# ノート (Note)

# Phenotypic variations among wild-type strains of the ectomycorrhizal fungus Tricholoma bakamatsutake when associated with Quercus serrata and cultivated in a barley-based substrate

Hitoshi MURATA<sup>1)\*</sup>, Noritaka NAKAMURA<sup>2)</sup>, Akira OHTA<sup>3)</sup> and Hiroyuki ICHIDA<sup>4)</sup>

Key words: Agaricales, mushroom cultivation, plant-microbe interactions, symbiosis

## Introduction

Tricholoma bakamatsutake is an ectomycorrhizal fungus that produces fruiting bodies, which resemble the prized mushroom matsutake, in association with trees in the Fagaceae family, such as Quercus serrata and Quercus stenophylla (Murata et al. 2023b). The colony morphology of T. bakamatsutake varies among wild-type strains when grown on agar media to produce "slow-growing brown" and "fast-growing white" mycelia (Fig. 1; Murata et al. 2023a). Herein, we examined how variable such wild-type T. bakamatsutake strains are when associated with Q. serrata seedlings in vitro and when cultured in barleybased substrates, which are used for producing spawn for fruiting of the ectomycorrhizal mushroom Lyophyllum shimeji (Ohta 1994, Murata et al. 2019).



Fig. 1. Variable mycelial morphology of Tricholoma bakamatsutake SF-Tf08 grown in semisolid MMN + V8 + 0.3% SeaKem<sup>®</sup> GTG agarose<sup>™</sup> plates at 23°C for 65 days. (A.) Brown and (B.) white mycelia.

#### Materials and methods

T. bakamatsutake strains SF-Tf05 and SF-Tf08, and SF-Tf09 were obtained from a Q. stenophylla forest in Yogomachi, Shiga on September 19th, 2005, and September 12th, 2008, respectively (Murata et al. 2013a, b, Ichida et al. 2023). These were cultured in MMN + V8 liquid medium or on MMN + V8 containing either 1.5% agar or 0.3% SeaKem® GTG agarose<sup>™</sup> at 23°C (Murata et al. 1999, 2023a). SF-Tf05 strain solely exhibits brown mycelia on the MMN+V8 1.5% agar plate, and little segregates into white ones on the MMN + V8 semisolid 0.3% SeaKem<sup>®</sup> GTG agarose<sup>™</sup> plate (Murata et al. 2023a). SF-Tf08 strain originally exhibited brown mycelia but tends to segregate into white ones on the media plate with 1.5% agar. SF-Tf08 strain segregates into brown and white mycelia at the highest frequency on the semisolid plate with 0.3%SeaKem<sup>®</sup> GTG agarose<sup>™</sup> (Fig. 1; Murata et al. 2023a). SF-Tf09 strain tends to retain brown mycelia on a 1.5% agar plate but segregates into white mycelia to some extent on the semisolid plate with 0.3% SeaKem<sup>®</sup> GTG agarose<sup>™</sup> (Murata et al. 2023a).

Dual cultivation using Q. serrata and T. bakamatsutake was axenically performed in vitro based on a protocol by Murata et al. (2013c), except for using vermiculate instead of granite soil. Briefly, axenic Q. serrata plants were generated from sterilized Q. serrata seeds followed by cottage propagation of branches in Murashge and Skoog (MS: Fujifilm) agar. An axenic Q. serrata plant and six  $5 \times 5$ -mm pieces of T. bakamatsutake

Received 23 August 2023, Accepted 13 September 2023

1) Department of Mushroom Sciences and Forest Microbiology, Forestry and Forest Products Research Institute (FFPRI)

2) Kyushu Research Center, FFPRI

3) Kansai Research Center, FFPRI

- 4) RIKEN Nishina Center for Accelerator-Based Science
- Department of Mushroom Sciences and Forest Microbiology, FFPRI,
- 1 Matsunosato, Tsukuba, Ibaraki, 305-8687 JAPAN; E-mail: murmur@ffpri.affrc.go.jp

