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### Education

Ph. D. (March, 1978), M. Agr. (March, 1975), B. Agr. (March, 1973): Kyoto University

### Academic Carrier

1978 (April): Researcher, Division of Genetics, National Institute of Agricultural Sciences, MAF.

1983 (March)-1984 (March): Visiting scholar, Plant Breeding Institute, Cambridge.

1985 (April): Senior Researcher, Department of Molecular Breeding, National Institute of Agrobiological Resources, MAFF.

1990 (April): Head of Laboratory, Laboratory of Breeding Engineering, Department of Crop Development, Hokuriku National Agricultural Station, MAFF.

1998 (October): Professor (Head of Laboratory of Dynamic Cell Biology), Department of Biotechnology, Faculty of Engineering, Osaka University

2002 (April)-2005 (March) : Visiting Professor, Department of Mechanical and Machinery Science, Graduate School of Engineering, University of Tokyo

2010-2013: Director of Modern GP program

2007-: Core member of Global Education and Research Center for Bio-Environmental Chemistry (Global COE Program) at Osaka University

### Awards and Honors

The Japanese Society of Breeding Award (1999), The Osaka University Award for General Education (2008), J. Biosci. Bioeng. Award (2003), Award for Biocompetition Japan (2003).

### Total Publications

Original papers: 150, Review papers: 120, Books and Bookchapters: 70

### Research Interests

From the beginning of my research career, extensive efforts have been devoted to elucidate higher-order structure of plant and animal chromosomes, which are the physical carriers of organized genetic information. Recently, however, we started molecular breeding of bio-diesel producing plants for these five years because of the increased demands for the low carbon dioxide emission and creation of a low carbon society. We use a tropical shrub, *Jatropha curcas* L. as the target plant. First, we introduced some useful genes to produce higher tolerant *Jatropha* lines for droughtiness by developing an effective transformation method. Second, all the genome information has been read for the first time. Third, many molecular markers which are useful for molecular breeding, have been isolated. The similarity of all *Jatropha* lines collected from different continents and isles of Africa, Asia, Philippines is also confirmed, which may be useful for phylogenetic research of *Jatropha*.

# Global Greening: Toward Low Carbon Society

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To reconcile increasing energy consumption with worsening global environmental conditions is a fundamental concern of the contemporary society. Fossil fuel deposits are rapidly diminishing, and their consumption raises carbon dioxide discharge levels. Alternative fuels, such as bioethanol and biodiesel, show great promise for alleviating the problems caused by the consumption of fossil fuel. *Jatropha curcas* L. is a plant belonging to the family Euphorbiaceae that is endemic to tropical America. It is now grown commercially in tropical and subtropical Africa and Asia. *Jatropha* has considerable potential for various uses including biofuels. The plant can grow at rainfall levels as low as 200 mm per annum. Medicinal compounds are found in various parts of the plant, but it is the potentially high yield of oil per unit land area, which is second only to oil palm, that makes *Jatropha* an outstanding biofuel plant. Furthermore, the quality of oil in its seeds is suitable for production of biodiesel as they contain more than 75% unsaturated fatty acids. Despite its cultivation throughout the tropical and subtropical world, the positive attributes of this plant are not fully understood in terms of breeding and utilization. This can be attributed mainly to the lack of information on its genetics and genomics. The genome size (~410 Mb) and the base composition have been estimated by flow cytometry, and karyotypes have been characterized. Expressed sequence tags (ESTs) from developing and germinating *Jatropha* seeds have been reported. Furthermore, the whole genome of *Jatropha curcas* was sequenced, using a combination of the conventional Sanger method and new-generation multiplex sequencing methods. Total length of the non-redundant sequences thus obtained was 285 858 490 bp consisting of 120 586 contigs and 29 831 singlets. They accounted for ~95% of the gene-containing regions with the average G + C content was 34.3%. A total of 40 929 complete and partial structures of protein encoding genes have been deduced. Comparison with genes of other plant species indicated that 1529 (4%) of the putative protein-encoding genes are specific to the Euphorbiaceae family. A high degree of microsynteny was observed with the genome of castor bean and, to a lesser extent, with those of soybean and *Arabidopsis thaliana* and a total of 21 225 unigene data have been generated. Further information on the genomic sequences and DNA markers is available at <http://www.kazusa.or.jp/jatropha/><sup>(1)</sup>. In parallel with genome sequencing, development of an effective transformation method was explored. Based on the method developed, several new transgenic *Jatropha* plants were developed and now are examined under the tropical conditions<sup>(2)</sup>.

## References

- (1) Sato, S. et al. *DNA Res.* **2012**, *18*, 65-76.
- (2) Khemkladngonen, N. et al. *Plant Biotech. Rep.* **2011**, *5*, 235-243.