Title of Papers Presented at the 128th Meeting of The JAPANESE SOCIETY Oral presentations

Oral Presentations

101 “Chikushi 90”, a new rice cultivar with medium late maturity, high yielding, fine palatability and tolerance to high temperature during ripening period

Wada, T. [1], T. Inoue [1,2], M. Tsubone [1,3], T. Ogata [1,4], K. Miyahara [1], Y. Hamachi [1,5], M. Furusho [1], M. Miyazaki [1,3], ○O. Yamaguchi [1], M. Ishibashi [1], H. Sato [6], Y. Matsue [1,7] (1.Fukuoka Agric. Forest. Res. Cent., 2.Fukuoka Pref. Keichiku Agric. Ext. Cent., 3.Fukuoka Pref. Gover. Office, 4.Fukuoka Pref. Iizuka Agric. Ext. Cent., 5.JA Zennoh Fukuren, 6.Fukuoka Agric. Forest. Res. Cent. Chikugo Branch, 7.Kyushu Univ.)

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102 Genetic relationships among A genomes of tetraploid wheat and two lineages in *T. urartu*

☆Takenaka, S. [1], M. Nitta [2], T. Kawahara [2], S. Nasuda [2] (1.Fac. Agri., Rukoku Univ., 2.Grad. Sch. Agri., Kyoto Univ.)

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103 Development of high-yielding common buckwheat line using genomic selection

☆Hara, T. [1], S. Yabe [2], M. Ueno [3], H. Enoki [4], T. Kimura [4], S. Nishimura [4], Y. Yasui [3], H. Iwata [5], R. Ohsawa [1] (1.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 2.NARO Agricultural Research Center, 3.Grad. Sch. Agr., Univ. Kyoto, 4.Future Project Div., TOYOTA MOTOR CORPORATION, 5.Grad. Sch. Agric. Life Sci. Univ. Tokyo)

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104 Evaluation of safflower genetic resources based on the major morphological traits investigated in 2012-2014

○Sasanuma, T., Y. Takahashi, Y. Aizawa, S. Aoyagi, T. Abe (Fac. Agr., Yamagata Univ.)

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105 Genetic studies on Bambuseae species in Japan. XXXVIII. Phenotypic characters of the intergeneric hybrids, and the possible parents of *Pseudosasa japonica*

○Muramatsu, M. (*)

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106 Genetic resources of Citrus in Yoron island: Diversity in Citrus rokugatsu

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

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107 Breeding of a new potato variety "Saikai 37" with high eating quality, high carotenoid content and combined resistance to disease and pest for warm region

Mori, K. [1], ☆Y. Sakamoto [1], Y. Matsuo [1], N. Mukojima [2], W. Watanabe [3], N. Sobaru [4], S. Tamiya [5], K. Hayashi [6], H. Watanuki [6], K. Nara [6], K. Yamazaki [6], T. Nakao [1] (1.Nagasaki Agricultural and Forestry Technical Development Center, 2.Nagasaki Ken'ou Development Bureau, 3.Nagasaki Goto Development Bureau, 4.Nagasaki Agriculture & Forestry Department, 5.National Agriculture and Food Research Organization Hokkaido Agricultural Research Center, 6.Tokyo Kasei Gukuin University)

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108 Development of a duplex (YYyy) parental potato "Aikei 230" with resistant gene *Rychc* to potato virus Y using marker assisted selection

☆Mori, K. [1], Y. Matsuo [1], W. Watanabe [2], Y. Sakamoto [1], N. Mukojima [3], T. Nakao [1] (1.Nagasaki Agricultural and Forestry Technical Development Center, 2.Nagasaki Goto Development Bureau, 3.Nagasaki Ken'ou Development Bureau)

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109 Adaptative trait of the natural hybrid in genus Vigna found in a limestone karst

○Naito, K. [1], Y. Takahashi [1], K. Iseki [1], K. Kitazawa [2], K. Irie [2], N. Tomooka [1] (1.Genetic Resource Center, NIAS, 2.Tokyo Univ. Agriculture)

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110 Breeding of a new rice cultivar "Yamagata112" with short-culmed, good taste and high quality rice

○Chuba, M. [1], K. Yuki [1], T. Sano [2], H. Goto [3], K. Watanabe [4], M. Moriya [5], K. Sato [2], M. Mitobe [5], N. Saito [6], Y. Abe [1], H. Saito [2], T. Homma [1], K. Saito [4], T. Suzuki [1], K. Watanabe [1] (1.Rice Breeding and Crop Sci. Exp. Stn.,Yamagata Integrated Agr. Res. Cent., 2.Shonai Area General Branch Administration Office, 3.Yamagata Integrated Agr. Res. Cent., 4.Former Rice Breeding and Crop Sci. Exp. Stn.,Yamagata Integrated Agr. Res. Cent., 5.Murayama Area General Branch Administration Office, 6.Shonai Branch, Yamagata Disease and Pest-Related Crop Damage Prevension Office)

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111 A New winter double low rapeseed [Brassica napus L.] cultivar, "Kirakiraginga", with high oil yield and ability of multi-directional use of seeds

○Honda, Y. [1], M. Kawasaki [2], M. Yamamori [3], M. Katou [3], M. Yui [2] (1.NARO, 2.NAROTARC, 3.NARONICS)

112 Evaluation of spike morphology and bread-making property on *Aegilops tauschii* genetic resource collected in North Caucasia

☆Akaike, R., A. Kakizaki, T. Sasanuma (Fac. Agr., Yamagata Univ.)

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113 Geographical variation of γ-oryzanol in rice genetic resources

○Ebana, K. [1], K. Sawada [2], Y. Harada [2], H. Hashimoto [2], R. Masuda [3], E. Araki [3], Y. Suzuki [3] (1.Natl. Inst. Agrobio. Sci., 2.Tsuno Food Industrial Co., Ltd., 3.NARO, Inst. Crop Sci.)

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114 Current on-farm diversity and core collection development of Khao Kai Noi, a Lao rice landrace (Oryza sativa L.)

☆Vilayheuang, K. [1,4], R. Machida-Hirano [2], C. Bounphanousay [4], K. Watanabe [2,3] (1.Grad. Sch. LES., Univ. Tsukuba, 2.Gene Res. Cen., Univ. Tsukuba, 3.Fac. LES., Univ. Tsukuba, 4.ARC, NAFRI, Vientiane, Lao P.D.R)

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115 Development of wheat variety LM12 for living-mulching and its characteristics

○Murai, K., K. Kato, M. Kinoshita, M. Kurosaka (Dep. Biosci., Fukui Pref. Univ.)

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116 Genomic prediction of breeding values for fruit-quality traits using single-step GBLUP and single-step GWAS methods

☆Imai, A. [1,6], T. Kuniga [1,2], T. Yoshioka [1], K. Nonaka [1], N. Mitani [1], N. Hiehata [1,3], M. Yamamoto [1,4], T. Hayashi [5,6] (1.NIFTS,NARO, 2.WARC,NARO, 3.Nagasaki Regional Development Bureau, 4.Faculty of Agriculture, Kagoshima University, 5.NARC, NARO, 6.Grad. Life Env. Sch., Univ. Tsukuba)

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117 Isolation of the non-Mendelian stay-green gene in soybean

☆Kohzuma, K. [1,2], Y. Sato [3], A. Okuzaki [3,4], Y. Masuda [1], H. Fukuoka [5], A. Kanazawa [6], Y. Tabei [3], M. Kusaba [1,2] (1.Grad. Sch. Sci. Hiroshima U., 2.CREST, 3.NIAS, 4.Fac. Agr., Tamagawa Univ., 5.NIVTS, 6.Res. Fac. Agr., Hokkaido Univ.)

---

118 An amino acid altering mutation of *NARROW LEAF 1* gene contributes natural variation of flag leaf morphology in rice

○Taguchi-Shiobara, F. [1], T. Ota [2], K. Ebana [1], T. Ookawa [3], M. Yamasaki [4], T. Tanabata [1,5], U. Yamanouchi [1], J. Wu [1], N. Ono [6], Y. Nonoue [1,6,7], K. Nagata [1], S. Fukuoka [1], H.

Hirabayashi [8], T. Yamamoto [1], M. Yano [1,9] (1.NIAS, 2.SOKENDAI, 3.Tokyo Univ. of Agr. and Tech., 4.Kobe Univ., 5.RIKEN CSRS, 6.STAFF, 7.Iwate Biotech. Res. Ctr., 8.NARO/NICS, 9.NARO/NICS)

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119 Identification of interactions among flowering time loci with the use of mutaions induced in rice variety Gimbozu

☆Fushimi, E. [1], T. Yokoo [1], H. Saito [1], Y. Yoshitake [1], T. Tsukiyama [1], M. Teraishi [1], T. Tanisaka [1,2], Y. Okumoto [1] (1.Grad. Sch. Agri., Kyoto Univ., 2.Dep. Agric. Regional Reclamation., Kibi Int. Univ.)

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120 Breeding for mineral in rice

☆Ohmori, Y., T. Fujiwara (Dept. of Appl. Biol. Chem., Grad. Sch. of Agric. Life Sci., Univ. of Tokyo)

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201 Modeling genotypic difference in the flowering characteristics of rice based on spikelet position on a panicle

☆Yabe, S. [1], H. Yoshida [1], S. Adachi [2], T. Mukouyama [3], Y. Arai-Sanoh [3], M. Okamura [3], M. Kondo [3], H. Nakagawa [1] (1.NARO Agricultural Research Center, 2.The Global Innovation Research Organization, Tokyo Univ. Agriculture and Technology, 3.NARO Institute of Crop Science)

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202 Roles of a semi-determinate habit gene Dt2 in flowering and stem termination of soybean

Zhu, J. [1], ☆R. Takeshima [1], C. Zhao [1], T. Hayashi [1], F. Kong [2], T. Yamada [1], J. Abe [1] (1.Grad. Sch. Agric., Hokkaido U., 2.Northeast Institute of Geography and Agroecology, China)

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203 Variation for root systems associated with seedling growth in soybean

☆Yoshikiyo, T. [1], Y. Oouchi [1], Y. Jitsuyama [1], D. Xu [2], R. Takahashi [3], T. Yamada [1], J. Abe [1] (1.Grad. Sch. Agr., Univ. Hokkaido, 2.JIRCAS, 3.Crop Sci Inst)

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204 Seed viability and lipid peroxidation in soybean

☆Nakaya, K. [1], K. Suzuki [2], M. Sato [1], T. Yamada [1], J. Abe [1] (1.Grad. Sch. Agri., Univ. Hokkaido, 2.HRO)

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205 Isolation of the pollen S candidate in a heterostylous flax, based on the k-mer comparison between the ngs sequence pools of different flower types

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

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206 The genetic basis of pollen number variation revealed by a genome-wide association study in Arabidopsis thaliana

☆Kakui, H. [1], T. Tsuchimatsu [1,2], M. Yamazaki [1], C. Marona [3], D. Meng [2,4], M. Kanaoka [5], T. Stadler [6], M. Lenhard [3], M. Nordborg [2,4], K. Shimizu [1] (1.University of Zurich, 2.Gregor Mendel Inst., 3.Univ. Potsdam, 4.Univ. Southern California, 5.Nagoya Univ., 6.ETH Zurich)

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207 Molecular analysis of the fertility restorer gene on chromosome 10 derived from wild rice

☆Kazama, T., K. Igarashi, M. Okazaki, K. Toriyama (Grad. Sch. Agri. Sci., Tohoku Univ.)

