

Curriculum Vitae

Shoshi KIKUCHI

Senior Researcher in Plant Genome Research Unit,
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Education:

BS:1974.4-1978.3: The Graduate School of College of Arts and Sciences, The University of Tokyo.

MS:1978.4-1980.3: The Department of Biophysics and Biochemistry, The School of Science, The University of Tokyo.

Ph, D 1980.4-1983.3: The Graduate school of Biophysics and Biochemistry, The School of Science, The University of Tokyo

Employment:

1983.4-1983.11: Researcher in Plant Virus Institute,

1983.12-1988.10: Researcher in National Institute of Agrobiological Resources

1988.10-1989.10: Abroad study in Berlin West. Institute fur Genbiologische Forschung,

1989.10-1992.4: Senior researcher in National Institute of Agrobiological Resources

1992.5-1994.9: Administrative position in Science and Technology Agency in Japan.

1999.4-Present: Head of Lab of Gene Expression

2000.1-Present As a Project leader:

Rice microarray project (1999~2004)

Rice full-length cDNA project (2000~2005)

Generation Challenge Program (2004~2009)

BRAIN virus transcriptome project (2007~2012)

MAFF international collaboration project (2010~2013)

2006.4-Present As a senior researcher of Plant Genome Research Unit

Research Thema

Plant Genomics: Full-length cDNA collection from japonica rice, mapping to rice genome, functional annotation, establishment of microarray system, gene expression analysis through microarray system, data mining, development of the tools for data mining.

Physiology: Analyses of abiotic and biotic stress-responsive genes. Transcriptome analysis of virus-infected rice cells

Collaborative research

PI of the Generation Challenge Program SP-2 Project (2008-)

coPI of the Generation Challenge Program SP-2 Project (2005-2007)

PI of the Generation Challenge Program SP-4 project (2005-)

PI of the rice full-length cDNA project (2000-2003)

PI of the rice microarray project (2000-2004)

Collaboration with Japan-Korea (RDA: NIAB), with IRRI, with CIRAD

Foreign Languages

Fluent English

Research Interest

Mainly to the functional genomics of rice. Contributed to the massive collection and sequence analysis of rice full-length cDNA clones and the established the microarray systems. Rice transcriptomic analysis is the main way for the functional genomics. For the establishment of good data mining process, we have also contributed to the establishment of the good and user-friendly research tools.

Using the genomic resources, transcriptome analyses in rice with several kinds of environmental stress treatments, with virus infection are the current research thema.

Relevant Publications:

Sharoni A.M et al. (2010) Gene structures, classification, and expression models of the AP2/EREBP transcription factor family in rice **Plant and Cell Physiology** (Advance Access)

Kim C et al. (2010) Genetic analysis of gene expression for pigmentation in Chinese cabbage (*Brassica rapa*) **BioChip Journal** 4(2):123-128

Nuruzzaman M et al. (2010) Genome-wide analysis of NAC transcription factor family in rice **Gene** 465(1-2):30-44

Goh C-H et al. (2010) Mitochondrial activity in illuminated leaves of chlorophyll-deficient mutant rice (*OsCHLH*) seedlings **Plant Biotechnology Reports** 4(4):281-291

Kim C et al. (2010) Computational identification of seed-specific transcription factors involved in anthocyanin production in black rice **BioChip Journal** 4(3):247-255

She K-C et al. (2010) A novel factor *FLOURY ENDOSPERM2* is involved in regulation of rice grain size and starch quality **The Plant Cell** 22(10):3280-3294

Kim C et al. (2010) Computational identification of anthocyanin-specific transcription factors using a rice microarray and maximum boundary range algorithm **Evolutionary Bioinformatics** 2010(6):133-141

Hakata M et al. (2010) Production and characterization of a large population of cDNA-overexpressing transgenic rice plants using Gateway-based full-length cDNA expression libraries **Breeding Science** 60(5):575-585

Lee J-H et al. (2010) Single nucleotide polymorphisms in a gene for translation initiation factor (eIF4G) of rice (*Oryza sativa*) associated with resistance to Rice tungro spherical virus **Molecular Plant-Microbe Interactions** 23(1):29-38

Satoh K et al. (2010) Selective modification of rice (*Oryza sativa*) gene expression by rice stripe virus infection **Journal of General Virology** 91(1):294-305

Mizuno H et al. (2009) Characterization of 2159 unmapped full-length cDNA sequences of *Oryza sativa* L. ssp. Japonica 'Nipponbare' **Plant Molecular Biology Reporter** (Online First)

