. Inst. Genet., 3.KIBR, Yokohama City Univ.)

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601 Assessing and reducing the impact of genomic prediction accuracy on breeding programs

☆Hamazaki, K.[1], H. Iwata[2], K. Tsuda[1,3] (1.Adv. Int. Proj., RIKEN, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Grad. Sch. Fro. Sci., Univ. Tokyo)

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602 Estimating the increase of genetic diversity through inter-family crosses

☆Kinoshita, S.[1], K. Sakurai[1], K. Hamazaki[2], T. Tsusaka[3], M. Sakurai[3], T. Kurosawa[3], K. Shirasawa[4], S. Isobe[4], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Adv. Int. Proj., RIKEN, 3.TSUMURA & CO., 4.Kazusa DNA Res. Inst.)

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603 Proposing optimal combinations of genotype and environment using batch Bayesian optimization

☆Mochizuki, H.[1], K. Hamazaki[2], C. Sato[3], A. Abe[4], C. Kim[5,6], H. Shimono[5], H. Iwata[1] (1.Grad. Sch. Agr. Life Sci., Univ., 2.Adv. Int. Proj., RIKEN, 3.Ifu-Rinrin, 4.Iwate Biotechnology Research Center, 5.Iwate University, 6.Sky Ocean Technology Co., Ltd.)

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604 Interactive Data Driven Breeding Platform (DDB) for GS, GWAS and Crossing Simulation

○Honda, K.[1], J. Diot[1], S. Honda[1], J. Pineda[1], J. Jennings[1], H. Iwata[2], S. Isobe[3], M. Minamikawa[2,4] (1.ListenField Inc., 2.Gard. Sch. Agr. Life Sci., Univ. Tokyo, 3.Kazusa DNA Research Inst., 4.IAAR, Chiba Univ.)

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605 Developing a genomic prediction model incorporating spatial effects for nationwide rice data

☆Taniguchi, S.[1], T. Hayashi[1], N. Hiroshi[1], K. Matsushita[2], H. Kajiya-Kanegae[1], M. Yano[1], J. Yonemaru[1,2], A. Goto[1,2] (1.Res. Cent. Agric. Info. Tech., NARO, 2.Inst. Crop Sci., NARO)

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606 Search for genes related to flowering in soybean and construction of a developmental prediction model based on this genetic information.

☆Mori, T.[1], K. Nishimura[2], S. Nakano[3], H. Kokaji[4], K. Motoki[2], E. Kumagai[3], A. Kaga[3], H. Iwata[5], Y. Iwahashi[1], K. Nagasaka[1], K. Murata[1], Y. Kinoshita[1], T. Maki[1], H. Inoue[1], R. Nakano[1], H. Nakagawa[3], T. Nakazaki[1] (1.Grad. Sch. Agr., Kyoto Univ., 2.Grad. Sch. Environ. Life. Sci. and Tech., Okayama Univ., 3.NARO, 4.GRA &GREEN Inc., 5.Grad. Sch. Agr. Life Sci., Univ. Tokyo.)

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607 Image Selection of Potted seedling from Strawberry Crossbreeding seedling through Machine Learning

○Yamada, H., T. Kawata, S. Mochizuki (Shizuoka Pref. Res. Inst. Agri. Forest . Station)

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608 Four-dimensional measurement of crop root systems using X-ray CT with backward prediction

○Teramoto, S., Y. Uga (Inst. Crop. Sci., NARO)

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609 Effects of the sucrose concentrations and incubation periods on in vitro pollen germination and pollen tube growth in three rice cultivars

☆Yohana, N.[1], A. Nakano[2], Y. Kishima[3], Y. Hoshino[1,2] (1.Division of Biosphere, Graduate School of Environmental Science, Hokkaido University, 2.Field Science Center for Northern Biosphere, Division of Biosphere, Graduate School of Environmental Science, Hokkaido University, 3.Division of Plant Breeding, Graduate School of Agriculture, Hokkaido University)

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610 Relationship between strawberry fruit firmness and polygalacturonase gene expression

○ASAO, H., S. ASANO, T. NISHIMOTO, H. YASUKAWA, K. MINE (Nara Pre. Agri. Res. Cen.)

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611 Chemical emasculation of cowpea and model plants

☆Sekiguchi, Y.[1], B. Ubi[2,3], T. Ishii[1,3] (1.Grad. Sch. Sustainability Sci. Tottori Univ., 2.Department of Biotechnology, Ebonyi State Univ., 3.Arid Land Research Center, Tottori Univ.)

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612 Development of Near-isogenic lines (NILs) with genetic background of ‘Nihonbare’ for development of rice version of ‘Micro-Tom’

○Tanaka, J.[1,2], Y. Taniguchi[2] (1.NARO, 2.Inst. Crop. Sci., NARO)

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613 Breeding of a new adzuki bean cultivar "Toiku180" with low harvesting losses by combine harvesters

☆Nagasawa, H.[1], Y. Horiuchi[1], K. Nakagawa[1], H. Sato[1], M. Okuyama[1], H. Sato[2], S. Hagihara[1], N. Yamaguchi[2], H. Kosaka[2], A. Tazawa[3], N. Murata[1] (1.Hokkaido Research Organization Tokachi Agricultural Experiment Station, 2.HRO Central agri. Exp. stn., 3.HRO Kitami agri. Exp. stn.)