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208 Transcriptome analysis of *Lilium longiflorum* pollen by RNA sequencing

☆Itabashi, E. [1,2], P. Bhalla [1], M. Singh [1] (1.Fac. Vet. Agric. Sci., Melbourne Univ., 2.Grad. Sch. Agric. Sci., Kobe Univ.)

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209 Investigation of historogical, cytogenetical and molecular genetic features in the production of *Brassica rapa* carrying *Diplotaxis tenuifolia* cytoplasm

☆Hayashi, T., S. Shim, S. Bang (Fac. Agric. , Utsunomiya U.)

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210 Production of cytoplasmic male sterile and fertility restorer lines in *Brassica rapa* carrying *Brassica maurorum* cytoplasm

☆Koike, H., K. Sunaga, S. Shim, S. Bang (Fac. Agric. , Utsunomiya U.)

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211 The relationship between training data sets with multiple years and the performance of genomic selection for the yield-related traits in rice

○Yonemaru, J. [1], K. Matsubara [2], T. Yamamoto [1], R. Mizobuchi [1], E. Yamamoto [1,3], H. Tsunematsu [2], N. Kobayashi [2], H. Kato [1,2], M. Yano [1,2] (1.Natl. Inst. Agr. Sci., 2.NARO Inst. Crop Sci., 3.NARO Inst. Veg. Tea Sci.)

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212 Utilization of leaf surface temperature for high throughput phenotyping of water status

☆Iseki, K. [1], C. Muto [1], Y. Takahashi [1,2], K. Naito [1], N. Tomooka [1] (1.National Institute of Agrobiological Sciences, 2.JSPS Research Fellow)

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213 Development of simulator software for genomic selection breeding

○Iwata, H., B. Galliot (Grad. Sch. Agr. Life Sci., Univ. Tokyo)

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214 A novel method for multi-trait genomic selection : application of multi-task learning

☆Hori, T. [1], M. Kobayashi [2,3], H. Ohyanagi [2,3,4], H. Takanashi [1,3], A. Nagano [5,6], T. Tokunaga [3,7], T. Sazuka [3,8], K. Yano [2,3], N. Tsutsumi [1,3], H. Iwata [1,3] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Fac. Agr., Meiji Univ., 3.CREST, JST, 4.Mitsubishi Space Software Co., Ltd., 5.Cent. Ecol. Res., Kyoto Univ., 6.PREST, JST, 7.EARTHNOTE Co., Ltd., 8.Biosci. Biotech. Cent., Nagoya Univ.)

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215 Prototype developments for recurrent selection using transgenic male sterility in rice, with the fluorescent protein accumulations in the endosperms

○Tanaka, J. [1], M. Akasaka [1], Y. Taniguchi [1], M. Oshima [2], Y. Tabei [2] (1.NARO Institute of Crop Science, 2.National Institute of Agrobiological Sciences)

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216 Plant Omics Data Center (PODC) : The Integrated Web Repository for Interspecies Gene Expression Networks and High Reliable Functional Annotation

☆Terashima, S. [1], T. Takano [1], T. Kudo [1], M. Kanno [1], M. Saito [1], N. Matsuda [1], S. Asano [1], S. Ozaki [1], Y. Sasaki [1], M. Kobayashi [1], K. Yokoyama [1], K. Suwabe [4], G. Suzuki [5], M. Watanabe [6], M. Matsuoka [3], H. Ohyanagi [1,2], K. Yano [1] (1.Sch. of Agri., Meiji Univ., 2.Mitsubishi Space Software Co., Ltd., 3.Bioscience and Biotechnology Center., Nagoya Univ., 4.Graduate School of Bioresources, Mie Univ., 5.Division of Natural Science, Osaka Kyoiku Univ., 6.Graduate School of Life Sciences, Tohoku Univ.)

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217 A web database WFI-DB for wheat- *Fusarium graminearum* interactions based on large-scale transcriptome analysis

☆Nakamura, Y. [1], A. Kosaka [2], A. Manickavelu [2], K. Yano [1] (1.Bioinformatics lab., Sch. of Agri., Meiji Univ., 2.Kihara Inst. Biol. Res., Yokohama City Univ.)

---

301 Analysis of rice endosperm mutant *abnormal aleurone layer 1* (*aal1*) which has supernumerary aleurone layers

☆Katoh, H. [1], M. Fukai [1], K. Kurotani [1], Y. Sato [2], H. Kitano [2], Y. Nagato [3], Y. Kobayashi [4], I. Kobayashi [4], S. Takeda [1], T. Hattori [1] (1.Biosci. Biotech. Ctr, Univ. Nagoya, 2.Grad. Sch. Bioagri, Univ. Nagoya, 3.Grad. Sch. Agri. Life, Univ. Tokyo, 4.Life Sci. Res, Univ. Mie)

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302 Wheat Vrs1 orthologues control floret development

☆Sakuma, S. [1,2], T. Ogawa [2], A. Tagiri [2], H. Kanamori [2], J. Wu [2], M. Pourkheirandish [2], T. Komatsuda [2] (1.KIBR/YCU, 2.NIAS)

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303 Analysis of water-repellency in wild-type and wet-leaf mutants of rice

☆Aiga, S., J. Itoh (Grad. Sch. Agric. Life Sci., U. Tokyo)

---

304 Simultaneous imaging of florigen and its downstream gene expression

○Tsuji, H. [1], A. Fujita [2], A. Matsumoto [2], Z. Shimatani [2,3], R. Terada [3], K. Shimamoto [2] (1.Kihara Institute for Biological Research, 2.Nara Institute of Science and Technology, 3.Faculty of Agriculture, Meijo Univ.)

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305 Regulation of inflorescence development by rice TFL1 homolog, RCN

☆Suzuki, M. [1], R. Ishikawa [2], K. Shimamoto [2], K. Taoka [1] (1.Kihara Institute for Biological Research, 2.Nara Institute of Science and Technology)

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306 Molecular mechanism for regulation of potato tuberization by tuberigen

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

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307 Genetic and morphological analysis of autopolyploids in rice

☆Iwaki, A. [1], J. Ito [1], T. Okamoto [2] (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Grad. Sch. Sci & Eng. Bio Sci., Tokyo Metropolitan Univ)

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308 Evolution of the seed dispersal system in barley

○Komatsuda, T., M. Pourkheirandish (Natl. Inst. Agrobiological Sciences)

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309 *heracles*: A semidominant suppressor of *giant embryo* (*ge*)

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

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310 Analysis of rice *fickle spikelet1* mutant showing an increase in the number of flower and spikelet organs

☆Suzuki, C. [1], W. Tanaka [1,2], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Frontier Sci., Univ. Tokyo)

---

311 Rice *TAB1* gene regulates tiller and panicle formation

☆Tanaka, W. [1,2], S. Kawano [2], H. Hirano [1] (1.Department of Biological Sciences, Graduate School of Science, The University of Tokyo, 2.Department of Integrated Bioscience, Graduate School of Frontier Science, The University of Tokyo)

---

312 Characterization of a rice mutant that produces verticillate primary branches

☆Ikeda, T. [1], W. Tanaka [1,2], M. Murai [3], T. Sakamoto [4], T. Kurata [4], H. Hirano [1] (1.Graduate School of Science, The University of Tokyo, 2.Graduate School of Frontier Sciences, The University of Tokyo, 3.Faculty of Agriculture, Kochi University, 4.Graduate School of Biological Sciences, NAIST)

---

313 *OsWOX4* plays multiple roles in leaf development

☆Yasui, Y. [1], Y. Ohmori [1,2], H. Hirano [1] (1.Grad. Sch. Sci., Univ. Tokyo, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo)

---

314 Visualization of auxin distribution in roots of the Arabiopsis heterotrimeric G-protein β subunit - deficient mutant *agb1*

☆Ogura, N. [1,2], D. Tsugama [2,3], T. Takano [1,2] (1.ANESC., Univ. Tokyo, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.JSPS Research Fellow(PD))

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315 Effect of *HvPhyC* sequence variation on expression patterns of downstream genes in barley

○Nishida, H. [1], K. Taniko [2], K. Kato [1] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Fac. Agr., Okayama U.)

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316 The causal gene for the rice mutant *endosperm defective 1* (*end1*) encodes the first enzyme in shikimic acid pathway

☆Kurotani, K. [1], H. Kato [1], Y. Takafuji [2], Y. Kobayashi [3], I. Kobayashi [3], Y. Sato [4], K. Hibara [5], Y. Nagato [5], H. Kitano [1], Y. In-Sun [6], S. Takeda [1], T. Hattori [1] (1.Biosci. &

Biotech. Center, Nagoya Univ., 2.Agri., Meijo Univ., 3.Life Sci. Res. Center, Mie Univ., 4.Bioagri., Nagoya Univ., 5.Agri. & Life Sci., Univ. of Tokyo, 6.Nat. Aca. of Agri. Sci., RDA)

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317 *Ehd2* mediated ambient temperature-dependent regulation of flowering in rice

☆Yoshitsu, Y. [1], Y. Takahata [1], S. Yokoi [2] (1.Fac. Agri., Iwate Univ., 2.Grad.Sch. Lif. Envi. Sci., Osaka Pref. Univ.)

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318 Identification of *Vrn-D4* gene reveals the origin of spring growth habit in ancient wheats from South Asia

○Kato, K. [1], N. Kippes [2], H. Harada [1], H. Nishida [1], J. Dubcovsky [2] (1.Grad. Sch. Environ. Life Sci., Okayama U., 2.Dept. Plant Sci., UC Davis, USA)

---

319 Expression analyses of photoperiodic pathway-related genes in extra early-flowering 2 (exe2) wheat mutant

☆Kitagawa, S. [1], A. Nishiura [1], N. Mizuno [2], S. Nasuda [2], Y. Kazama [3], T. Abe [3], K. Murai [1] (1.Dep. Biosci., Fukui Pref. Univ., 2.Grad. Sch. Agr., Kyoto Univ., 3.RIKEN, Nishina Cent.)

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320 Mapping of QTLs associated with awn length in sorghum recombinant inbred lines

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

---

321 Characterization of stay green phenotype and QTL mapping in a sorghum RIL population

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

---

401 Genetic analysis for whiteness of cooked rice

○Kobayashi, A. [1], Y. Machida [1], T. Kataoka [2], K. Tamura [2], K. Tomita [1] (1.Fukui Agr. Exp. Stn., 2.NARO/KARC)

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402 Relationship between alkali disintegration of the rice grain and the chain-length distribution of amylopectin

☆Machida, Y., A. Kobayashi, K. Tomita (Fukui Agr. Exp. Stn.)

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403 Qualitative and quantitative variation of the main γ-oryzanol components of brown rice in the world core collection

○Suzuki, Y. [1], R. Masuda [1], K. Sawada [2], Y. Harada [2], H. Hashimoto [2], E. Araki [1], K. Ebana [3] (1.NARO, Inst. Crop Sci., 2.Tsuno Food Industrial Co., Ltd., 3.Natl. Inst. Agrobio. Sci.)

