Environmental responses of plants: Biological interactions in the homogenous population or community (mixed populations)

Tsuyoshi Mizoguchi^{1,*}, Masatoshi Funabashi²

¹International Christian University (ICU), Osawa 3-10-2, Mitaka, Tokyo 181-8585, Japan; ²Sony Computer Science Laboratories, Inc. (Sony CSL), Shinagawa-ku, Tokyo 141-0022, Japan *E-mail: mtsuyoshi@icu.ac.jp

"Environmental responses of plants" is not a new topics but it has been studied for many years by many researchers. However, how to deal with the topics after the genome era is completely different from that before the completion of whole genome sequencing of model plant species.

Over 15 years have already passed since the completion of a whole genome sequencing of a model plant, *Arabidopsis thaliana* (Arabidopsis Genome Initiative 2000). Since then, whole genome sequencing of several other plant species such as *Oryza sativa* (International Rice Genome Sequencing Project 2005) and *Solanum lycopersicum* (The Tomato Genome Consortium 2012) has been reported.

The 1990's was an era of identification of genes whose mRNA levels increased or decreased in response to various environmental changes. Differential screening and differential display methods were often used for this purpose. Genetic screening of mutants whose responses to various environmental conditions were altered was performed and genes corresponding to the mutant phenotypes were identified with genetic mapping or T-DNA/transposon tagging methods. After identification of genes, we often realized that mRNA levels of these genes themselves changed in response to the conditions used to screen the mutants.

This special issue mainly focuses on the biological interactions in the i) homogenous population (Harper 1977; Pacala and Weiner 1991) or ii) community (mixed and heterogenous populations, Funabashi 2011; Funabashi et al. 2015) and includes responses of plants to 1) population density under artificial laboratory conditions (Takahashi et al., pp 333–339; Yamamoto et al., pp 323–331) and 2) eco-system under natural environmental conditions (Funabashi, pp 213–234; Ohta et al., pp 277–279).

Light quantity and quality changes during a variety

of direct and indirect interactions in the homogenous and heterogenous populations. The changes often affect both the biosynthesis and signaling of plant hormones. Therefore cellular and individual responses of the plants to changes of i) light conditions in their living circumstances and ii) hormones in their own cells play important roles in the biological interactions. This issue also includes responses of plants to 3) plant hormones (jasmonate, Chung et al., pp 235-243; auxin, Naramoto et al., pp 309-314; brassinosteroid, Suzuki et al., pp 315-321), 4) quantity and quality of lights (Tsukamoto et al., pp 297-307; Yoshida et al., pp 267-276) and 5) salinity stress (Chikha et al., pp 287-295). Novel methods to analyze 6) the membrane trafficking in plant cells by using GFP- and RFP-tagged proteins (Ito et al., pp 281-286) and 7) developmental processes by using overexpression of the transcription factors with the chimeric repressor or VP16 activation domains (Chung et al., pp 245-253; Fujiwara et al., pp 255-265) are also included in this volume.

Although this special volume could only introduce primary steps about the following issues, these would be of growing importance in the research areas of the biological interactions in the i) homogenous population and ii) community in the near future.

- Identification and functional analysis of unidentified sensor molecules or mechanisms (complexes) for abiotic factors such as temperature (high, low, ambient, etc), humidity, light quality (ultra-violet A (UVA), UVB, green light, etc) light quantity (strong and weak), and biotic factors such as bacteria, viruses and insects, etc, along with synergetic effect of those in natural environment toward the elucidation of ecological niche formation.
- II) Application of both knowledge and technologies obtained through them on food production of the

This article can be found at http://www.jspcmb.jp/ Published online October 26, 2016

next generation that could secure productivity and food quality in face of population growth, biodiversity loss and climate change. Especially those that could resolve fundamental trade-off between productivity and environmental load by making integrative use of plants environmental responses at community level.

We hope the information in this special issue will be useful not only for researchers currently working on the research area "Interactions between plants and their environment", but also for young investigators who are planning to jump in it with novel ideas and techniques in the near future.

References

Arabidopsis Genome Initiative (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* 408: 796–815 Funabashi M (2011) Foundation of Synecoculture: Toward an agriculture of synthetic and profitable ecosystems. *Actes du colloque Transversalités de l'agriculture biologique* 23&24 juin 2011, pp500-506

Funabashi M, Hanappe P, Isozaki T, Maes AM, Takahiro Sasaki T, Steels L, Yoshida K (2015) Foundation of CS-DC e-laboratory: Open Systems Exploration for Ecosystems Leveraging", Proceedings of CS-DC'15, Springer. http://cs-dc-15.org/ papers/territories/sys-explo-socio-eco/foundation-of-cs-dc-elaboratory-open-systems-exploration-for-ecosystems-leveraging/ Harper JL (1977) Population biology of plant. Academic Press

- Pacala SW, Weiner J (1991) Effects of competitive asymmetry on a local density model of plant interference. *J Theor Biol* 149: 165–179
- Sato S, Tabata S, Hirakawa H, Asamizu E, Shirasawa K, Isobe S, Kaneko T, Nakamura Y, Shibata D, Aoki K, et al.; The Tomato Genome Consortium (2012) The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485: 635–641
- Sequencing Project IRG; International Rice Genome Sequencing Project (2005) The map-based sequence of the rice genome. *Nature* 436: 793–800