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614 Breeding of Miyazaki Prefctural original squash [Hyuga Kabocha] - A F_1 new line achieved by varities' crosing

○Chen, L.[1,2], T. Hori[1], S. Joukan[1], K. Yoshimura[2], M. Matsuse[1], T. Naruki[1], R. Kubota[1] (1.Fac. Environ. Hirt., Minami Kyusyu U., 2.Grad. Sch. Hort. Food Sci., Minami Kyusyu U.)

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615 Pollinator lines of hybrid wheat utilizing photoperiod-sensitive cytoplasmic male sterility

○Murai, K.[1], H. Tada[1], Y. Takenouchi[2] (1.Dep. Sus. Agri., Fukui Pref. U., 2.HOKUREN)

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616 Evaluation of varieties in the production field using molecular markers capable of classifying Zoysiagrass

○Tanaka, H.[1], Y. Uozumi[2], S. Yamada[2] (1.Fac. Agr., Tottori Univ., 2.Chubu Co., Ltd.)

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617 Trend of the use of silkworm genetic resources in the Genebank Program, NARO

○SHIBATA, S. (Research Center of Genetic Resources, NARO)

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618 Genome-wide association study for plant architecture of *Amaranthus tricolor* genetic resource

☆Hoshiakwa, K.[1,2], Y. Lin[2], Y. Yoshioka[3], H. Okubo[4], R. Schafleitner[2], K. Shirasawa[5], S. Isobe[5] (1.JIRCAS, 2.World Vegetable Center, 3.Inst. Life Environ. Sci., Univ. Tsukuba, 4.Grad. Sch. Sci. Tech., Univ. Tsukuba, 5.Kazusa DNA Res. Inst.)

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619 Evaluation of tocopherol composition of a subset of soybean world minicore collection grown in Hokkaido

○Dwiyanti, M.[1], F. Aurelia[2], S. Christin[1] (1.Res. Fac. Agr., Hokkaido Univ., 2.Swiss German Univ.,)

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620 Genetic structure analysis of 2500 tea germplasm in Shizuoka prefecture

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621 Phylogenetic analysis of edible yams in Japan using genome-wide SNPs

☆Minoji, K.[1], A. Ohta[1], Y. Sugihara[2], A. Kudoh[1], T. Sakai[1], R. Terauchi[1,3] (1.Grad. Sch. Agr., Kyoto Univ., 2.The Sainsbury Laboratory, 3.Iwate Biotechnology Research Center)

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622 Comparative plastid genome analysis of *Hippophae* species

○Asakura, N.[1], Y. Takahashi[2], M. Noda[2], S. Ueno[2], N. Arai[1], Y. Kawai[3] (1.Fac. Chem and Biochem, Kanagawa Univ., 2.Fac. Engin, Kanagawa Univ., 3.Fac. Agr, Tokyo Univ. of Agriculture)

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623 The source of the *Ppo-A1* null allele in Japanese wheat varieties

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624 A high-throughput phenotyping of the hexaploid wheat NAM population during tillering stage by UAVs and their correlation with yield-related traits.

☆Yoshioka, S.[1], K. Kuroki[1,2], M. Nitta[1], J. Nie[1], M. Ishii[3], H. Kakui[1,3], M. Okada[4,5,7], S. Takenaka[6], K. Simizu[4,5], H. Iwata[3], G. Wei[3], S. Nasuda[1] (1.Grad. Sch. Agri., Kyoto Univ., 2.Grad. Sch. Sci., Univ. Tokyo, 3.Grad. Sch. Agri and Life Sci., Univ. Tokyo, 4.Kihara Inst. of Biol., Yokohama City Univ., 5.Dept. of Evo. Biol. and Env. Studies, Univ. Zurich, 6.Fac. Agri., Ryukoku Univ., 7.Grad. Sch. Sci. Tech., Niigata U.)

Poster Presentations

P001 Validation of QTL and epistatic QTL mapping using SHAP

☆Ishibashi, T., A. Onogi (Faculty of Agr., Ryukoku Univ.)

P002 Establishment of speed breeding method for rapids production of interspecific *Pennisetum* hybrids

☆Terada, K.[1], T. Ishii[2], S. Sakuma[3] (1.Grad. Sch. of Sustainability Sci., Univ.Tottori, 2.Arid Land Research Center., Univ.Tottori , 3.Agri., Univ.Tottori)

P003 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)

P004 Utilizing gibberellin treatment for scion elongation in Brassicaceae Plant grafting techniques

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

P005 Relationship between relative illuminance and yield using soybean lines derived from Japanese-American hybridization.