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404 QTL analysis of leaf and stem biomass related genes in sorghum

○Kawahigashi, H. [1], J. Yonemaru [1], M. Kitahara [2], S. Kasuga [2] (1.NIAS, Japan, 2.Shinshu University)

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405 Is it possible to predict the heterosis from parental genetic distance in Chinese cabbage ?

Kawamura, K. [2], T. Kawanabe [1], N. Saeki [2], S. Konno [3], A. Nagano [4,5,6], M. Honjyo [5], M. Yasugi [5], H. Kudo [5], T. Yasuda [1], M. Kaji [3], K. Okazaki [2], ○R. Fujimoto [1,6] (1.Grad. Sch. Agric. Sci., Kobe Univ., 2.Grad. Sch. Sci. Tech., Niigata Univ., 3.Watanabe Seed Co., Ltd, 4.Fac. Agric., Ryukoku Univ., 5.Cent. Ecol. Res., Kyoto Univ., 6.PRESTO)

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406 Effect of genetic variation of rootstocks for the protein content in soybean seeds

☆Shimbo, D. [1], D. Tanabe [1], T. Hirata [2], S. Watanabe [3], J. Abe [1], T. Yamada [1] (1.Grad.Sch.Agric.,Univ.Hokkaido, 2.Field Science Center for Northern Biosphere, Hokkaido University, 3.Fac.Agric.,Univ.Saga)

---

407 Biochemical and physiological characterization of stay-green soybean seeds

☆Tokumitsu, Y. [1], M. Tsuchida [1], M. Kusaba [2], J. Abe [1], T. Yamada [1] (1.Grad. Sch. Agr., Univ. Hokkaido, 2.Grad. Sch. Sci., Univ. Hiroshima)

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408 Difference of saccharification yields among organs and harvesting stages

Abe, T. [1], K. Ito [1], A. Matsuzaka [1], T. Sonoki [2], ○Y. Ito [1] (1.Graduate School of Agricultural Science, Tohoku University, 2.Faculty of Agriculture and Life Science, Hirosaki University)

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409 Characterization of transgenic rice introduced cyanobacterial *FBP/SBPase* in isolation field

○Komatsu, A. [1], M. Tamoi [2], M. Ohtake [1], K. Ohtori [2], M. Ohshima [1], S. Shigeoka [2] (1.NARO Inst. of Crop Sci., 2.Faculty of Agric., Kinki Univ.)

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410 Effects of microwave irradiation on growth of Arabidopsis

☆Hasegawa, Y., N. Suzuki, S. Horikoshi (Sophia University, Faculty of Sciences and Technology)

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411 Mapping QTLs for traits related to low-phosphorus tolerance using introgression lines derived from wild relatives of *Oryza sativa*

☆Kokaji, H. [1], M. Kudo [2], K. Oda [3], H. Hirabayashi [4], A. Shimizu [1] (1.Grad. Sch. Environ. Sci., Univ. Shiga Pref., 2.Environ. Sci., Univ. Shiga Pref., 3.Grad. Sch. Agr. Kyoto Univ., 4.NARO Natl. Inst. Crop Sci.)

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412 Identification of clubroot resistance genes using a *Brasica napus- Raphanus sativus* chromosome addition line, and introduction of the clubroot resistance

☆Ohtsu, F., K. Tsutsui, M. Akaba, S. Bang (Fac. Agric., Utsunomiya U)

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413 Acetate confers drought tolerance by inducing pseudo-acclimation state in rice

☆Ogawa, D. [1,5], J. Kim [2,5], M. Muramatsu [1], E. Kato [1], J. Ma [3], M. Kusano [2,4], H. Kaya [1], M. Miyao [1], M. Seki [2,5], Y. Ogo [1,5], Y. Habu [1,5] (1.NIAS, 2.CSRS, 3.Okayama Univ, 4.Univ of Tsukuba, 5.JST CREST)

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414 Ethylene-dependent/independent aerenchyma formation in rice roots

☆Yamauchi, T. [1], A. Tanaka [1], I. Takamure [2], K. Kato [3], M. Nakazono [1] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Grad. Sch. Agr., U. Hokkaido, 3.Obihiro. Univ. Agric. & Vet. Med.)

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415 Mechanism of auxin signaling-mediated constitutive aerenchyma formation in rice roots

☆Tanaka, A. [1], T. Yamauchi [1], H. Inahashi [1], H. Mori [1], Y. Nagamura [2], N. Nishizawa [3,4], Y. Inukai [5], M. Nakazono [1] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Natl. Inst. Agr. Sci., 3.Res. Inst. Bioresource Biotech., Ishikawa Pref. U., 4.Grad. Sch. Agric. Life Sci., U. Tokyo., 5.ICCAE., Nagoya U.)

416 Fine mapping of the clubroot resistance gene, *PbBo(Anju)1*, in *Brassica oleracea*

☆Kawamura, K. [1], T. Kodama [1], M. Shimizu [1], A. Md. [2], H. Tomita [1], K. Sasaki [1], R. Fujimoto [3], E. Fukai [1], K. Okazaki [1] (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Fac. Agri., Sylhet Agric. Univ., 3.Grad. Sch. Agric. Sci., Kobe Univ.)

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417 Improvemant of cold tolerance of rice seedlings by cold acclimation treatment

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

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418 Kihara Afghan wheat landraces (KAWL), a treasure for osmotic stress tolerance

☆Zaheri, E. [1,2], B. Behnam [1], H. Tsuji [1], A. Manickavelu [1], T. Ban [1] (1.Kihara Institute for Biological Research, 2.Ministry of Agriculture, Forestry, Irrigation and Livestock, Afghanistan)

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419 Analysis of some wheat WRKY transcription factor genes up-regulated in interspecific triploids showing hybrid incompatibilities

☆Kuki, Y. [1], R. Ohno [2], K. Yoshida [2], S. Takumi [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Org. Adv. Sci. Tech., Kobe Univ.)

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501 Production of an alloplasmic *Brassica napus* line carrying *Diplotaxis erucoides* cytoplasm, and its agronomically useful traits

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

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502 A gain-of-function Bushy dwarf tiller 1 mutation in rice microRNA gene miR156d caused by insertion of the DNA transposon nDart1

○Tsugane, K. [1], M. Tsugane-Hayashi [1], M. Maekawa [2] (1.Nat. Inst. Basic Biol., 2.Okayama Univ.)

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503 Development of hexaploid wheat mutant populations for the crop improvement through a reverse genetic, nontransgenic approach

○Oono, Y., F. Kobayashi, Y. Hanawa, D. Kawada, K. Sugimoto, H. Handa (NIAS)

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504 Comparison of off-target mutation frequency using Cas9 Nuclease or Cas9 Nickase

☆Mikami, M. [1,2], M. Endo [2], S. Toki [1,2] (1.Gra. Sch. Nanobiol., Yokohama City Univ., 2.Natl. Inst. Agrobiol. Sci.)

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505 Analysis of a rice virescent mutant induced by heavy-ion beam

☆Morita, R. [1], M. Nakagawa [2], S. Usuda [1], K. Ichinose [1], Y. Hayashi [1], H. Tokairin [1], H. Takehisa [3], T. Sato [1,4], T. Abe [1] (1.RIKEN, Nishina Cent., 2.Ishinomaki Senshu Univ., 3.NIAS, 4.Grad. Sch. Agric. Sci., U. Tohoku)

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506 Identification of artificially induced mutations in tomato with next-generation sequencing technology

○Shirasawa, K. [1], H. Hirakawa [1], T. Nunome [2], S. Isobe [1] (1.Kazusa DNA Res Inst, 2.NIVTS)

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507 Flowering habits in dominant male sterile rice plants created by a gene recombinant technology

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

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508 Identification of the genome region responding to transformation in barley

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

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509 Production of transgenic ornamental Ipomoea obscura by introduction of astaxanthin biosynthesis genes

○Otani, M. [1], H. Ishikuro [1], J. Hattan [1], K. Kitayama [1], T. Maoka [2], N. Misawa [1] (1.Res. Inst. Biores., Ishikawa Pref. U., 2.Res. Inst. Prod. Dev.)

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510 COMET: A sensitive and accurate motif discovery tool that uses a multiple length enumerative approach and a multiple control-defined method

☆Sasaki, Y. [1], S. Terashima [1], H. Ohyanagi [1,3,4], N. Yamamoto [1], M. Kobayashi [1], T. Takano [1], M. Otani [5], E. Nambara [2], K. Yano [1] (1.School of Agri., Meiji University, 2.Department of Cell & Systems Biology, University of Toronto, 3.Tsukuba Division, Mitsubishi Space Software Co., Ltd., 4.Plant Genetics Laboratory, National Institute of Genetics, 5.Department of Botany & Plant Sciences, University of California)

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511 Identification of reference gene candidates for quantitative expression analysis using large-scale RNA-seq data of Arabidopsis thaliana and crop plants

☆Kudo, T., S. Terashima, Y. Sasaki, T. Takano, N. Matsuda-Imai, M. Kanno, M. Saito, S. Ozaki, S. Asano, K. Yokoyama, K. Yano (Sch. of Agri., Meiji Univ.)

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512 Production and analyses of transgenic wheat plants overexpressing the 4-HPPD inhivitor sensitive gene 1 (HIS1)

○Abe, F. [1], M. Tougou [1], I. Ashikawa [1], A. Yamazaki [2], K. Sekino [2], S. Hirose [1], M. Kawata [1] (1.NARO Inst. Crop Sci., 2.SDS Biotech K.K.)

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513 Production and analyses of transgenic soybean plants overexpressing the 4-HPPD inhivitor sensitive gene 1 (HIS1)

○Tougou, M. [1], F. Abe [1], N. Takahashi [1], A. Yamazaki [2], K. Sekino [2], S. Hirose [1], M. Kawata [1] (1.NARO Inst. Crop Sci., 2.SDS Biotech K.K.)

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514 Comparative analysis of low input whole genome bisulfite sequencing methods

○Kawakatsu, T. [1,2], J. Nery [2], J. Ecker [2,3] (1.NIAS, 2.SALK, 3.HHMI)

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515 Expression level of a flavonoid 3'-hydroxylase gene determines pathogen-induced color variation in sorghum

○Mizuno, H. [1], T. Yazawa [1], S. Kasuga [2], Y. Sawada [3], J. Ogata [1], T. Ando [1], H. Kanamori [1], J. Yonemaru [1], J. Wu [1], M. Yokota-Hirai [3], T. Matsumoto [1], H. Kawahigashi [1] (1.NIAS. Agrogenomics Res. Center, 2.Shinshu Univ., Fac. of Agriculture, 3.RIKEN, Center for Sus. Res. Sci.)

