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Educational Qualifications

Ph. D. in Agriculture, Tohoku University, March 2011

M. S. in Agriculture, Tohoku University, March 2008

B. S. in Agriculture, Tohoku University, March 2006

Professional Experiences

Research Assistant Professor in University of Shizuoka (2017-)

Postdoctoral fellow of Tohoku University (2011-2017)

Research Fellow of the Japan Society for the Promotion of Science (2009-2011)

Honors and Awards

1. The Tohoku Branch of the Japan Society for Bioscience, Biotechnology and Agrochemistry Society Award for Scientists (2015)

2. The Tohoku Branch of the Japan Society for Bioscience, Biotechnology and Agrochemistry Society Award for Young Scientists (2012)

Research Interests

Regulation of gene expression in filaments fungi

Cellular response to the high expression of secretory proteins in filaments fungi

Heterologous protein production using filaments fungi and yeast

Publications

Review and Book

1) Mizuki Tanaka*, Masafumi Tokuoka, Katsuya Gomi* (*Corresponding author): Effects of codon optimization on the mRNA levels of heterologous genes in filamentous fungi. *Appl. Microbiol. Biotechnol.*, 98: 3859–3867 (2014).

2) Mizuki Tanaka and Katsuya Gomi: Strategies for increasing the production level of heterologous proteins in *Aspergillus oryzae*. *Microbial production: From genome design to cell engineering*, Chapter 14: 149-164 (2014).

Original papers

(†Equally contributed)

1) Zhang S, Sato H, Ichinose S, Tanaka M, Miyazawa K, Yoshimi A, Abe K, Shintani T, Gomi K.

Cell wall α -1,3-glucan prevents α -amylase adsorption onto fungal cell in submerged culture of *Aspergillus oryzae*.

J. Biosci. Bioeng., in press.

2) Yokota JI, Shiro D, Tanaka M, Onozaki Y, Mizutani O, Kakizono D, Ichinose S, Shintani T, Gomi K, Shintani T.

Cellular responses to the expression of unstable secretory proteins in the filamentous fungus *Aspergillus oryzae*.

Appl. Microbiol. Biotechnol., 101: 2437-2446, 2017.

3) Zhang S, Ban A, Ebara N, Mizutani O, Tanaka M, Shintani T, Gomi K.

Self-excising Cre/mutant lox marker recycling system for multiple gene integrations and consecutive gene deletions in *Aspergillus oryzae*.

J. Biosci. Bioeng., 123: 403-411, 2017.

4) Tanaka M†, Yoshimura M†, Ogawa M, Koyama Y, Shintani T, Gomi K.

The C₂H₂-type transcription factor, FlbC, is involved in transcriptional regulation of *Aspergillus oryzae* glucoamylase and protease genes specifically expressed in solid-state culture.

Appl. Microbiol. Biotechnol., 100: 5859-5868, 2016.

5) Tanaka M, Shintani T, Gomi K

Unfolded protein response is required for *Aspergillus oryzae* growth under conditions inducing secretory hydrolytic enzyme production.

Fungal Genet. Biol., 85: 1-6, 2015.

6) Hiramoto T†, Tanaka M†, Ichikawa T, Matsuura Y, Hasegawa-Shiro S, Shintani T, Gomi K.

Endocytosis of a maltose permease is induced when amylolytic enzyme production is repressed in *Aspergillus oryzae*.

Fungal Genet. Biol., 82: 136-144, 2015.

7) Suzuki K[†], Tanaka M[†], Konno Y, Ichikawa T, Ichinose S, Hasegawa-Shiro S, Shintani T, Gomi K.

Distinct mechanism of activation of two transcription factors, AmyR and MalR, involved in amylolytic enzyme production in *Aspergillus oryzae*.

Appl. Microbiol. Biotechnol., 99: 1805-1815, 2015.

8) Ugai T, Minami A, Fujii R, Tanaka M, Oguri H, Gomi K, Oikawa H.

Heterologous expression of highly reducing polyketide synthase involved in betaenone biosynthesis.

Chem. Commun., 51: 1878-1881, 2015.

9) Tagami K, Minami A, Fujii R, Liu C, Tanaka M, Gomi K, Dairi T, Oikawa H.

Rapid reconstitution of biosynthetic machinery for fungal metabolites in *Aspergillus oryzae*: Total biosynthesis of Aflatrem.

ChemBioChem., 15: 2076–2080, 2014.

10) Ichinose S[†], Tanaka M[†], Shintani T, Gomi K.

Improved α -amylase production by *Aspergillus oryzae* after a double deletion of genes involved in carbon catabolite repression.

Appl. Microbiol. Biotechnol., 98: 335–343, 2014.

11) Tanaka M, Tokuoka M, Shintani T, Gomi K.

Transcripts of a heterologous gene encoding mite allergen Der f 7 are stabilized by codon optimization in *Aspergillus oryzae*.

Appl. Microbiol. Biotechnol., 96: 1275-1282, 2012.

12) Tanaka M[†], Sakai Y[†], Yamada O, Shintani T, Gomi K.

In silico analysis of 3'-end-processing signals in *Aspergillus oryzae* using expressed sequence tags and genomic sequencing data.

DNA Res., 18: 189-200, 2011.

13) Tokuoka M, Tanaka M, Ono K, Takagi S, Shintani T, Gomi K.

Codon optimization increases steady-state mRNA levels in *Aspergillus oryzae* heterologous gene expression.

Appl. Environ. Microbiol., 74: 6538-6546, 2008.