○Yamada, T.[1], A. Onogi[2], K. Hirata[1], A. Hishinuma[3], K. Takahashi[1], Y. Nanjo[1], J. Yonemaru[4] (1.Inst. Crop. Sci., NARO, 2.Fac. Agric., Ryukoku Univ., 3.Tohoku Agric. Res. Cent., NARO, 4.Res. Cent. Agric. Info. Tech., NARO)

P006 Fusion of UAV remote sensing data and hand-measured data based on a nonlinear growth model

☆Fukumoto, Y.[1], T. Chen[2,8], ユ. トダ[2], Y. Oomori[2], Y. Yamasaki[3], H. Takahashi[4], H. Takanashi[2], M. Tsuda[5], M. Hirai[6], H. Tsujimoto[3], A. Kaga[7], M. Nakazono[4], T. Fujiwara[2], H. Iwata[2] (1.Fac. Agr., Univ. of Tokyo, 2.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 3.Arid Land Res. Ctr., Tottori Univ., 4.Grad. Sch. Bioagri. Sci., Nagoya Univ., 5.T-PIRC, Univ. Tsukuba, 6.Ctr. for Sustainable Resource Sci., RIKEN, 7.Inst. Crop Sci., NARO, 8.Inst. Vegetable and Floriculture Sci., NARO)

P007 Exploration of environments for evaluating traits of high-yielding rice cultivars using growth chambers.

☆Wada, K., H. Yamashita, J. Yonemaru, H. Itoh (Inst. Crop. Sci., NARO)

P008 Breeding new strawberry varieties "oonoaguri81ou18-166" and "oonoaguri81ou18-547" for fresh eating with large and high yields.

○Tamaki, M., M. Morino, R. Tamaki, S. Sano, W. Hashimoto (Oono Development Co., Ltd.)

P009 Establishment of an ovule culture system to enhance the utilization of cowpea genetic resources via wide crosses

☆OFEM, N. (Grad. Sch. of Sus. Sci., Tottori University)

P010 Soybean cultivar "Sumisayaka" for soymilk.

○Takada, Y., K. Komatsu, T. Sayama, K. Yamashita, M. Saruta (WARC, NARO)

P011 Metaborome analysis in *Leymus racemosus* addition lines of common wheat

☆Ono, T.[1], M. Kishii[2], M. Hirai[3], H. Tsujimoto[4], M. Okamoto[1,3,5] (1.Univ. Utsunomiya, 2.JIRCAS, 3.CSRS., RIKEN, 4.Univ. Tottori, 5.Univ. Yokohama City)

P012 RE:phenotyping analysis of visible characteristics from the large mutant pools of the NBRP-Tomato.

○Sugimoto, K., Y. Fujimori, T. Ariizumi, H. Ezura (Univ. Tsukuba, T-PIRC)

P013 Project on Prof. Masatake Tanaka's archival materials and links to wheat genetic resources

○Ohta, A.[1,2], M. Nitta[1,2], A. Saito[3], M. Hirazawa[3], Y. Matsuoka[4], K. Kawaura[5], S. Ohta[6], Y. Ishikawa[1], K. Yoshida[1,2], S. Nasuda[1,2], R. Terauchi[1,2] (1.Grad. Sch. Agri., Kyoto Univ., 2.NBRP-Wheat, 3.Kyoto Univ. Museum, 4.Grad. Schl. Agri. Sci., Kobe Univ., 5.KIBR, Yokohama City Univ., 6.Professor emeritus, Fukui Pref. Univ.)

P014 Gene structure analysis of the *Puroindoline* gene in hard grain mutants of the bread wheat cultivar "Fukui-kendai3(Fukukomugi)"produced by heavy ion-beam

☆Fueki, R.[1], M. Hatashita[2], K. Murai[1] (1.Grad.Sch.Biosci.Biotech.,Fukui Pref. Univ, 2.Wakasa Wan Energy Research Center)

P015 System to 'back up' biological resources in IBBP center

○Tsugane, K., A. Kato, N. Matsubayashi, C. Tsuzuki, A. Hamatani, K. Naruse (National Institute for Basic Biology, IBBPセンター)

P016 QTL analysis of fruit morphology and sex expression in a population between two varieties in melon

☆Nashiki, A.[1], H. Matsuo[1], K. Takano[1], S. Isobe[2], K. Shirasawa[2], Y. Yoshioka[3] (1.Grad. Sch. Science & Tech., Univ. Tsukuba, 2.Kazusa DNA Research Institute, 3.Inst. Life Env. Sci., Univ. Tsukuba)

P017 The geographic distribution of *WAPO-A1* genotypes controlling spikelet number per spike and *GNI-A1* genotypes controlling floret fertility in wheat.

☆Kasama, M., K. Takahashi, K. Tanaka, M. Kawase, Z. Nishio (Grad. Sch. Agr., Tokyo Univ. Agr)

P018 Dough Property and Protein Composition of "Tousan 57" and "Tousan 62", Successor Candidate Lines of Wheat for Hard Bread "Yumekaori"

☆Nakazawa, R.[1], T. Ikeda[2], H. Maezima[1] (1.Agri. Exp. Sta., Nagano. Pref, 2.WARC., NARO)

P019 Effect of red pericarp extract on anti-bacterial ability in wild rice (*Oryza rufipogon*)

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

P020 Genetic analysis of foxtail millet leaf sheath pigmentation and geographic distribution of its variants

☆Tsuji, M.[1], S. Matsuyama[2], K. Itou[3], K. Oikawa[3], A. Abe[3], K. Fukunaga[1] (1.Grad. Sch. Arts and Sci., Pref. Univ. Hiroshima, 2.Life and Envi. Sci., Pref. Univ. Hiroshima, 3.Iwate Biotech. Res. Center)

P021 Genetic analysis of domestication-associated traits of spike and plant type using backcross derived lines in emmer wheat.