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516 Analysis of candidate factors for plant mitochondrial division

☆Hajime, E., N. Yamashita, K. Katayama, N. Tsutsumi, M. Fujimoto, S. Arimura (Grad. Sch. Agric. Life Sci., Univ. Tokyo)

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517 Comparative transcriptome analysis among diploid ancestors of common wheat

☆Kajita, Y. [1], T. Tanaka [2], K. Kawaura [1], S. Sakuma [1], K. Mishina [1,2], H. Tarui [3], N. Suzuki [3], M. Tagami [3], J. Kawai [3], Y. Ogihara [1] (1.KIBR,Yokohama City Univ., 2.NIAS, 3.Riken OSC)

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518 Detection of alternatively spliced transcripts based on RNA-seq data from seedling leaves and young spikes in *Aegilops tauschii*

○Takumi, S. [1], C. Iehisa [1], M. Okada [1], K. Sato [2] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.IPSR, Okayama Univ.)

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519 Relationship between gradual 1A chromosome deletion and glutenin expression in common wheat

○Tanaka, H., E. Shimizu (Fac. Agr., Tottori Univ.)

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601 Genomic region on rice chromosome 1 associated with root system development identified by 2D & 3D root-phenotyping systems

○Uga, Y. [1], I. Assaranurak [2], B. Larson [3], E. Craft [3], J. Shaff [3], Y. Kitomi [1], S. McCouch [2], L. Kochian [3] (1.NIAS, 2.Cornell Univ., 3.USDA-ARS)

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602 Analysis of 200 wild Oryza genomes reveals their diversity and evolutionary relationships

○Kurata, N. [1,6], A. Toyoda [2], M. Shenton [1], M. Fujita [1], H. Ohyanagi [1], K. Ikawa [1], M. Kobayashi [3], T. Takano [3], S. Terashima [3], K. Yano [3], T. Kubo [1,6], H. Furuumi [1], M. Niihama [4], K. Nonomura [4,6], D. Copetti [5], W. Rod [5], A. Fujiyama [2,6] (1.Plant Genetics, NIG, 2.Comparative Genomics, NIG, 3.Sch. Agri., Meiji Univ., 4.Experimental Farm, NIG, 5.AGI, Arizona Univ., 6.Grad. Sch. Life Sci. SOKENDAI)

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603 *De novo* assembly of a wild rice *Oryza officinalis* genome

☆Kobayashi, M. [1], H. Ohyanagi [2], N. Kurata [2,4], M. Fujita [2], A. Toyoda [3], A. Fujiyama [3], D. Copetti [5], R. Wing [5], K. Yano [1] (1.Sch. of Agri., Meiji Univ., 2.Plant Genetics Laboratory, National Institute of Genetics, 3.Comparative Genomics Laboratory, National Institute of Genetics, 4.Department of Genetics, SOKENDAI, 5.Arizona Genomics Institute, Arizona University)

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604 Genetic diversity in the Oryza officinalis complex

☆Shenton, M. [1], M. Fujita [1], H. Ohyanagi [1], M. Kobayashi [3], T. Takano [3], S. Terashima [3], K. Yano [3], A. Toyoda [2], A. Fujiyama [2,5], D. Copetti [4], R. Wing [4], N. Kurata [1,5] (1.National Institute of Genetics, Plant Genetics Laboratory, 2.National Institute of Genetics, Comparative Genomics Laboratory, 3.Meiji University School of Agriculture, 4.Arizona Genomics Institute, University of Arizona, 5.Graduate School of Life Sciences, SOKENDAI)

605 Molecular evaluation of a mini core collection of Japanese wheat varieties and its application to association analysis using by GBS (genotyping-by-sequencing)

○Handa, H., F. Kobayashi, T. Tanaka, H. Kanamori, J. Wu, Y. Katayose (National Institute of Agrobiological Sciences)

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606 Verification of QTL for the occurrence of milky-white rice kernel under high temperature stress during ripening period

○Miyahara, K. [1], M. Ishibashi [1], O. Yamaguchi [1], T. Wada [1], M. Miyazaki [2], J. Sonoda [3], T. Tsukaguchi [4], M. Kondo [5] (1.Fukuoka Agric. Forest. Res. Cent., 2.Fukuoka Pref. Gover. Office, 3.Kagoshima Pref. Inst. Agric. Dev., 4.Ishikawa Pref. Univ., 5.Naro, Inst. Crop Sci.)

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607 Sequence analysis of the mitochondrial genome of a male-sterile onion

☆Tsujimura, M. [1], T. Kaneko [2], M. Shigyo [3], H. Izumotani [4], T. Terachi [2] (1.Kyoto Sangyo U. Plant Organelle Genomics R. C., 2.Fac. Life Sci., Kyoto Sangyo U., 3.Fac. Agr., Yamaguchi U., 4.Grad. Sch. Life Sci., Kyoto Sangyo U.)

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608 Resequencing of rice organelle genomes

☆Ohnishi, T. [1], T. Takamatsu [2,3], K. Oikawa [2,3], T. Inomata [3], K. Tanaka [4], H. Furuumi [5], N. Kurata [5], H. Kobayashi [4], T. Mitsui [2,3], T. Kinoshita [1] (1.Kihara Inst. for Biol. Res., Yokohama City Univ., 2.Department of Appl. Biol. Chem., Niigata Univ., 3.Grad. Sch. Sci. Tech., Niigata Univ., 4.NODAI Genome Research Center, Tokyo Univ. of Agr., 5.Plant Genet. Lab., Natl. Inst. Genet.)

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609 Genome-wide association study of anthocyanin pigmentation in sorghum leaf sheath

☆Shichijo, M. [1], H. Takanashi [1,2], Y. Sano [1], M. Fujimoto [1,2], H. Kanegae [1], M. Kobayashi [2,3], K. Yano [2,3], T. Koshiba [2,4], T. Tokunaga [2,4], H. Iwata [1,2], N. Tsutsumi [1,2] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.CREST, JST, 3.Sch. of Agri., Meiji Univ., 4.Earth Note, Co. Ltd.)

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610 Genome-wide SNP survey based on RNA-seq data from seedling leaves of 10 *Aegilops tauschii* accessions

☆Nishijima, R. [1], K. Yoshida [2], K. Sato [3], S. Takumi [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Org. Adv. Sci. Tech., Kobe Univ., 3.IPSR, Okayama Univ.)

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611 Identification of the gene controlling heading date of rice cultivars adapted to the northern Tohoku Region of Japan

☆Nonoue, Y. [1,2], H. Takagi [1], H. Yaegashi [1], H. Kikuchi [1], S. Natsume [1], H. Utsushi [1], Y. Ogasawara [1], Y. Yoshitsu [2], S. Yokoi [2], R. Terauchi [1], A. Abe [1] (1.Iwate Biotech. Res. Ctr., 2.United Grad. Sch. Agric. Sci., Iwate U.)

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612 MutMap identified a novel gene related to endosperm amylose content in rice

○Abe, A. [1], H. Takagi [1], H. Utsushi [1], H. Yaegashi [1], H. Kikuchi [1], Y. Ogasawara [1], A. Uemura [1], S. Kawadai [2], R. Terauchi [1] (1.Iwate Biotechnol. Res. Ctr., 2.Iwate Agric. Res. Ctr.)

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613 Origin of rice varieties grown in Hokkaido

○Fujino, K., M. Obara (Hokkaido Agr Res Cent)

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614 Diversity of rice landrace in Hokkaido

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

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615 Genetic diversity among a local rice varieties in Hokkaido revealed by genome sequences

☆Takano, S., K. Fujino (NARO/HARC)

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616 Genome-wide association study of complex agronomic traits based on multi-environmental trials using soybean mini-core collections

Tsuda, M. [1], S. Watanabe [1,2], T. Shimizu [1], N. Oki [3], M. Hajika [4], T. Yamada [4], A. Kikuchi [5], S. Kato [5], T. Sugimoto [6], N. Yamaguchi [7], M. Saruta [8], K. Okano [9], K. Kosuge [9,10], K. Takahashi [4], N. Yamada [11], N. Tomooka [1], T. Hori [12], H. Iwata [12], M. Ishimoto [1], ○A. Kaga [1] (1.NIAS, 2.Univ. Saga, 3.NARO/KARC, 4.NARO/NICS, 5.NARO/TARC, 6.Hyogo Pref. Tech. Cent. for Agric. Forest. and Fish., 7.HRO Tokachi Agric. Exp. Stn., 8.NARO/WARC, 9.Agri. Res. Inst. Ibaraki Agri. Cent., 10.Ibaraki Pref. Rokkou Agri. & For. Management Office, 11.Nagano Pref. Vegetable and Ornamental Crops Exp. Stn., 12.Grad. Sch. Gric. Life Sci., U. Tokyo)

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617 Genome sequencing of sub clover (Trifolium subterraneum)

○Hirakawa, H. [1], P. Kaur [2], K. Shirasawa [1], S. Nagano [1], P. Nichols [3], R. Appels [4], S. Tabata [1], W. Erskine [2], S. Isobe [1] (1.Kazusa DNA Research Institute, 2.University of

Western Australia, 3.Department of Agriculture and Food Western Australia, 4.Murdoch University)

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618 De novo whole genome assembly and SNP discovery in horsegram

Shirasawa, K. [1], H. Hirakawa [1], R. Chahota [2], S. Nagano [1], T. Sharma [2], ○S. Isobe [1] (1.Kazusa DNA Research Institute, 2.CSK Himachal Pradesh Agricultural University)

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619 Analysis of genomic structure of wheat chromosome 6B based on BAC physical map and survey sequence

☆Kobayashi, F., T. Tanaka, H. Kanamori, Y. Mukai, S. Katagiri, W. Karasawa, Y. Katayose, J. Wu, H. Handa (NIAS)

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620 Development of twelve sets of chromosomal segment substitution lines that enhance allele mining in cultivated rice

☆Nagata, K. [1], Y. Nonoue [1,2,3], R. Mizobuchi [1], N. Ono [3], T. Shibaya [1], K. Ebana [1], K. Matsubara [1,4], E. Ogiso-Tanaka [1], T. Tanabata [1,5], K. Sugimoto [1], F. Taguchi-Shiobara [1], J. Yonemaru [1], Y. Uga [1], A. Fukuda [1], T. Ueda [1], S. Yamamoto [1], U. Yamanouchi [1], T. Takai [1,4], T. Ikka [1,6], K. Kondo [1,7], T. Hoshino [1,8], E. Yamamoto [1,9], S. Adachi [1,10], J. Sun [1], N. Kuya [1], Y. Kitomi [1], S. Choi [1], K. Iijima [1], H. Nagasaki [1,11], A. Shomura [1], T. Mizubayashi [1], N. Kitazawa [1], K. Hori [1], T. Ando [1], T. Yamamoto [1], S. Fukuoka [1], M. Yano [1,4] (1.NIAS, 2.Iwate Biotech. Res. Ctr., 3.STAFF, 4.NARO/NICS, 5.RIKEN CSRS, 6.Shizuoka Univ., 7.JIRCAS, 8.Yamagata Univ., 9.NARO/NIVTS, 10.Tokyo U. Agr. Tec, 11.NIG)

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621 A photoperiod-sensitivity QTL on chromosome 7A in tetraploid wheat interacts with *Ppd-A1*

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

Poster presentations

P001 A gene based crop model to predict heading date of progeny populations in unknown environment

☆Aoike, T. [1], M. Watanabe [1], A. Onogi [1], O. Ideta [2], T. Yoshioka [3], K. Ebana [4], M. Yamasaki [3], H. Nakagawa [5], H. Iwata [1] (1.Grad. Sch. Agric. Life Sci., U. Tokyo, 2.Natl.