Berri S et al. (2009) Characterization of WRKY co-regulatory networks in rice and Arabidopsis **BMC Plant Biology** 9:120

Encabo J.R et al. (2009) Suppression of two tungro viruses in rice by separable traits originating from cultivar Utri Merah **Molecular Plant-Microbe Interactions** 22(10):1268-1281

Tanaka A et al. (2009) BRASSINOSTEROID UPREGULATED1, encoding a Helix-Loop-Helix protein, is a novel gene involved in brassinosteroid signaling and controls bending of the lamina joint in rice **Plant Physiology** 151(2):669-680

Madamba M.R.Set al. (2009) A recessive mutation in rice conferring non-race-specific resistance to bacterial blight and blast **Rice** 2(2-3):104-114

Kim C et al. (2009) Genetic analysis of seed-specific gene expression for pigmentation in colored rice **BioChip Journal** (3) 125-129

Masuo Y et al. (2009) Omic analyses unravels global molecular changes in the brain and liver of a rat model for chronic Sake (Japanese alcoholic beverage) intake **Electrophoresis** 30 1259-1275

Cho K et al. (2008) Integrated transcriptomics, proteomics, and metabolomics analyses to survey ozone responses in the leaves of rice seedling **Journal of Proteome Research** 7(7):2980–2998

Yamada-Akiyama H et al. (2008) Analysis of expressed sequence tags in apomictic guineagrass (*Panicum maximum*) **Journal of Plant Physiology** (Article in Press):Corrected Proof

Doi K et al. (2008) Development of a novel data mining tool to find cis-elements in rice gene promoter regions **BMC Plant Biology** 8 20.

Nagata T, Iizumi S, Satoh K, Kikuchi (2008) Comparative molecular biological analysis of membrane transport genes in organisms. **Plant Mol Biol.** 66. 565-585.

Satoh K, Doi K, Nagata T, Kishimoto N, Suzuki K, et al (2007) Gene Organization in Rice Revealed by Full-Length cDNA Mapping and Gene Expression Analysis through Microarray. **PLoS ONE** 2(11): e1235.

Nagata T. et al. (2005) Microarray analysis of genes that respond to r-irradiation in Arabidopsis. **J Agric. Food Chem.** 53, 1022-1030.

Nagata T. et al. (2004) Radial expansion of root cells and elongation of root hairs of Arabidopsis thaliana induced by massive doses of gamma irradiation. **Plant Cell Physiol** 45, 1557-1565.

Nagata T. et al. (2004) Comparative analysis of plant and animal calcium signal transduction element using plant full-length cDNA data. **Mol. Biol. Evol.** 21, 1855-1870.

Yazaki J. et al. (2004) Transcriptional profiling of genes responsive to abscisic acid and gibberellin in rice: phenotyping and comparative analysis between rice and Arabidopsis. **Physiol Genomics** 17, 87-100.

Sugimoto H. et al. (2004) The virescent mutation inhibits translation of plastid transcripts for the plastid genetic system at an early stage of chloroplast differentiation. **Plant Cell Physiol.** 45, 985-996.

Yang G-X. et al. (2004) Microarray analysis of brassinosteroids- and gibberellin- regulated gene expression in rice seedlings. **Mol Gen Genomics** 271, 468-478.

Yazaki J. et al. (2004) The Rice PIPELINE: a unification tool for plant functional genomics. **Nucleic Acids Research** 32, DB issue D383-D387

Ooka H. et al. (2004) Comparative analysis of NAC family genes in *Oryza sativa* and *Arabidopsis thaliana*. **DNA research** 10, 239-247.

Yazaki J. et al. (2004) Genomic approach to abscisic acid- and gibberellin- responsive genes in rice. **DNA research** 10, 249-261.

Kikuchi S. et al. (2003) Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice. **Science** 301:376-379.

Shimono M, et al. (2003). cDNA microarray analysis of gene expression in rice plants treated with probenazole, a chemical inducer of disease resistance. **J Gen Plant Pathol** 69,76-82

Otsuki S. et al. (2003) Novel gene encoding a Ca²⁺-binding protein and under hexokinase-dependent sugar regulation. **Biosci Biochem Biochem** 67, 347-353,

Yazaki, J. et al. (2002). The Rice Expression Database: gateway to rice functional genomics. **Trends in Plant Science** 7:563-564

Demura T, et al. (2002) Visualization by comprehensive microarray analysis of gene expression programs during transdifferentiation of mesophyll cells into xylem cells. **PNAS** 26;99(24):15794-15799.