☆Morioka, M.[1], S. Kasubuchi[1], S. Shimada[1], K. Gyu[1], C. Vladutu[1], S. Kianian[2], N. Mori[1] (1.Grad. Sch. Agr. Sci., Kobe U., 2.USDA-ARS, Univ. Minnesota, U.S.A)

P022 Estimation of a novel locus associated with seed-shattering degree in African cultivated rice, *Oryza glaberrima*

☆Yamazaki, M.[1], A. Maeda[1], S. Lim[1], T. Ishii[1], Y. Yamagata[2], Y. Koide[3], D. Fujita[4], R. Ishikawa[1] (1.Grad. Sch., Agr. Sci., Kobe Univ., 2.Fac. Agr. Grad. Sch., Kyushu Univ.,

3.Grad. Sch. Agr., Hokkaido Univ., 4.Fac. Agr., Saga Univ.)

P023 A mutant line with lower pasting temperature of endosperm starch than the rice variety “Ichihomare”.

☆Nakaoka, F.[1,2], A. Kobayashi[1], S. Watanabe[1], Y. Morozumi[1], Y. Machida[1], G. Chaya[1], K. Miura[3], M. Yamasaki[2] (1.Fukui Agr. Exp. Stn., 2.Niigata Univ., 3.Fukui Pref. Univ.)

P024 Evaluation of basic morphological characters and variation analysis of red pigment synthesis gene in safflower genetic resources

☆Hosono, K.[1], H. Suzuki[2], S. Kimura[2], T. Sasanuma[1,2] (1.Grad. Sch. Agr., Yamagata Univ., 2.Fac. Agr., Yamagata Univ.)

P025 Genetic analysis of yield-related traits on the long arm of chromosome 4 derived from *Oryza longistaminata*

○Hirabayashi, H.[1], K. Matsubara[1], S. Fukuoka[1,2], Y. Takeuchi[1], K. Sugimoto[1] (1.Inst. of Crop Sci., NARO, 2.Core Technology Research Headquarters, NARO)

P026 Using next-generation sequencing to identify homoeologous recombination sites in Brassica napus.

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

P027 Whole genome sequence comparison between three wild soybeans from Japan against reference genomes Williams 82(*Glycine max*) and W05(*G. soja*)

☆Nishimura Carmo, E.[1], M. Dwiyanti[2] (1.Hokkaido University, Grad. Sch. Agr., 2.Hokkaido University, Res. Fac. Agr.)

P028 The development and efficient utilization of molecular markers for the major quantitative trait locus of bacterial wilt resistance in potato

○Habe, I., Y. Sakamoto, K. Matsumoto (Nagasaki Agri. Fore. Tech. Dev. Ctr.)

P029 Development of a rapid and simple protocol for construction of MIG-seq library using unpurified DNA

☆Nishimura, K.[1], K. Motoki[1], K. Nagasaka[2], R. Takisawa[3], Y. Chang[2], T. Mori[2], R. Nakano[2], T. Nakazaki[2] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama Univ., 2.Grad.

Sch. Agr., Kyoto Univ., 3.Fac. Agr., Ryukoku Univ.)

P030 Development of imputation and correction algorithms for marker genotype data using graph theory and hidden Markov models

○Inamori, M.[1], M. Minamikawa[1,2], T. Shimizu[3], M. Kunihisa[3], K. Nonaka[3], S. Moriya[3], K. Abe[3], H. Iwata[1] (1.The University of Tokyo, Graduate School of Agricultural and Life Sciences, 2.Chiba University, Institute for Advanced Academic Research, 3.National Agriculture and Food Research Organization, Institute of Fruit Tree and Tea Science)

P031 Genome-wide association study for strawberry anthracnose resistance using multiple isolated populations and validation of SNP markers

○Taguchi, M.[1], Y. Kashiwaya[1], S. Yasuno[1,2], T. Abe[1,3], A. Toyoda[1], T. Shigeno[1,4], Y. Nakazawa[1,5] (1.Tochigi Pref. Agric. Exp. Stn., 2.Haga Agric. Promotion Office, 3.Tochigi Agric. Prod. Mktg. Assoc., 4.Tochigi Pref. Govt. Mgm. Technol. Dept, 5.Shimotsuga Agric. Promotion Office)

P032 Development of Recombinant Inbred Lines （RILs）and construction of a linkage mapping between *Setaria italica* and *S. viridis* using GRAS-Di technology

☆Watanabe, I.[1], S. Nakamura[2], Y. Monden[3], K. Fukunaga[1] (1.Fac. Biores. Sci., Pref. U. Hiroshima, 2.Sch. Agr., Okayama U., 3.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P033 Phenotypic evaluation and genetic mapping of seminal root angle in the Japanese Wheat Core Collection

☆Nakano, Y.[1], K. Nishimura[2], R. Nishijima[1] (1.Facul. Biosci. Biotech., Fukui Pref. U., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P034 Mutant alleles of *Tof11* are frequently detected in early-planting adaptable Japanese summer type soybeans

○Komatsu, K., T. Sayama, K. Yamashita, Y. Takada (Western Region Agricultural Research Center, NARO)

P035 Identification of QTLs for grain yield-related traits using three connected segregating mapping populations of tetraploid wheat (*Triticum turgidum* L.)