Agr. Res. Ctr., Western Region, 3.Food Resources Education and Research Ctr., Grad. Sch. Agric. Sci., Kobe U., 4.Natl. Inst. Agrobiological Sci., 5.NARO/NARC)

P002 Heading date prediction of two BIL families 'Koshihikari' × 'Nipponbare' and 'Koshihikari' × 'Takanari' based on a gene-based crop model

☆Kajiya-Kanegae, H. [1], T. Aoike [1], J. Tanaka [2], T. Kataoka [3], K. Hori [4], H. Iwata [1] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.NARO Institute of Crop Science, 3.NARO KARC, 4.National Institute of Agrobiological Sciences)

P003 A novel selection criterion for genomic selection: Bayesian optimization

☆Tanaka, R. [1], A. Onogi [1], S. Yabe [2], H. Iwata [1] (1.Grad. Ach. Agric. Life Sci., Univ.Tokyo, 2.NARO Agricultural Research Center)

P004 New evaluation method of multiplexed soybean breeding lines

☆Yamada, T. [1], T. Nagaya [1], K. Hirata [2], K. Takahashi [1], A. Hishinuma [1] (1.NARO Institute of Crop Science, 2.NARO Tohoku Agricultural Research Center)

P005 Selection-system for breeding lines of soybean having good characteristics of processing to 'Natto' estimating with a small amount of steamed sample

☆Iwahashi, M. [1], C. Ikeda [1], T. Noguchi [2], Y. Kubo [2], H. Hasegawa [2], R. Nakagawa [2], K. Kosuge [3], M. Takahashi [4], M. Sakurai [5], K. Okamoto [1] (1.Plant Biotech. Inst. Ibaraki Agri. Cent., 2.Ibaraki Pref. Ind. Tech. Inst., 3.Ibaraki Pref. Rokko Agri. & For. Manegement Office, 4.National Center for Seeds and Seedlings Hokkaido-Chuo Station, 5.Ibaraki Pref. Fish. Exp. Sta.)

P006 Development and application of new method for polymorphism detection from shot reads of next-generation sequencer

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

P007 A field information management system for large-scale phenotyping and genotyping data

☆Asano, S. [1,2], K. Kamatsuki [1,2,3], H. Ohyanagi [1,2,3], M. Kobayashi [1,2], H. Kanegae [2,4], H. Takanashi [2,4], T. Tokunaga [2,5], T. Sazuka [2,6], H. Iwata [2,4], N. Tsutsumi [2,4], K. Yano

[1,2] (1.Sch. of Agri., Meiji Univ., 2.CREST, JST, 3.Mitsubishi Space Software Co., Ltd., 4.G. Sch. of Agricultural and Life Sci., The Univ. of Tokyo, 5.Earth Note, Co. Ltd., 6.Bioscience and Biotechnology Center, Nagoya Univ.)

P008 Resequencing analysis of rice 41 landraces and development of the allele mining tool

○Sakai, H., J. Yonemaru, H. Kanamori, Y. Katayose, T. Itoh, J. Wu (National Institute of Agrobiological Sciences, Japan)

P009 TOMATOMICS: An Integrated Database for Comprehensive Omics Infomation in Tomato

○Yano, K. [1], S. Ozaki [1], S. Terashima [1], M. Katayama [1], M. Kanno [1], S. Asano [1], M. Saito [1], M. Kobayashi [1], H. Ohyanagi [1], K. Aoki [2] (1.Sch. of Agri., Meiji Univ., 2.Grad. Sch. of Life and Env. Sci., Osaka Pref. Univ.)

P010 Genomic prediction and genome-wide association studies of sorghum seed morphology quantified using image analysis

☆Sakamoto, R. [1], H. Kanegae [1], K. Noshita [1], M. Ishimori [1], M. Kobayashi [2,3], H. Takanashi [1,3], A. Nagano [4,5], T. Tokunaga [3,6], T. Sazuka [3,7], K. Yano [2,3], N. Tsutsumi [1,3], H. Iwata [1,3] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Fac. Agr., Meiji Univ., 3.CREST, JST, 4.Cent. Ecol. Res., Kyoto Univ., 5.PREST, JST, 6.EARTHNOTE Co., Ltd., 7.Biosci. Biotech. Cent., Nagoya Univ.)

P011 Preliminary approach for development of core collection set based on the polymorphism data of SSR markers and CAPS markers among strawberry cultivars

○Wada, T. [1], Y. Noguchi [2], S. Isobe [3], M. Kunihisa [2,4], T. Sueyoshi [1], K. Shimomura [1] (1.Fukuoka Agric. Forest. Res. Cent., 2.NIVTS, NARO, 3.Kazusa DNA Res. Inst., 4.NIFTS, NARO)

P012 PGDBj—Integration of genome information in 80 plant species—

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

P013 The application of Semantic Web for plant genome information

☆Ichihara, H. [1], S. Shirasawa [1], A. Nakaya [2], Y. Nakamura [1], E. Asamizu [3], H. Hirakawa [1], S. Tabata [1] (1.Kazusa DNA Res. Inst., 2.Grad. Sch. Med., Osaka Univ., 3.Fac. Agr., Ryukoku Univ.)

P014 “Yukiminori”, a high-yielding waxy rice cultivar for rice cracker

○Nagaoka, I. [1], M. Yamaguchi [2], H. Sasahara [1], K. Matsushita [1], A. Shigemune [3], K. Miura [5], Y. Uehara [1], A. Goto [2], Y. Komaki [4] (1.NARO Agricultural Research Center, 2.NARO Institute of Crop Science, 3.NARO Western Region Agricultural Research Center, 4.Kagoshima Prefectural Government, 5.once NARO Institute of Crop Science)

P015 A new soybean cultivar 'Tatsumaro' with resistance to seed coat mottling and seed transmission to soybean mosaic virus

○Takada, Y. [1], M. Saruta [1], A. Okabe [1], A. Kikuchi [2] (1.NARO/WARC, 2.NARO/TARC)

P016 Developing of near isogenic lines of ‘Sachiyutaka’ with virus resistance

○Saruta, M., Y. Takada (NARO/WARC)

P017 A genealogy and agronomic traits of rice parental lines “Furukawa Taireichubo 104~110” with an extremely high cold tolerance at the booting stage

☆Saeki, K., T. Endo, H. Sato, Y. Nakagomi (Miyagi Prefectural Furukawa Agricultural Experiment Station)

P018 The development of a novel high amylose rice cultivar 'Amichanmai' with noodle making quality

○Matsushita, K. [1,2], S. Hagita [3], M. Yamaguchi [4], K. Miura [5], H. Sasahara [1], A. Shigemune [6], I. Nagaoka [1], A. Goto [4] (1.NARO/ARC Hokuriku Cent., 2.Grad. Sch. Sci. Tech., Niigata Univ., 3.Japan Grain Inspection Association, 4.NICS, 5.Ex. NARO/ARC Hokuriku Cent., 6.NARO/WARC)

P019 Development of cytoplasmic male sterile IR24 using CW-CMS/Rf17 system

○Toriyama, K., T. Kazama (Grad. Sch. Agri. Sci., Tohoku Univ.)

P020 Recent Development in Nagoya Protocol and revision of SMTA of ITPGRFA

○Yamamoto, A. (Minister's Secretariat, Ministry of Agriculture, Forestry and Fisheries)

P021 Evaluation of seed traits of azuki bean “KOMOIKE dainagon” cultivated in Kyoto

Inui, H. [1], ○Y. Yoshida [2] (1.Fac. Agr., Kobe Univ., 2.Food Resources Education and Research Center, Grad. Sch. Agr. Sci., Kobe Univ.)

P022 Evaluation of stigma exsertion in world rice core collection

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

P023 Study on genetic diversity of wild rice in the Mekong delta

☆Tamura, N. [1], I. Nakamura [2], S. Makabe [2], K. Toriyama [3], K. Igarashi [3], H. Pham [4], N. Lang [4], D. Lam [5], B. Buu [5], R. Ishikawa [1] (1.Fac. Agri. Life Sci.Hirosaki Univ., 2.Grad. Sch. Hort. Chiba U., 3.Grad. Sch. Agri. Sci, Univ. Tohoku, 4.Cuu Long Delta Rice Res. Inst., 5.Inst. Agri. South. Viet Nam)

P024 Screening for soil rot resistant genetic resources of sweetpotato

○Kobayashi, A. [1], Y. Kobayashi [1], Y. Okada [1], M. Yoshida [2], T. Sakai [1], Y. Kai [1], Y. Takahata [1] (1.Naro Kyushu Okinawa Agricultural Research Center, 2.Sch. Agr., Univ. Tokai)

P025 Metabolic responses to carbonate stress in the carbonate-tolerant plant Puccinellia tenuiflora and the carbonate-sensitive plant Poa annua

☆Nakamura, S. [1,2], S. Kobayashi [1], D. Tsugama [2,3], S. Liu [4], T. Takano [1,2] (1.ANESC., Univ. Tokyo, 2.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 3.JSPS Research Fellow (PD), 4.Northeast Forestry, Univ. China)

P026 Evaluation of parthenocarpic ability and fruit traits in parthenocarpic melon lines (*Cucumis melo* L. var. *makuwa*)

Zaelani, A. [1], M. Sugiyama [2], Y. Kawazu [2], K. Shimomura [2], R. Ohsawa [3], ○Y. Yosuke [3] (1.Grad. Sch. Life & Env. Sci., Univ. Tsukuba, 2.NIVTS, 3.Faculty Life & Env. Sci., Univ. Tsukuba)

P027 Ionome variation in Afghan wheat landraces and its association with genome-wide markers

☆Hattori, T. [1], K. Yoshimura [1], M. Alagu [2], Y. Kondo [3], M. Matsui [4], T. Ban [2], H. Iwata [1] (1.Grad.Sch.Agric.Life.Sci., Univ.Tokyo, 2.Kihara Institution for Biological Research,

Yokohama City Univ., 3.Sci., Kanto Gakuin Univ., 4.RIKEN Center for Sustainable Resource Science)

P028 Relationships between differentiations of seed coat types and mucilage in *Brassica rapa*

☆Maeda, T. [1], H. Yamagishi [2] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Fac. Life Sci., Kyoto Sangyo U.)

P029 The relationship between fruit color and polymorphism of *Psy* and *Ccs* genes, involved in carotenoid biosynthesis pathway, in pepper

☆Tsurumaki, K. [1], Y. Inaba [2], Y. Matsumoto [2], T. Sasanuma [1,2] (1.United Grad. Sch. Agr. Sci., Iwate Univ., 2.Fac. Agr., Yamagata Univ.)

P030 Pedigree analysis of sweetpotato cultivars in Japan

○Tabuchi, H., M. Tanaka, T. Sakai, Y. Takahata (NARO Kyushu Okinawa Agr. Res. Cent.)