宿主共培養時および押し麦培地上でのバカマツタケ野生株表現型多型

- 村田 仁 1)\*、中村 慎崇 2)、太田 明 3)、市田 裕之 4) 原稿受付:令和 5 年 8 月 23 日 原稿受理:令和 5 年 9 月 13 日
- 1)森林総合研究所きのこ・森林微生物研究領域 2)森林総合研究所九州支所
- 3) 森林総合研究所 関西支所
- 4) 理化学研究所 仁科加速器研究センター

森林総合研究所 きのこ・森林微生物研究領域 〒 305-8687 茨城県つくば市松の里 1、E-mail: murmur@ffpri.affrc.go.jp

mycelia grown in MMN + V8 agar were coinoculated into substrates containing vermiculite and 1/4 MS liquid medium with 0.1% glucose and 0.5% sucrose (Murata et al. 2013a). Cocultivation was performed for 27 months at 23°C under daylight for 16 h per day and at 16°C under darkness for 8 h per day. At least three replicates were prepared per treatment. No control plants were used due to the limited numbers of axenic plants. Fresh weight (g) and above-ground height (mm) were measured. Significant differences (P < 0.05) among plants associated with different *T. bakamatsutake* strains were statistically analyzed using the Tukey–Kramer test. Fresh weight was measured, rather than dry weight, as plants were acclimatized with *T. bakamatsutake* mycorrhizas in open pots.

*T. bakamatsutake* was axenically cultivated with barleybased substrate prepared in 450-mL capped jar; the cap had an 8-mm vent sealed with MilliSeal (0.45 mm in pore size; Merck) to enable aeration without contamination (Murata et al. 2019, 2020) and had originally been developed for fruiting of *L. symeji* (Ohta 1994). At least two replicates were prepared per treatment.

## **Results and discussion**

Three T. bakamatsutake strains conferred three different responses on *Q. serrata* plants (Fig. 2). SF-Tf05 allowed the Q. serrata plants to wilt completely (Fig. 2A). SF-Tf08 with brown mycelia allowed two Q. serrata plants to grow while one seedling to wilt (Fig. 2B). SF-Tf08 with white mycelia allowed all three plants to completely wilt (Fig. 2C). SF-Tf09 with both brown and white mycelia, however, allowed all Q. serrata plants to apparently show better growth than any other plants with SF-Tf08 or SF-Tf09, exhibiting no sign of wilting (Fig. 2D and E). As it is difficult to axenically propagate Q. serrata plants, we could not establish control plants without T. bakamatsutake, which would have allowed us to examine how the association influenced plants in comparison with uninoculated plants. However, Q. serrata plants clearly responded in different ways to the three T. bakamatsutake strains.

SF-Tf09 with white mycelia conferred the highest total shoot growth, whereas SF-Tf05 with brown mycelia conferred least total shoot growth, between which the statistically significant differences were observed (Fig. 3A). SF-Tf08 with both brown and white mycelia and SF-Tf09 with brown mycelia conferred no significant total shoot growth in the plants as compared with all the *T. bakamatsutake* strains tested (Fig. 3A). Although plant response to different *T. bakamatsutake* strains visually differed from each other (see above, Fig. 2), which also reflected the difference in the total shoot length of plants with different *T. bakamatsutake* strains (Fig. 3A), there was no statistical difference in the total plant fresh weight among





Fig. 2. Quercus serrata plants axenically associated with Tricholoma bakamatsutake SF-Tf05, SF-Tf08 and SF-Tf09. SF-Tf05 only formed brown mycelial colonies and such mycelia were used for the experiment. SF-Tf08 and SF-Tf09 formed brown and white mycelia, which were separately inoculated in the rhizosphere of Q. serrata plants. Q. serrata plants with (A.) SF-Tf05, (B.) SF-Tf08 (brown mycelia), (C.) SF-Tf08 (white mycelia), (D.) SF-Tf09 (brown mycelia) and (E.) SF-Tf09 (white mycelia).



Fig. 3. Total shoot length (mm) and total fresh weight (g) of *Q. serrata* plants axenically associated with *T. bakamatsutake* strains. Significant difference (*P* < 0.05) was determined using the Tukey–Kramer test. Fresh weight, rather than dry weight, was measured because of the acclimatization of *Q. serrata* plants associated with *T. bakamatsutake* SF-Tf09 in soil in the open air.