☆Chen, T.[1], K. Nishimura[2], K. Nagasaka[1], Y. Iwahashi[1], K. Murata[1], T. Maki[1], Y. Kinoshita[1], H. Inoue[1], R. Nakano[1], T. Nakazaki[1] (1.Grad. Sch. Agr., Kyoto Univ, 2.Grad.

Sch. Environ. Life Nat. Sci. and Tech., Okayama Univ.)

P036 Simultaneous selection for multiple fruit traits using genomic selection and GWAS in strawberry.

○Toyoda, A.[1], Y. Kashiwaya[1], Y. Matsushima[1], S. Yasuno[1,2], A. Inaba[1], S. Isobe[3], K. Shirasawa[3], M. Sato[3], E. Yamamoto[3], K. Tasaki[1], K. Iimura[1,4], T. Shigeno[1,5], Y. Nakazawa[1,4] (1.Tochigi Pref.Agric.Exp.Stn, 2.Haga Agric. Promotion Office, 3.Kazusa DNA Res. Inst., 4.Shimotsuga Agric. Promotion Office, 5.Agricultural Management Division)

P037 Exploration of genes responsible for monogerm seeds by genome wide association study (GWAS) in Japanese sugar beet (*Beta vulgaris* L.).

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

P038 Consideration of using modified MIG-seq and re-evaluation of ethylene synthesis lelated loci in melon

○Kageyama, R.[1], K. Nishimura[1], R. Nakano[2], K. Ikeda[3], K. Kato[1], Y. Kubo[1], T. Akagi[1], K. Ushijima[1] (1.Grad. Sch. Environ. Life Nat. Sci. Tech., Univ. Okayama, 2.Grad. Sch. Agr., Univ. Kyoto, 3.Fac. Agr., Univ. Yamagata)

P039 Re-sequencing analysis of genes involved in specialized metabolisms in tea cultivars.

☆Funakawa, N.[1], H. Yamashita[2,3], Y. Ishiguro[1], J. Kawaki[4], T. Ikka[2,3,5] (1.Grad. Agr., Univ. Shizuoka, 2.Fac. Agr., Univ. Shizuoka, 3.Shizuoka Univ. Res. Inst. Tea Sci., 4.Shizuoka Tea Res. Cent., 5.Shizuoka Univ. Res. Inst. Green Sci. Tech.)

P040 Development of high-quality/yield DNA extraction methods adaptable to long-read sequencing from crop seeds

☆Shioya, N.[1], E. Ogiso-Tanaka[2], M. Watanabe[1], T. Anai[3], T. Hoshino[1] (1.Grad. Sch. Agr., Yamgata Univ., 2.Ctr. Mol. Biodivers. Res., Natl. Mus. Nat. Sci., 3.Grad. Sch. Agri., Kyusyu Univ.)

P041 Enhancing alignment accuracy in RNA-seq analysis for allopolyploid plants

☆Saiga, S., T. Segawa, R. Kumazawa, M. Hara, M. Yoshizumi, K. Fukuoka, H. Takagi (Ishikawa Prefectural University)

P042 Gene identification and characterization of days to heading in mutant lines of glutinous rice variety “Hiyokumochi” (*Oryza sativa* L.)

☆YA, M.[1], T. ANAI[2], S. Zheng[1], D. Fujita[1] (1.Grad. Sch. Agr., Saga Univ., 2.Grad. Sch. Agr., Kyushu Univ.)

P043 Dosage effect and heterosis of QTLs predicted by GWAS of segregation progenies from interspecific hybrid tetraploid rice

Oka, T.[1], T. Furuta[1], H. Mu[1], K. Kashihara[1], K. Nagaki[1], Y. Kishima[2], ○T. Yamamoto[1] (1.IPSR, Grad. Sch. Environ. Life Sci., Okayama Univ., 2.Grad. Sch. Agr., Hokkaido Univ.)

P044 Comparison of gene expression profiles between interspecific tetraploid rice and its cultivated rice parents

☆MU, H.[1], T. Furuta[1], T. Oka[1], K. Nagaki[1], Y. Kishima[2], T. Yamamoto[1] (1.IPSR, Grad. Sch. Environ. Life Sci., Okayama Univ., 2.Grad. Sch. Agr., Hokkaido Univ.)

P045 Transcriptome analysis to elucidate the high sugar content of sorghum juice using multiple reference genome sequences.

☆Okada, S.[1], M. Ikezaki[2], S. Hashimoto[3,4], T. Kikuchi[2], S. Araki-Nakamura[1], K. Ohmae-Shinohara[1], T. Sazuka[1] (1.Biosci. and Biotech. Center, Nagoya Univ., 2.Grad. Sch. Bioagri., Nagoya Univ., 3.Grad. Sch. Agric. Life Sci., U. Tokyo, 4.JSPS Research Fellowship for Young Scientists PD)

P046 Ectopic expression of a phosphate transporter gene improves phosphate absorption and utilization efficiency of plants?

○Tada, Y., Y. Noike, A. Shimizu (Sch. Biosci. Biosci., Tokyo Univ. Technol.)

P047 Characterization of callus types and establishment of the efficient tissue culture system in *Echinochloa phyllopogon*

○Gondo, T.[1], M. Sugahara[2], S. Iwakami[3] (1.FSRC, Univ. Miyazaki, 2.Grad. Sch. Agr., Univ. Miyazaki, 3.Grad. Sch. Agr., Kyoto Univ.)