P031 Evaluation of genetic variation among wild and cultivated rice in Cambodia

☆Orn, C. [1,2], R. Shishido [3], M. Akimoto [4], R. Ishikawa [1], H. Than Myint [1,5], R. Nishioka [1], S. Men [6], S. Sakhan [2], M. Ouk [2], T. Ishii [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Cambodian Agr. R&D Inst., 3.Coll. Biores. Sci., Nihon Univ., 4.Obihiro Univ. Agr. Vet. Med., 5.Yezin Agr. Univ., Myanmar, 6.Royal Univ. Agr., Cambodia)

P032 Chromosome behaviors during meiosis in interspecific hybrid of J. curcas and J. integerrima

☆Fukuhara, S. [1], M. Narathid [2], S. Kikuchi [1], T. Patcharin [2], P. Srinives [2], H. Sassa [1], T. Koba [1] (1.Grad. Sch. Hort., Chiba Univ., 2.Fac. Agri. Kamphaengsean, Kasetsart Univ.)

P033 Relationship of seed shattering and panicle spreading in the genetic background of wild rice, *Oryza rufipogon*

Inoue, C. [1], H. Than Myint [1,2], T. Ishii [1], ○R. Ishikawa [1] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Yezin Agr. Univ., Myanmar)

P034 Development of backcross inbred lines with genetic background of wild emmer wheat

○Mori, N. [1], K. Gyu [1], C. Vladutu [1], T. Ishii [2], S. Kianian [3] (1.Lab. of Crop Evol., Grad. Sch. Agr. Sci., Kobe Univ., 2.Lab. of Plant Breed., Grad. Sch. Agr. Sci., Kobe Univ., 3.USDA-ARS Cereal Disease Lab., Univ. Minnesota, U. S. A.)

P035 Genetic analysis of domestication traits using backcross derived lines with the genetic background of domesticated emmer wheat

☆Miyazaki, Y. [1], N. Pham-Minh [1], C. Vladutu [1], T. Ishii [2], S. Kianian [3], N. Mori [1] (1.Lab. Crop Evol., Grad. Sch. of Agric. Sci., Kobe Univ., 2.Lab. Plant Breed., Grad. Sch. of Agric. Sci., Kobe Univ., 3.USDA-ARS Cereal Disease Lab., Univ. Minnesota, U. S. A.)

P036 Diversity and relationships between root shape and hypocotyl/root in Japanese radish

☆Otsubo, K. [1], Y. Yoshida [2] (1.Grad. Sch. Agr. Sci., Kobe Univ., 2.Food Resources Education and Research Center, Grad. Sch. Agr. Sci., Kobe Univ.)

P037 Development and characterization of DEB-induced mutants in a rice cultivar "Tsuyahime" for a reverse genetic approach, TILLING

☆Kawakami, T. [1], T. Yoshida [1], E. Ishikawa [1], K. Abe [1], H. Goto [2], M. Chuba [3], T. Hoshino [1] (1.Fac. Agr., Yamagata Univ., 2.Yamagata Int. Agr. Res. Cent., 3.Rice Breed. Crop Sci. Exp. Stn., Yamagata Int. Agr. Res. Cent.)

P038 Effect of high LET ion-beam irradiation on mutation induction in rice

○Hayashi, Y. [1], R. Morita [1], K. Ichinose [1], S. Usuda [1], H. Toukairin [1], T. Sato [2], T. Abe [1] (1.Nishina Center, RIKEN, 2.Grad. Sch. Agric. Sci., Univ. Tohoku)

P039 Heavy-ion beam-induced deletion mutant library provides the map of essential chromosomal regions in *Arabidopsis thaliana*

☆Ishii, K. [1], Y. Kazama [1], T. Hirano [1,2], Y. Shirakawa [1], S. Ohbu [1], M. Yamada [1], T. Wakana [1], T. Abe [1] (1.RIKEN Nishina Cent., 2.Fac. Agric., Univ. Miyazaki)

P040 Alteration of flowering time by utilization of soybean EMS mutant library

○Nishizawa, K. [1], T. Sayama [2], T. Yamada [1], Y. Nanjo [1], A. Hishinuma [1], K. Takahashi [1], M. Hajika [1], T. Shimizu [2], A. Kaga [2], T. Anai [3], M. Ishimoto [2] (1.NARO Institute of Crop Science, 2.NIAS, 3.Saga University)

P041 Effects of genome editing by TALEN on the DNA methylation state of target region

☆Kaya, H. [1], H. Numa [2], A. Yokoi [1], D. Ogawa [1], S. Toki [1], Y. Habu [1] (1.NIAS, 2.NIAS)

P042 Natural variations in crossing ability and hybrid incompatibility with tetraploid wheat in *Aegilops umbellulata*

☆Okada, M. [1], K. Yoshida [2], S. Takumi [3] (1.Fac. Agr., Kobe Univ., 2.Org. Adv. Sci. Tech., Kobe Univ., 3.Grad. Sch. Agr., Kobe Univ.)

P043 *Nicotiana rustica* L. enhanced tumorigenesis compared to the progenitors of *N. rustica* in hybridization with *N. langsdorffii* Weinmann

○Takanashi, H., W. Marubashi (Sch. Agr., Univ. Meiji)

P044 Viable hybrids are produced at high frequency in lethal crosses between *Nicotiana amplexicaulis* and *N. tabacum*

☆Itakura, H., R. Nakamura, T. Morikawa, M. Yanase, S. Yokoi, T. Tezuka (Grad. Sch. Life Envi. Sci., Osaka Pref. U.)

P045 Morphological, histological and cytogenetical investigations of alloplasmic *Brassica oleracea* lines carrying each cytoplasm of four wild relative species

☆Taniguchi, K., S. Miyauchi, A. Kadota, S. Shim, S. Bang (Fac. Agric. , Utsunomiya U.)

P046 Genetic characteristics of calli and regenerated plants derived from anther culture in hybrids between *Oryza sativa* L. and *O. glaberrima* Steud

☆Kanaoka, Y. [1], D. Kuniyoshi [1], I. Masuda [1], E. Inada [1], Y. Okamoto [2], Y. Hoshino [3], Y. Kishima [1] (1.Res. Fac. Agri., Hokkaido U., 2.Rakuno Gakuen University, 3.Field Science Center for Northern Biosphere, Hokkaido U.)

P047 Studies on the variegated tobacco plants appeared in the chloroplast transformation experiment. III. Multipartite chloroplast genome

☆Uemura, K. [1], S. Morita [2], M. Yamamoto [3], T. Takami [4], W. Sakamoto [4], T. Terachi [1] (1.Fac.Life Sci., Kyoto Sangyo U., 2.Grad. Sch. Life and Envi., Kyoto Pref. U., 3.Kansai U. Welf. Sci., 4.IPSR, Okayama U.)

P048 Targeted genome editing in onion (*Allium cepa* L.)

☆Makabe, S. [1], T. Igawa [1], S. Imai [2], T. Kamoi [2], I. Nakamura [1] (1.Grad. Sch. Hort., Chiba U., 2.House foods Group Inc.)

P049 Production of a transplastomic tobacco plant expressing the sweet protein *Thaumatin* in the chloroplast

○Omori, K. [1], T. Terachi [2] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Fac. Life Sci., Kyoto Sangyo U.)

P050 Variations of pollen fertility and flower morphology in progenies of somatic hybrids between cabbage and *Arabidopsis thaliana*

☆Kanayama, J. [1], M. Tsujimura [2], H. Yamagishi [3] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Kyoto Sangyo U. Plant Organelle Genomics R. C., 3.Fac. Life Sci., Kyoto Sangyo U.)

P051 Construction of a linkage map and identification of *Plasmodiophora brassicae* pathotype specific CR QTLs

☆Kodama, T. [1], K. Kawamura [1], A. Md [2], M. Shimizu [1], R. Fujimoto [3], E. Fukai [1], K. Okazaki [1] (1.Grad. Sch. Sci. Tech., Niigata Univ., 2.Fac. Agri., Sylhed Agric. Univ., 3.Grad. Sch. Agric. Sci., Kobe Univ.)

P052 Identification and linkage analysis of bacterial blight resistance gene from XM14, a mutant line

☆Busungu, C. [1], K. Ichitani [2], J. Sakagami [2], T. Anai [3], Y. Kawaguchi [2], T. Tanaka [2], K. Kawabe [4], S. Taura [4] (1.Grad. Sch.Agri.Sci., Kagoshima Univ., 2.Fac.Agri.,Kagoshima Univ., 3.Fac.Agri.,Saga Univ., 4.Div.Gene Res.,Kagoshima Univ.)

P053 Toward identification of genetic factors regulating resistance to spikelet sterility under high temperature in rice

☆Hakata, M., H. Wada, C. Masumoto-Kubo, R. Tanaka, H. Sato, S. Morita (NARO Kyushu Okinawa Agricultural Research Center)

P054 The role of the acidic domain of chloroplast RNA binding protein CP31A involved in cold tolerance

○Okuzaki, A. [1,2], C. Schmitz-Linneweber [1] (1.Humboldt Univ. of Berlin, 2.Fac. Agr., Tamagawa Univ.)

P055 Relationship between salt stress and flowering pathways in *Arabidopsis thaliana*

☆Goto, Y. [1], Y. Takahata [1], S. Yokoi [2] (1.Fac. Agri., Iwate Univ., 2.Grad. Sch. Lif. Envi. Sci., Osaka Pref. Univ.)

P056 Heat stress response of Arabidopsis deficient in heat sensors during vegetative stage

☆Katano, K., R. Kataoka, M. Takahashi, M. Fujii, N. Suzuki (Sophia University, Faculty of Sciences and Technology)

P057 Functional analysis of miRNA528 for chilling tolerance in rice

☆Shimakage, R. [1], T. Komoto [1], H. Shimono [1], Y. Takahata [1], S. Yokoi [2] (1.Lab of Plant Breeding Faculty of Agriculture, Iwate University, 2.Lab of Plant Applied Biology Faculty of Agriculture, Osaka Prefecture University)

P058 Map-based cloning of a reduced culm number mutant gene RCN11 in rice

Takano, S. [1], S. Matsuda [1], A. Funabiki [1], J. Furukawa [2], T. Yamauchi [3], Y. Tokuji [1], M. Nakazono [3], Y. Shinohara [2], I. Takamure [4], ○K. Kato [1] (1.Agri. & Vet. Med., Univ. Obihiro, 2.Grad. Sch. Adv. Life Sci., Univ. Hokkaido, 3.Grad. Sch. Bioagr. Sci., Univ. Nagoya, 4.Res. Fac. Agri., Univ. Hokkaido)

P059 Sustained low abscisic acid levels increase seedling vigor under cold stress in rice

○Sato, Y. [1], R. Mega [2], A. Meguro-Maoka [3], A. Endo [4], E. Shimosaka [1], S. Murayama [5] (1.NARO Hokkaido Agricultural Research Center, 2.Arid Land Research Center, Tottori University, 3.Amino Up Chemical Co., Ltd., 4.National Institute of Agrobiological Sciences, 5.Alpine Plant Culture Center)

P060 Gene expression analysis of salt tolerant Arabidopsis expressing glycine-rich RNA-binding protein from S. virginicus

○Tada, Y. [1], M. Katsuhara [2], S. Ozaki [3], S. Terashima [3], C. Endo [1], K. Yano [3], T. Kurusu [1] (1.Sch. of Biosc. Biotechnol., Tokyo Univ. of Technol., 2.Inst. of Plant Sci. Resources, Okayama Univ., 3.Sch. of Agri., Meiji Univ.)