Fig. 4. Dissecting and differential-interference-contrast micrographs of roots associated with *T. bakamatsutake* SF-Tf09. (A.) Dissecting micrographs, (B.) Differentialinterference-contrast micrographs. A large number of chlamydospores were observed; however, the Hartig net was not found.

the tested *T. bakamatsutake* strains (Fig. 3B). Although further open pot acclimatization experiment of plants with SF-Tf09 did not allow us to do so, dry weight analysis should be able to provide more statistically meaningful results.

Dissecting microscopic analysis revealed that the Q. serrata plants associated with SF-Tf09 contained carbonized mycorrhiza-like root tips without root hairs surrounded by fungal mycelia (Fig. 4A). By contrast, Q. serrata plants associated with SF-Tf05 and SF-Tf08 exhibited carbonized root tips but rare fungal association. Differential-interferencecontrast microscopy revealed that most of the mycorrhizallike tips with SF-Tf09 had a limited Hartig net, the hallmark structure of ectomycorrhizas, but did have many chlamydospores filled with mycorrhizal-like tips (Fig. 4B). We found a few ectomycorrhizas with a Hartig net in the plants associated with SF-Tf09, which indicates the occurrence of the ectomycorrhizal association between Q. serrata and SF-Tf09. Yamada et al. (2010, 2014) showed the occurrence of ectomycorrhizal association between Q. serrata seedlings and T. bakamatsutake B1 (NBRC 33138) in a soil condition with limited nutrients similar to that used in the present study. By observing the variability of such plant association profiles, we conclude that T. bakamatsutake could form a straindependent association with the native host *Q. serrata*. Notably, T. matsutake also differentially associates with the native hosts Pinus densiflora and Pinus sylvestris inhabiting Asia and Europe, respectively; a fungal isolate from Scandinavia can associate with both P. densiflora and P. sylvestris, and an isolate from Japan can associate with P. densiflora but not with P. sylvestris (Yamada et al. 2010, 2014).

Axenic cultivation of the fungal strains with the barleybased substrate showed that the thick brown mass of the SF- Tf05 mycelia grew rather irregularly or randomly in the substrate (Fig. 5A and B). By contrast, the thin white hyphae of *T. bakamatsutake* SF-Tf08 and SF-Tf09 grew more uniformly in the substrate (Fig. 5C and D). The brown mycelia of SF-Tf08 and SF-TF09 grew poorly in the substrate.

The behavior of *T. bakamatsutake* is complex and depends upon the fungal strains, association with a host plant, and growth in substrate cultivation, even with those from the same forest. Whether the phenomena presented in this study are relevant to the growth of phenotypic variants in an agar culture is unknown. The *T. bakamatsutake* strains SF-Tf05, SF-Tf08 and SF-Tf09 tested here did not exhibit any correlations between growth and morphology on an agar plate (Murata et al. 2023a) or with their behaviors in association with host plants or in substrate cultivation.

Our unpublished genomic analyses, using the nearlycomplete *T. bakamatsutake* SF-Tf05 genome sequences as a reference (Ichida et al. 2023), revealed that a high number of point mutations and deletions could occur in the genome of *T. bakamatsutake*. Although these could enable differentiation between the SF-Tf05, SF-Tf08 and SF-Tf09 genomes, we cannot specify which mutations are responsible for variable phenotypes among these strains. The current study implies that the population of *T. bakamatsutake* is highly variable, and strains suitable for both field and substrate cultivation could exist.

#### References

Ichida, H., Murata, H., Hatakeyama, S., Yamada, A. and Ohta, A. (2023) Near-complete de novo assembly of *Tricholoma bakamatsutake* chromosomes revealed the structural divergence and differentiation of *Tricholoma* genomes.



Fig. 5. Mycelial growth of *T. bakamatsutake* strains with barley-based substrate prepared in a 450-mL capped jar as described by Murata et al. (2019). (A and B.) SF-Tf05, (C.) SF-Tf08 (white mycelia) and (D.) SF-Tf09 (white mycelia).

G3; Genes, Genomes, Genetics, jkad198. https://www.doi. org/10.1093/g3journal/jkad198.