P048 Development of novel evergreen zoysiagrass variety via genome editing: Production and evaluation of *NYC1*-knockout *Zoysia matrella*

☆Ng, H.[1], M. Hirata[2], T. Gondo[3], R. Akashi[4] (1.Interdiscip. Grad. Sch. Agr. & Engr., Univ. Miyazaki, 2.Grad. Sch. Agr., Univ. Miyazaki, 3.FSRC, Univ. Miyazaki, 4.Univ. Miyazaki)

P049 Genetic characterization of re-differentiated genome-edited potato

○Endo, A.[1], S. Yasumoto[2], H. Sasaki[3], T. Igarashi[3], N. Umemoto[4], T. Muranaka[2], M. Mori[3], T. Yamada[1] (1.Grad. Sch. Agric., Hokkaido Univ., 2.Grad. Sch. Eng., Osaka Univ., 3.Calbee Potato, Inc., 4.CSRS, RIKEN)

P050 An attempt of the multiplex gene editing in rice

○Saika, H.[1], K. Negishi[1,2], H. Kaya[1,3], M. Endo[1], S. Toki[1,4,5,6] (1.Institute of Agrobiological Sciences, NARO, 2.Present; Institute of Fruit Tree and Tea Science, NARO, 3.Present; Fac. Agr., Ehime Univ., 4.Grad. Sch. Nanobio., Yokohama City Univ., 5.KIBR, Yokohama City Univ., 6.Fac. Agr., Ryukoku Univ.)

P051 Attempts to create novel cleistogamous rice by amino acid substitution genome editing technology

☆Nozaka, A., T. Kuroha, M. Kimizu, S. Chechetka, H. Yoshida (National Agriculture and Food Research Organization, NARO)

P052 Studies on the male sterility and abnormal floral organs observed in the BC3 line of a mutable tobacco plant.

☆Hanamoto, S.[1], T. Terachi[2], M. Nishimoto[2], H. Terada[2] (1.Grad. Sch. Life Sci., Kyoto Sangyo Univ., 2.Fac. Life Sci., Kyoto Sangyo Univ.)

P053 Whole-genome sequence analysis of neutron-irradiated rice in the M2 generation using the J-PARC accelerator

☆Kojima, K.[1], K. Ishibasi[2], N. Kikuchi[2], T. Kohzuma[3], A. Hoshikawa[4], T. Kuboyama[1] (1.Col. Agr., Ibaraki U., 2.QFF, 3.Col. Sci., Ibaraki U., 4.iFRC, Ibaraki U.)

P054 Activation of LTR retrotransposons in a rice nested association mapping population.

○Fukai, E.[1], A. Abe[2], K. Okazaki[1] (1.Graduate School of Science and Technology, Niigata University, 2.Iwate Biotechnology Research Center)

P055 Effect of genomic region associated with light-independent anthocyanin accumulation in the turnip cultivar ‘Akamaru’ on the transcriptome and methylome

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

P056 Studies on the Koubou radish showing mitochondrial heteroplasmy found in the Yonezawa city (Yamagata prefecture).

○Terachi, T., R. Takii, A. Yamakawa (Fac. Life Sci., Kyoto Sangyo Univ.)

P057 Development a technology for the induction of plant-organelle-genome-specific random mutagenesis in 2 ways

☆Kosaka, N.[1], Y. Harada[1], I. Nakazato[1], M. Okuno[2], T. Itoh[3], W. Yamori[1], N. Tsutsumi[1], S. Arimura[1] (1.Grad. Sch. Agri. and Life Sci., Univ. Tokyo, 2.Sch. Med., Univ. Kurume, 3.Sch. Life Sci. and Tech., Tokyo Inst. Tech.)

P058 Bacterial blight resistant mutant lines induced by ion beam irradiation in rice with special reference to agronomic traits and reaction to multiple races

☆Takahashi, R.[1], K. Kato[1], Y. Maeda[1], Y. Shibata[1], Y. Gatayama[2], S. Taura[3], K. Ichitani[4] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.KIAD Tokunoshima, 3.Inst. Gene Res., Kagoshima Univ., 4.Fac. Agr., Kagoshima Univ.)

P059 Effect of bacterial blight resistance genes from mutants on agronomic traits in rice

☆Maeda, Y.[1], R. Takahashi[1], Y. Shibata[1], S. Taura[2], K. Ichitani[3] (1.Grad. Sch. Agr. Forest. Fish., Kagoshima Univ., 2.Inst. Gene Res., Kagoshima Univ., 3.Fac. Agr., Kagoshima Univ.,)

P060 Screening method of resistance to gray leaf spot disease caused by *Neopestalotiopsis* sp in loquat fruit

○Hiehata, N.[1], R. Sakaguchi[1,2], M. Komine[1] (1.Fruit Tree & Tea Res. Unit, Nagasaki Agri. Forest. Tech. Dev. Ctr., 2.Nagasaki Prefectural Government Ken'ou Development Bureau)

P061 Genetic characterization and preliminary mapping of *Cucumber mosaic virus* resistance in spinach

☆Wu, Y.[1], H. Hirakawa[2], C. Masuta[3], Y. Onodera[3] (1.Grad. Sch. Agr., Hokkaido Univ., 2.Kazusa DNA Res. Inst., 3.Res. Fac. Agr., Hokkaido Univ.)

