



Asst. Prof.
FURUTA Tomoyuki



Boosting up crop breeding by integrated bioinformatics and statistical genetics

Along with drastically changing our lives, computers have also brought a paradigm shift in plant breeding. “Genomic breeding” is a state-of-the-art method which integrates genome-wide genotype information to model and predict phenotypic variation in populations. Although modern computer-based methods have strong potential for accelerating the development of new varieties, statistical models used in the method still need improvements to capture in detail events happening in real nature. At present, we try to integrate all useful environmental and biological data into new statistical models for genomic breeding that will allow accurate phenotype prediction within relatively small datasets. We apply a large variety of modeling methods that also include machine learning strategies. We hope that our work will boost up breeding in the future, helping to overcome the global shortage in food production experienced worldwide.



Exploring genetic diversity for discovery of novel beneficial genes and improved crop productivity



In addition to methodological approaches, we also use real plants to discover novel genes leading to practical improvements of rice. Currently, African cultivated rice *Oryza glaberrima* is our main genetic target and source for variety of stress tolerance-related genes. In particular, we hope that *O. glaberrima* will provide us with beneficial genes to promote rice yield even under harsh environments that spread as a result of global warming in the current era.