- Murata, H., Nakamura, N., Ohta, A. and Ichida, H. (2023a) A semisolid plate method to isolate mycelia maintaining chlamydospore formation in *Tricholoma bakamatsutake*. Bull. FFPRI. 22(1), 13–16. https://www.doi.org/10.20756/ ffpri.22.1\_13.
- Murata, H., Nakano, S., Yamanaka, T., Shimokawa, T., Abe, T., Ichida, H., Hayashi, Y. and Ohta, A. (2019) Conversion from mutualism to parasitism: a mutant of the ectomycorrhizal agaricomycete *Tricholoma bakamatsutake* that induces stunting, wilting and root degeneration in seedlings of its symbiotic partner, *Pinus densiflora*, in vitro. Botany, 97(8), 463–474. https://www. doi.org/10.1139/cjb-2019-060.
- Murata, H., Ota, Y., Yamada, A., Ohta, A., Yamanaka, T. and Neda, H. (2013a) Phylogenetic position of the ectomycorrhizal basidiomycete *Tricholoma dulciolens* in relation to species of *Tricholoma* that produce "matsutake" mushrooms. Mycoscience, 54(6), 438–443. https://www. doi.org/10.1016/j.myc.2013.02.003.
- Murata, H., Ota, Y., Yamaguchi, M., Yamada, A., Katahata, S., Otsuka, Y., Babasaki, K. and Neda, H. (2013b)
  Mobile DNA distributions refine the phylogeny of "matsutake" mushrooms, *Tricholoma* sect. *Caligata*, 54(6), Mycorrhiza, 23(6), 447–461. https://www.doi. org/10.1007/s00572-013-0487-x.
- Murata, H., Yamada, A. and Babasaki, K. (1999) Identification of repetitive sequences containing motifs of retrotransposons in the ectomycorrhizal basidiomycete *Tricholoma matsutake*. Mycologia, 91(5), 766–775. https://www.doi.org/10.1080/00275514.1999.12061082.
- Murata, H., Yamada, A., Ichida, H., Nakamura, N. and Neda,

H. (2023b) Biodiversity of *Tricholoma matsutake* (syn. *T. nauseosum*) and its related species based on repetitive DNA and genomics Botany, 101(5), 138–154. doi. org/10.1139/cjb-2022-0122.

- Murata, H., Yamada, A., Maruyama, T., Endo, N., Yamamoto, K., Ohira, T. and Shomokawa, T. (2013c) Root endophyte interaction between ectomycorrhizal basidiomycete *Tricholoma matsutake* and arbuscular mycorrhizal tree *Cedrela odorata*, allowing in vitro synthesis of rhizospheric "shiro." Mycorrhiza, 23(3), 235–242. https:// www.doi.org/10.1007/s00572-012-0466-7.
- Murata, H., Yamanaka, T., Shimokawa, T. and Ohta, A. (2020) Morphological changes in a γ-ray irradiation-induced mutant of the ectomycorrhizal agaricomycete *Tricholoma matsutake* during in vitro spawning on barley-based substrates. Bulletin of FFPRI 19(2) 153–157. https:// www.doi.org/10.20756/ffpri.19.2\_153.
- Ohta, H. (1994) Production of fruit-bodies of a mycorrhizal fungus, *Lyophyllum shimeji*, in pure culture. Mycoscience, 35, 147–151. https://www.doi.org/10.1007/BF02318492.
- Yamada, A., Endo, N., Murata, H., Ohta, A. and Fukuda, M. (2014) *Tricholoma matsutake* Y1 strain associated with *Pinus densiflora* shows a gradient of in vitro ectomycorrhizal specificity with Pinaceae and oak hosts. Mycoscience, 55(1), 27–34. https://www.doi.org/10.1016/ j.myc.2013.05.004.
- Yamada, A., Kobayashi, H., Murata, H., Kalmiş, E., Kalyoncu, F. and Fukuda, M. (2010) *In vitro* ectomycorrhizal specificity between the Asian red pine *Pinus densiflora* and *Tricholoma matsutake* and allied species from worldwide Pinaceae and Fagaceae forests. Mycorrhiza, 20(5), 333–339. https://www.doi.org/10.1007/s00572-009-0286-6.