P062 Comparison of the transcriptional response between komatsuna cultivars upon *Albugo candida* infection

Akter, M.[1], N. Miyaji[2], M. Shimizu[2], I. Chuma[3], ○R. Fujimoto[1] (1.Grad. Sch. Agric. Sci., Kobe Uni, 2.Iwate Biotechnol. Res. Ctr., 3.Obihiro Univ. Agric. Vet. Med.)

P063 Identification of blast resistance genes in foxtail millet

☆Ito, K.[1], H. Kan[2], Y. Yoshitsu[2], A. Abe[1], T. Osato[2], R. Terauchi[1], M. Shimizu[1] (1.IBRC, 2.Iwate Agric.Res.Ctr.)

P064 A QTL, *Resistance to Burkholderia glumae 1* (*RBG1*) confers resistance to bacterial seedling rot through negative regulation of ABA

○Mizobuchi, R.[1], K. Sugimoto[1], S. Tsushima[2], S. Fukuoka[3], C. Tsuiki[1], M. Endo[4], M. Mikami[4], H. Saika[4], H. Sato[1] (1.Inst. Crop. Sci., NARO, 2.Strategic Planning Headquaters, NARO, 3.Core Technology Research Headquarters, NARO, 4.Institute of Agrobiological Sciences, NARO)

P065 The effects of rice cleistogamy to occurrence of Bacterial grain rot and Bacterial seedling rot caused by *Burkholderia glumae*

○OHMORI, S.[1], H. NAKAJIMA[2], K. SAKAI[3], K. KOMAKI[3], M. SABA[1], R. MIZOBUCHI[1] (1.Institute of Crop Science, NARO, 2.Nagano Agricultural Experiment Station, 3.Saitama Agricultural Technology Reseach Center)

P066 Identification of aquaporins and transcriptome analysis of salt and osmotic stress response in common wheat

☆Moriya, H., M. Safi, W. Ahmadzai, R. Nakayama, Y. Kamiya, K. Kanako (KIBR, Yokohama City Univ.)

P067 Comparison of salt stress response genes in synthetic hexaploid wheat

☆Yokota, A., H. Moriya, R. Watanabe, Y. Kamiya, K. Kawaura (KIBR, Yokohama City Univ.)

P068 MBF1c-dependent regulation of long-range signaling in response to heat stress in Arabidopsis thaliana.

☆Morizane, I., N. Suzuki (Grad.Sch.Sci.,Univ.Sophia)

P069 Evaluation of waterlogging tolerant in wheat using vegetation indexes measured with UAV

☆Kakitsuka, Y., O. Uchikawa, A. Onoue, H. Kai (Fukuoka Agric. Res. Cent.)

P070 Evaluation of waterlogging tolerance in wheat by field flooding treatment at the early stage of growth

☆Onoue, A., H. Kai, Y. Kakitsuka, O. Uchikawa (Fukuoka Agric. Res. Cent.)

P071 Exploration of wild emmer wheat intraspecific heat stress tolerance variation in a background of durum wheat

☆Balla, M.[1,2], N. Kamal[1,2], Y. Gorafi[1,2], M. Abdalla[2], I. Tahir[1,2], H. Tsujimoto[1] (1.Arid Land Research Center, Tottori Univ., 2.Agricultural Research Corporation, Sudan)

P072 Analysis of the quantitative trait locus *Na-QTL1* involved in the control of Na^+ accumulation in the leaf blades of rice under salinity stress.

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P073 Selection and physiological analysis of water-saving drought-tolerant genotypes from the wheat TILLING population

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P074 Investigation of conditions for mutation breeding to produce heat tolerant of licorice (*Glycyrrhiza uralensis* L.)

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P075 Elucidation of the drought response mechanisms of rice "Nipponbare" by multi-omics analysis

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P076 Evaluation of grain-filling-related traits using Taichung 65 x DV85 chromosome segment substitution lines (TD-CSSLs) of rice

☆MABREJA, A., V. Reyes, S. Nishiuchi, K. Doi (Grad. Sch. Bioagri. Sci., Nagoya U.)

P077 Evaluation of heritability of medicinal compound contents in *Glycyrrhiza uralensis*

☆Tsusaka, T., Y. Aoki, M. Sakurai (Tsumura & Co.)

P078 Production of antimicrobial peptides persulcatusin and CCL28 in rice for therapeutic use for livestock

Fujita, G., G. Watarai, S. Shimoda, M. Koseki, Y. Iwai, H. Yoneyama, ○Y. Ito (Grad Sch Agri Sci, Tohoku Univ)

P079 Genome-wide association study for ephedrine alkaloid in medicinal plant *Ephedra sinica*

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P080 Increased methylation levels observed in the 5' region of *18S rDNA* during the early growth of rice hybrids

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P081 Semi-dwarf gene identified in the Rht8 region from spelt wheat.

☆Shimada, S.[1], T. Abe[1], W. Takanishi[1], I. Chuma[1], M. Chono[2], K. Hatta[2], K. Onishi[1] (1.Obihiro U. Agr. & Vet. Med., 2.Institute of Crop Science, NARO)

P082 Multi-allelic variants in FT-B1 region responsible for heading time in hexaploid wheat

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P083 Effect of auxin biosynthesis inhibitor on seminal root length and the difference among strains in common wheat.