P061 Searching signals involved in response of Arabidopsis plants to a combination of heat stress and drought

☆Kumazaki, A., R. Nakano, M. Endo, N. Suzuki (Sophia University, Faculty of Materials and Sciences)

P062 Molecular mechanisms of aquaporin internalization induced by salt stress in *Arabidopsis thaliana*

☆Ueda, M. [1], M. Fujimoto [1], M. Fujiwara [2,3], Y. Fukao [2,4], N. Tsutsumi [1] (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.Plant Global Education Project, Grad. Sch. Biol. Sci., Nara Inst. Sci. Technol., 3.Inst. Adv. Bio., Keio Univ., 4.Col. Life Sci., Ritsumeikan Univ.)

P063 Effect of TaABA8'OH1 for wheat seed dormancy

○Matsunaka, H. [1], M. Chono [2], K. Nakamura [1], Z. Nishio [1], M. Okami [1] (1.NARO/KARC, 2.NARO/NICS)

P064 Response of Arabidopsis plants deficient in ROS regulatory systems to a combination of heat stress and drought

☆Fukui, G., N. Suzuki (Sophia University Faculty of Materials and Sciences)

P065 Effect of the quality of polished rice having high eating quality on rice cooking potential for the food-service industry and the home-meal replacement industry

☆Doman, K. [1], K. Nakamichi [2], H. Sato [2], T. Nishimura [1], Y. Hirayama [1], T. Yanagihara [2], T. Sato [1] (1.Kamikawa Agri. Exp. Stn., HRO, 2.Central Agri. Exp. Stn., HRO)

P066 Analysis of resistant starch content of long-chain type amyropectin rice variety, "Konayukinomai"

○Maeda, H. [1], K. Matsushita [1], I. Nagaoka [1], H. Sasahara [1], A. Ryuichiro [2], N. Wataru [2], Y. Masayuki [1] (1.NARO Agricultural Research Center, 2.Niigata Agricultural Research Institute, 3.NARO Institute of Crop Sience)

P067 Characteristic evaluation of genetic resources containing high level of β-glucan in breeding of barley cultivars for high functional foods

○Tonooka, T. [1], H. Araki [1], N. Kawada [1,2] (1.NARO Kyushu Okinawa Agric. Res. Cent., 2.Kyoto Gakuen Univ.)

P068 Varietal difference in *S*-methylmethionine (Vitamin U) Concentration in soybean seed

○Yamada, N. [1], Y. Miyazaki [2], S. Yamanaka [2], A. Morisaki [2], K. Matsui [2] (1.Nagano Vegetable and Ornamental Crops Exp. Stn., 2.Grad. Sch. Med., Univ. Yamaguchi)

P069 Characteristics of extraction in *Camellia* species using by Direct Analysis Real Time

☆Ogawa, S. [1], T. Oshikawa [2], K. Yoshino [2], A. Ogino [3], K. Furukawa [2] (1.National Institute of Technology, Numazu college, Adbanced Engineering Course, 2.National Institute of Technology, Numazu college, 3.National Agriculture and Food Research Organization, Institute of Vegetable and Tea Science)

P070 High spatial resolution of rice seed storage reserves by infrared micro-spectroscopy using synchrotron radiation

○Yoshida, K. [1], H. Sakai [2], F. Ishizuna [1], O. Yatou [3], T. Moriwaki [4], Y. Ikemoto [4] (1.Grad. Sch. Agr. Life Sci., Univ. Tokyo, 2.Fac. Agr., Univ. Tokyo, 3.NARO Agric. Res. Ctr., Hokuriku Res. Ctr., 4.SPring-8)

P071 Genetic variability in the yield and functional assessment of Yacon

○Matsuda, Y., S. Yasuda, T. Murata (Sch. Agri. Tokai U.)

P072 Rice variety selection for whole grain flour production with improved rice yield

○Suzuki, K., T. Ishii, Y. Takemoto-Kuno, Y. Takeuchi (NARO, Inst. Crop Sci.)

P073 Isolation of two new leucoanthocyanidin reductase (*LAR*) genes in buckwheat

○Matsui, K. [1], K. Katsu [1], T. Hisano [1], M. Mori [2], Y. Yasui [3] (1.NARO/KARC, 2.Res. Inst. Biores. Biotec. Ishikawa Pref. Univ., 3.Grad. Sch. Agric. Kyoto Univ.)

P074 Characterization of NERICA and local varieties cultivated in Africa on upland field

☆Agata, A. [1], T. Hobo [3], T. Kunishima [1], S. Ota [1], M. Doi [2], K. Doi [1], Y. Inukai [4], D. Makihara [4], H. Kitano [3] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Fac. Agr., Nagoya U., 3.Biosci. Biotec. Ctr., Nagoya U., 4.ICCAE, Nagoya U.)

P075 Identification of QTLs characterizing the panicle traits of the indica type multi-grain cultivar, VT-101

☆Ota, S. [1], T. Hobo [2], T. Touyama [1], K. Ando [1], A. Agata [1], D. Tran [3], D. Tran [4], H. Le [4], H. Kitano [2] (1.Grad. Sch. Bioagr. Sci., Nagoya U., 2.Biosci. Biotec. Ctr., Nagoya U., 3.Grad. Sch. IDEC, Hiroshima U., 4.Dep. Mol. Biol. Agric. Genet. Inst., Ha Noi, Vietnam)

P076 Mutants for saponin composition detected in the seeds of mutagen EMS treated soybeans by LC-PDA/MS/MS analysis

○Ohashi, U. [1], H. Abe [1], M. Itabashi [1,2], J. Kim [3], S. Maita [4], A. Kaga [4], T. Anai [5], J. Song [3], J. Lee [3], G. Chung [2], M. Ishimoto [4], C. Tsukamoto [1] (1.Fac. Agri. Iwate Univ., 2.Chonnam Natl. Univ., Rep. Korea, 3.Kyungpook Natl. Univ., Rep. Korea, 4.NIAS, 5.Fac. Agri. Saga Univ.)

P077 Characteristic of cell wall polysaccharide in mutant of hulless barley cultivar Shikokuhadaka 97

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

P078 Analysis of panicle structure formation by qSRN7 affecting grain number in rice

○Hobo, T. [1], Y. Fujishiro [2], R. Ishihara [2], S. Ota [2], T. Kunishima [2], A. Agata [2], I. Inari [1], J. Kyozuka [3], H. Kitano [1] (1.Biosci. Biotech. Ctr., Nagoya U., 2.Grad. Sch. Bioagar. Sci., Nagoya U., 3.Grad.Sch. Agric. Life Sci., U.Tokyo)

P079 Rice small seed mutants are due to the shorten cell length or the reduced cell number in lemma

Segami, S. [1,2], K. Miura [1], ○Y. Iwasaki [1] (1.Departemnt of Bioscience, Fukui Prefectural University, 2.JSPS research fellow)

P080 Search of the factors that control the antigravitropism of rhizomes from wild rice Oryza longistaminata

☆Uehara, K., J. Dominicus, H. Kondo, M. Ashikari (Bioscience and Biotechnology center)

P081 Change in the expression of flowering related genes of sugar beet by the de-vernalization treatment

○Kuroda, Y., H. Takahashi, K. Okazaki, K. Taguchi (NARO / HARC)

P082 Analysis of histone-methylation in *VRN1* gene of an alloplasmic wheat line showing late-flowering

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

P083 Evaluation of chilling requirement and narrow-sense earliness of barley cultivars

○Seki, M., T. Nagamine (NARO Agricultural Research Center)

P084 Roles of Arabidopsis group I bZIP proteins in regulating root tropisms - effects of multiple knockouts of them and visualization of PIN auxin transporters

☆Tsugama, D. [1,2], T. Takano [3] (1.Grad. Sch. Agric. Life Sci., Univ. Tokyo, 2.JSPS Research Fellow (PD), 3.ANESC., Univ. Tokyo)

P085 Copy number effect of *Oma1*-like gene clustered in *Rf1* locus on fertility restoration in sugar beet

☆Arakawa, T., H. Katsuyama, T. Kadowaki, T. Mikami, T. Kubo (Res. Fac. Agr., Univ. Hokkaido)

P086 Light suppression of shoot regeneration is induced by higher accumulation of endogenous abscisic acid in callus cultures derived from barley immature embryos

○Rikiishi, K., T. Matsuura, Y. Ikeda, M. Maekawa (Inst. Plant Sci. Res., Okayama Univ.)

P087 Culture conditions of hypocotyles and leaves in eggplant cultivars

☆Ibaraki, R. [1], H. Yamagishi [2] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Fac. Life Sci., Kyoto Sangyo U.)

P088 Variations of the Ogura cytoplasmic male-sterility gene (*orf138*) and its fertility restorer genes in cultivated radishes

☆Jikuya, M. [1], T. Terachi [2], H. Yamagishi [2] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Fac. Life Sci., Kyoto Sangyo U.)

P089 Is substoichiometric DNA molecule in mitochondria implicated in the evolution of wild-beet derived cytoplasmic male sterility?

○Kubo, T., T. Arakawa, R. Yui-Kurino (Res. Fac. Agr., Hokkaido Univ.)

P090 RNA-seq analysis of differentially expressed genes between RT98A CMS line and T65 maintainer line in rice

☆Igarashi, K. [1], T. Kazama [1], T. Kurata [2], K. Toriyama [1] (1.Grad. Sch. Agri. Sci., Tohoku Univ., 2.Grad. Sch. Life Sci., Tohoku Univ.)

P091 Identification of map position for male sterile genes (*ms-1~ ms-4*) in Cryptomeria japonica

○Moriguchi, Y. [1], K. Uchiyama [2], S. Ueno [2], T. Ihara [2], A. Matsumoto [2], M. Saito [3], J. Iwai [4], D. Miyajima [4], Y. Higuchi [5], S. Itoo [5], M. Sato [6], Y. Tsumura [7] (1.Niigata Univ. Grad. School Sci. & Tech., 2.FFPRI, 3.Toyama For. Res. Inst., 4.Niigata For. Res. Inst., 5.Ex. Niigata For. Res. Inst., 6.Ex. Niigata Univ. Fac. Agr., 7.Tsukuba Univ. Fac. Life and Environm. Sci.)

P092 Microsatellite markers linked to salt tolerance in barley "Hordeum vulgare L.

○Elakhdar, A. [1,2,3], K. Amer [3], A. Abdelsattar [2], T. Kumamaru [1] (1.Fac., Agric., Kyushu Univ., 2.Fac., Agric., Alex., Univ., Egypt., 3.Field Crops Res. Inst., ARC, Egypt.)

P093 Exploration of papaya leaf distortion mosaic virus resistance gene in *Vasconcellea cundinamarcensis*

○Tarora, K. [1], Y. Yabiku [1], R. Kaneshima [1], S. Kawano [1], K. Yasuda [1], H. Ueno [2], H. Matsumura [3], N. Urasaki [1] (1.Okinawa Pref. Agric. Res. Ctr., 2.Dep. Biosci. Tex. Tech., Shinshu Univ., 3.Gene Res. Ctr., Shinshu Univ.)

