Prof. Kiyohiko Igarashi

Department of Biomaterial Sciences, Graduate School of Agricultural and Life Sciences
The University of Tokyo
1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan
+81-3-5841-5258; aquarius@mail.ecc.u-tokyo.ac.jp

Biography: Kiyohiko Igarashi (Kiyo) is an Associate Professor of Forest Chemistry Laboratory, Department of Biomaterial Sciences, Graduate School of Agricultural and Life Sciences in the University of Tokyo. Before receiving Ph. D., he focused on the kinetic analysis of cellobiose dehydrogenase, extracellular flavocytochrome produced by filamentous fungi, with Professor Masahiro Samejima (University of Tokyo) and the late Professor Karl-Erik L. Eriksson (University of Georgia). After receiving the degree, he stayed in Uppsala University (Sweden) as a Postdoc, and returned to the University of Tokyo as an Assistant Professor. He also started his visiting professor position in VTT Technical Research Centre of Finland from 2016. Currently he is doing biochemical and structural analysis of cellulase and other Carbohydrate-Active enZymes, and microbiology of wood-rotting fungi, in addition to the single molecular observations of cellulase and chitinase acting at the solid/liquid interface. He is the Associate Editor of "Journal of Applied Glycoscience", and Editorial Board Member of "Applied Environmental Microbiology" and "Journal of Wood Science". He also contributed to this field as a chair of Gordon Research Conference in Cellulosomes, Cellulases & Other Carbohydrate Modifying Enzymes 2015.

This is why I don't like introns - searching for good enzymes –

So far, wood-rotting fungi, such as white-rot and brown-rot fungi, are the only organisms known to grown on wood. They produce various enzymes outside of their cell, extracellular part of the mycelia, to degrade major components of plant cell wall such as cellulose, hemicellulose and lignin. There are many enzymes, which can be utilized for the biomass conversion, in those fungi, as well as the proteins helping and/or accelerating the degradation of the plant cell wall. Therefore, combination of correct annotation of these genes and the proteome analysis of the extracellular enzymes are quite important for biomass utilization.

In the present study, we have cultivated the white-rot basidiomycetes *Flammulina velutipes* (Enoki-take, winter mushroom) and *Phanerochaete chrysosporium* in various biomass-degrading culture, and the transcriptome databases were constructed by sequencing of the cDNA library using 454 sequencer. In *F. velutipes*, we identified 19 novel biomass-degrading enzymes including 12 carbohydrate-active enzymes (CAZymes) by 2-dimentional gel electrophoresis of extracellular proteins from cellulose-grown culture, using the transcriptome data as a reference sequence. In the case of *P. chrysosporium*, the transcriptome sequence data was also used to improve the gene annotation, and more than 1,000 genes are newly annotated by the algorithms refined by cDNA sequences. The improvement of gene annotation caused accurate prediction of introns and showed unique monodispersed distribution of intron length in this fungus.