Accelerator Applications Research Division
Beam Mutagenesis Group
Plant Genome Evolution Research Team

1. Abstract

Established in May 2018 and succeed in October 2020, the plant genome evolution research team studies the effect of heavy-ion induced mutations on plant and microbial phenotypes. Chromosome rearrangements including translocations, inversions, and deletions are thought to play an important role in evolution and have a greater potential to achieve large phenotypic changes. However, this potential has not been fully investigated due to the lack of an effective method to induce and analyze complexed mutations. We employ the population genomics approach with robust molecular biology and bioinformatics techniques to characterize genomic mutations in model and non-model plant and microbial species, and create the future of mutation breeding.

2. Major Research Subjects

(1) Genomics-based approach to revolutionize the mutagenesis in model and non-model plants and microbes
(2) De novo genome sequencing and assembly of cultivars and isolates, and its application to evolution and breeding studies

3. Summary of Research Activity

(1) Genomics-based approach to revolutionize the mutagenesis in model and non-model plants and microbes

Recent advances in genome sequencing and bioinformatics technology enabled us to obtain a genome-wide view of the induced mutations in unselected populations. We chose baker's yeast and a legume *Lotus japonicus* as model systems, irradiated different doses of carbon-ion beams to these organisms, and determined the dose-survival correlation. We isolated a semi-dwarf *L. japonicus* mutant, identified the responsible mutation by whole-genome sequencing, and started to characterize the phenotypic traits of this mutant. Phenotyping analysis indicated that the isolated semi-dwarf mutant shows significantly shortened internode length while still maintaining good seed production equivalent to the wild-type plants. The semi-dwarf *L. japonicus* mutant is suitable for high-density cultivation in the laboratory environment and may serve as an efficient model platform for legume- *Rhizobium* symbiosis.

(2) *De novo* genome sequencing and assembly of new cultivars and isolates, and its application to evolution and breeding studies

We apply the latest *de novo* genome sequencing technology to elucidate genome sequences in different cultivars and isolates and successfully created some high-quality draft genome sequences. The determined and assembled draft genome sequences are subjected to gene predictions and functional annotations, then shared in a searchable data visualization and analysis system accessible through the internet. With these fundamental genome information resources, we and our collaborators work together to achieve new findings that will achieve major advances in both science and practical applications. These resources as well as the overall experimental techniques and the analysis pipeline are essential to further expand our genome-wide mutation and evolution approach to previously uncharacterized non-model species.

Members

Team Leader

Hiroyuki ICHIDA

Postdoctoral Researcher

Ni LEI

Administrative Part-time Workers

Yusaku NISHIMIYA
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List of Publications & Presentations

Publications

[Original Papers]

H. Ichida, T. Kazama, S. Arimura, and K. Toriyama, "The mitochondrial and plastid genomes of *Oryza sativa* L. cv. Taichung 65," Plant Biotechnol. **40**, 109 (2023).

H. Murata, N. Nakamura, A. Ohta, and H. Ichida, "A semisolid plate method to isolate mycelia maintaining chlamydospore formation in *Tricholoma bakamatsutake*," Bulletin of FFPRI **22**, 13 (2023).

[Review Article]

H. Murata, A. Yamada, H. Ichida, N. Nakamura, and H. Neda, "Biodiversity of *Tricholoma matsutake* (syn. *T. nauseosum*) and its related species based on repetitive DNA and genomics," Botany (April 5, 2023), `https://doi.org/10.1139/cjb-2022-0122` .

Presentations

[International Conference/Workshop]

T. Abe (invited), Y. Hayashi, R. Morita, Y. Shirakawa, and H. Ichida, “Ion-beam mutagenesis for creation of new varieties and discovery of genes,” Bangabandhu International Conference on Sustainable Agriculture through Nuclear and Frontier Research, Online, January, 2022.

[Domestic Conferences/Workshops]

高塚歩, 風間智彦, 市田裕之, 阿部知子, 鳥山欽哉, 「Tadukan 型細胞質雄性不稔性イネのミトコンドリア RNA プロセッシングに関わる PPR 遺伝子の推定」, 第 10 回 植物 RNA 研究ネットワーク シンポジウム, 文京区, 2022 年 12 月.

市田裕之, Ni Lei, 森田竜平, 阿部知子, 「機械学習による変異バリデーション法の開発と検証」, 日本育種学会 第 142 回講演会, 帯広市, 2022 年 9 月.

稲田裕介, 高塚歩, 市田裕之, 鳥山欽哉, 「CW 型細胞質雄性不稔性イネに対するインディカ品種 Samba Mahsuri 由来の新規稔性回復遺伝子のマッピング」, 日本育種学会 第 142 回講演会, 帯広市, 2022 年 9 月.

高塚歩, 風間智彦, 市田裕之, 阿部知子, 鳥山欽哉, 「Tadukan 型細胞質雄性不稔性イネを稔性回復させる遺伝子の探索」, 日本育種学会 第 142 回講演会, 帯広市, 2022 年 9 月.

高塚歩, 風間智彦, 市田裕之, 阿部知子, 鳥山欽哉, 「Tadukan に由来する細胞質雄性不稔性イネの稔性回復候補遺伝子」, 第 39 回日本植物バイオテクノロジー学会（堺）大会, 堺市, 2022 年 9 月.

武田信哉, 市田裕之, 阿部知子, 有村慎一, 風間智彦, 陳孫禄, 金岡義高, 貴島祐治, 鳥山欽哉, 「台中 65 号の細胞質とアフリカイネの核を持つ TG-CMS の原因遺伝子とその稔性回復様式の調査」, 第 39 回日本植物バイオテクノロジー学会（堺）大会, 堺市, 2022 年 9 月.