P094 Development and application of DNA markers derived from NGS data in soybean

○Watanabe, S. [1], C. Tsukamoto [1], T. Yamada [2], A. Kaga [3], T. Anai [1] (1.Fac. Agr., Univ. Saga, 2.Grad. Sch. Agr., Univ. Hokkaido, 3.NIAS)

P095 Linkage map construction in bitter gourd (Momordica charantia) using RAD-seq

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

P096 The draft genome sequence of bitter gourd (*Momordica charantia*)

○Urasaki, N. [1], H. Takagi [2], S. Natsume [2], A. Uemura [2], N. Taniai [1], N. Miyagi [1], M. Fukushima [3], S. Suzuki [3], K. Tarora [1], M. Tamaki [1], M. Sakamoto [1], R. Terauchi [2], H. Matsumura [3] (1.Okinawa Pref. Agric. Res. Ctr., 2.Iwate Biotech. Res. Ctr., 3.Gene Res. Ctr., Shinshu Univ.)

P097 Comparative analysis of chromosome structure using RADseq between Azuki and wild relatives and searching of salt tolerant genes

☆Ogiso-Tanaka, E., K. Naito, H. Sakai, A. Kaga, N. Tomooka (National Institute of Agrobiological Sciences)

P098 Trial of rice variety identification using INDEL (insertion and deletion) markers

○Yamashita, H. [1], K. Kogou [1], H. Yasue [2,3], A. Miyao [2], M. Nakagome [2] (1.KURABO INDUSTRIES LTD., 2.National Institute of Agrobiological Sciences, 3.Tsukuba GeneTechnology Laboratories Inc.)

P099 Improvement of gene annotation on barley genome by deciphering genomic sequence of Haruna Nijo

○Sato, K. [1], T. Tanaka [2], S. Shigenobu [3], Y. Motoi [1], J. Wu [2], T. Ito [2] (1.IPSR, Okayama Univ., 2.NIAS, 3.NIBB)

P100 Mapping of the black lemma and pericarp locus by exome capture in barley

☆Sakamoto, K., H. Hisano, Y. Motoi, K. Sato (IPSR, Univ. Okayama)

P101 High-density genotyping for rice recombinant inbred lines by whole genome sequencing

☆Oikawa, K., A. Uemura, H. Yaegashi, H. Kikuchi, A. Abe, R. Terauchi, H. Takagi (Iwate Biotechnology Research Center)

P102 Extraordinarily widespread horizontal genome transfers of a pararetrovirus into Poaceae species

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

P103 Association study of the QTLs for occurrence of hull-cracked grains to sink-source balance in Japanese malting barley

☆Haraguchi, Y., M. Hamada, H. Kai (Fukuoka Agric. Forest. Res. Cent.)

P104 Characteristics of QTLs for seed yield components and the application for improving sink capacity in soybean

☆Fujii, K. [1], S. Kato [2], K. Komatsu [3], T. Sayama [1], K. Takagi [4], R. Yano [1,5], K. Kosuge [6], K. Okano [6], C. Ikeda [6], M. Takahashi [7], N. Oki [7], A. Kaga [1], M. Ishimoto [1] (1.NIAS,

2.NARO/TARC, 3.NARO/HARC, 4.NARO/ARC, 5.Tsukuba Univ., 6.Ibaraki Plant-Biotec. Inst., 7.NARO/KARC)

P105 Detection of novel QTLs regulating grain size from extremely large-grain rices (*Oryza sativa* L.)

☆Segami, S. [1,2], T. Yamamoto [1], K. Oki [1], T. Noda [3], H. Kanamori [4], H. Sasaki [4], S. Mori [4], M. Ashikari [3], H. Kitano [3], Y. Katayose [4], Y. Iwasaki [1], K. Miura [1] (1.Faculty of Biotech., Fukui Pref. Univ., 2.JSPS Research Fellow, 3.Biosci. Biotech. Cent., Nagoya Univ., 4.NIAS)

P106 The verification of QTLs for White Core expression rate which “Yamadanishiki”, a brewing cultivar has

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

P107 Genetic analysis of biorefinery traits in rice straw

☆Goda, T. [1], H. Teramura [2], M. Suehiro [1], K. Kanamaru [3], K. Hori [4], M. Maeda [1], R. Takayama [5], D. Saisho [6], H. Yamamoto [7], A. Onogi [8], H. Iwata [8], H. Kawaguchi [2], C. Ogino [2], A. Kondo [2], M. Yamasaki [1] (1.Food Resour. Educ. and Res. Cent., Grad. Sch. of Agric. Sci., Kobe Univ., 2.Grad. Sch. of Eng., Kobe Univ., 3.Grad. Sch. of Agric. Sci., Kobe Univ., 4.Natl. Inst. of Agrobiol. Sci., 5.RMSB.inc, 6.IPSR, Okayama Univ., 7.FCR&Bio CO.,LTD., 8.Grad. Sch. Agric. Life. Sci., Univ. Tokyo)

P108 Fine mapping and BAC contigs construction of the susceptible gene to Alternaria blotch in apple

○Terakami, S. [1], S. Moriya [1], Y. Adachi [1], H. Fujisawa [2], S. Katagiri [2], H. Sasaki [2], K. Kurita [2], H. Kanamori [2], J. Wu [2], Y. Katayose [2], M. Kunihisa [1], C. Nishitani [1], K. Abe [1], T. Yamamoto [1] (1.NIFTS, 2.NIAS)

P109 Genetic analysis of Nekode gene in foxtail millet by QTL-seq

Masumoto, H. [1], H. Takagi [2], Y. Mukainari [1], R. Terauchi [2], ○K. Fukunaga [1] (1.Fac.Life & Environ. Sci., Pref. U. Hiroshima, 2.Iwate Biotech.Res.Center)

P110 Fine genetic and physical mapping of a major locus for monoecism in *Spinacia oleracea* L.

☆Iwabuchi, K. [1], S. Takahata [1], Y. Onodera [2] (1.Grad.Sch.Agr., Hokkaido Univ, 2.Res. Fac. Agr., Hokkaido Univ)

P111 Genetic linkage analysis for identifying root-knot nematode (*Meloidogyne incognita*) resistance gene in sweetpotato

☆Kishimoto, K. [1], R. Sasai [1], Y. Monden [2], Y. Okada [3], H. Tabuchi [3], A. Kobayashi [3], O. Jahana [4], S. Onaga [4], S. Isobe [5], H. Hirakawa [5], K. Shirasawa [5], M. Tahara [2] (1.Fac. Agri., Univ. Okayama, 2.Grad. Sch. Env. & Life Sci., Univ. Okayama, 3.KONARC, 4.OPARC, 5.Kazusa DNA Res. Inst)

P112 RNASeq analysis in sexual and apomictic guinea grass (Panicum maximum)

○Chen, L. [1], K. Yoshida [2], T. Suzuki [3], T. Higashiyama [3] (1.Fac. Environ. Horti. Sci., Minami Kyushu U., 2.Fac. Agri., U. Tokyo, 3.Fac. Sci., Nagaya U.)

P113 Reevaluation of DNA markers associated with sex differentiation in seaberry *Hippophae rhamnoides* L.

○Asakura, N. [1], K. Kondo [2], Y. Kawai [3] (1.Fac. Engin., Kanagawa Univ., 2.The Research Institute of Evolutionary Biology, 3.Fac. Agr., Tokyo Univ.of Agriculture)

P114 Assessment of genetic diversity of *Brassica napus* populations in Japan using SSR markers

☆Chen, R. [1], Y. Yoshioka [1], A. Shimono [2], M. Aono [3], N. Nakajima [3], R. Ohsawa [1] (1.Graduate School of Life and Environmental Sciences, University of Tsukuba, 2.Faculty of Science, Toho University, 3.National Institute for Environmental Studies)

P115 SNP detection and marker constructuion based on barley RNA-Seq

○Tanaka, T. [1,2], K. Okada [3], T. Kato [3], K. Namai [3], K. Sato [4], T. Matsumoto [1], S. Oda [2,5], M. Yano [2,5] (1.NIAS, 2.ACGRC, 3.Tochigi Prefectural Agricultural Experiment St., 4.Okayama University, 5.NICS)

P116 Comparative genome analysis of Koshihikari-related cultivars and comparative transcriptome analysis between Koshihikari and a disease resistant NIL

○Kawahara, Y. [1], N. Tanabe [2], T. Izawa [2] (1.Agrogenomics Res. Center, NIAS, 2.Div. of Plant Sci., NIAS)

P117 Comparison of gene expression patterns between homeologs in common wheat by RNA-seq analysis

☆Mizuno, N. [1], K. Sato [2], S. Nasuda [1] (1.Grad. Sch. Agri., Kyoto Univ, 2.IPSR, Okayama U.)

P118 A novel binary vector for genome editing of rice and a versatile idea for high-density crop hydroponics in a plant incubator

○Kuroda, M. [1], T. Yamaguchi [1], H. Yamakawa [1], S. Ikenaga [2] (1.NARO Agric. Res. Cent., 2.NARO Tohoku Agric. Res. Cent.)

P119 Coexpression-analysis based functional prediction of nutrient-deficiency response genes in rice

☆Takehisa, H., Y. Sato, B. Antonio, Y. Nagamura (NIAS)

P120 Identification of cis-motif in the TAM3 that regulates inhibition of nuclear import of TAM3 TPase in Antirrhinum

☆Zhou, H., M. Hirata, K. Makiya, K. Fujino, Y. Kishima (Hokkaido University)

P121 The positive-feedback loop established by transcription factors modified *mPing* insertions in rice

☆Yasuda, K. [1,2], T. Tsukiyama [1], Y. Okumoto [1] (1.Grad. Sch. Agri., Univ. Kyoto, 2.JSPS Research Fellow)

P122 Cytosine methylation dynamics of the petunia chalcone synthase genes in cosuppression and epigenetic reversion of the altered phenotype

☆Fukumoto, S., M. Kasai, A. Kanazawa (Res. Fac. Agr., Hokkaido Univ.)

P123 Production of green callus for chloroplast transformation of wheat

☆Nakamura, Y. [1], M. Tsujimura [2], H. Tsujimoto [3], T. Terachi [4] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Kyoto Sangyo U. Plant Organelle Genomics R.C., 3.ALRC, Tottori Univ., 4.Fac. Life Sci., Kyoto Sangyo U.)

P124 Production of a transplastomic lettuce containing a radish *gsh1* gene in the chloroplast genome

☆Abe, K. [1], T. Terachi [2], K. Uemura [2] (1.Grad. Sch. Life sci., Kyoto Sangyo U., 2.Fac. Life Sci.,Kyoto Sangyo U.)

P125 Determination of mitochondrial genome sequence of *Brassica oxyrrhina*

☆Mukai, A. [1], M. Tsujimura [2], T. Terachi [1], H. Yamagishi [1] (1.Grad. Sch. Life Sci., Kyoto Sangyo U., 2.Kyoto Sangyo U. Plant Organelle Genomics)