☆Ozawa, K., Y. Kamiya, K. Kawaura (KIBR, Yokohama City Univ.)

P084 Effect of cytokinin oxidase/dehydrogenase inhibitor CPPU treatment on a new frill mutant of Torenia

☆Mayuzumi, T.[1], M. Hatashita[2], K. Takagi[2], T. Abe[3], Y. Kazama[1,3] (1.Fac. Biosci. Biotech., Fukui Pref. Univ, 2.Wakasa-wan Ener. Cent, 3.RIKEN Nishina Center)

P085 Breaking seed dormancy by physical stimulations and changes in amounts of phyto-hormones in barley

○Kai, H.[1], A. Onoue[1], T. Matsuura[2], D. Saisho[2], T. Tanaka[3], Y. Haraguchi[1], T. Todoroki[4], T. Abiko[5] (1.Fukuoka Agric. Res. Cent., 2.IPSR, Okayama Univ., 3.NAAC, NARO, 4.Fukuoka Pref. Office, 5.Kyushu Univ.)

P086 Changes in nuclear structure during abortion in the barley inflorescence meristem

☆Matsumoto, H.[1], J. Ito[1], Y. Nomura[1], M. Wakazaki[2], M. Sato[2], N. Takeda-Kamiya[2], D. Saisho[3], K. Toyooka[2], H. Tsuji[1,4] (1.KIBR, Yokohama City Univ., 2.CSRS, RIKEN, 3.IPSR, Okayama Univ., 4.Bioscience and Biotechnology Center, Nagoya Univ.)

P087 Interaction among mechanism by heading time genes of durum wheat revealed by expression analysis

☆Fujioka, A.[1], Y. Monden[2], K. Nishimura[2], H. Nishida[2], K. Kato[2] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P088 The exploration of causal genes that affect heading time by exome-sequencing and genetic analysis of mutant genes in barley mutants

☆Okuma, M.[1], K. Nishimura[2], Y. Monden[2], K. Kato[2], H. Nishida[2] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Grad. Sch. Environ. Life Nat. Sci. Tech., Okayama U.)

P089 Phenotypic evaluation of ricewheat (*Oryzawheat*) under the sandy filed condition

☆Sugiura, R.[1], R. Nakao[1], H. Tarutani[2], T. Maryenti[3,4], J. Liu[5], T. Okamoto[3], R. Kimura[5], T. Ishii[5] (1.Under. Sch. Agri., Tottori Univ., 2.Grad. Sch. Dry., Tottori Univ., 3.Grad. Sch. Biol., Tokyo Metro. Univ., 4.Grad. Sch. Math., Univ. Indonesia, 5.Arid Land Research Center., Tottori Univ.)

P090 Novel QTL responsible for seminal root elongation in wheat

☆Manaka, C.[1], K. Inoshita[1], K. Hatta[2], G. Ishikawa[2], K. Onishi[1] (1.Obihiro U. Agr. & Vet. Med., 2.Institute of Crop Science, NARO)

P091 Selection of individuals suitable for genetic breeding experiments from the self-pollinated buckwheat backcross inbred lines.

☆Nemoto, K.[1], S. Ishikawa[1], O. Ueda[1], S. Ito[1], K. Ishikawa[1], H. Maruyama[1], S. Akiyama[1], T. Funaki[2], H. Nakamura[2], T. Kaizu[2], A. Nakano[1], J. Aii[1] (1.NUPMLS, 2.Niigata City Agri. Dev. Res. Cent.)

P092 Research to restore fertility in CMS potato varieties.

☆Nakajima, R.[1], K. Kuwabara[1], T. Ariizumi[2], S. Arimura[3], K. Shirasawa[4] (1.Grad. Sch. Life Environ Sci., Univ. Tsukuba, 2.Fac. Life Environ Sci., Univ. Tsukuba, 3.Grad. Sch. Agri. and Life. Sci., Univ. Tokyo, 4.Kazusa DNA Res. Inst.)

P093 Histological evaluation of fertility restoration lines against cytoplasmic male sterile tomato.

☆Mashita, S.[1], K. Shirasawa[2], H. Takei[4], I. Harada[4], Y. Iki[4], K. Kuwabara[1], H. Suzuki[3], S. Iioka[3], T. Ariizumi[4] (1.Grad. Sch. Life and Env. Sci., Univ. Tsukuba, 2.Kazusa DNA Res. Inst, 3.Tokita Seed Co., Ltd, 4.Fac. Life Env. Sci., Univ. Tsukuba)

P094 A proposed model for the molecular mechanism of Tadukan-type cytoplasmic male sterility based on morphological observation and transcriptomic analysis

☆Takatsuka, A.[1], T. Kazama[2], K. Toriyama[1] (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Fac. Agri. Sci., Kyushu Univ.)

P095 Phenotypic effects of sugar beet *Restorer-of-fertility 1* gene on pollen development and male fertility of normal cytoplasm line

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P096 Detection of overcoming hybrid weakness in an intraspecific cross of *Arabidopsis thaliana*

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P097 Development of a self-pollinated buckwheat mutant population by heavy ion beam irradiation.

☆Ishikawa, S.[1], K. Nemoto[1], K. Kawakami[1], R. Morita[2], T. Abe[2], A. Nakano[1], J. Aii[1]
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