Phylogenetic analysis of strains originally assigned to *Bullera variabilis*: descriptions of *Bullera pseudohuiaensis* sp. nov., *Bullera komagatae* sp. nov. and *Bullera pseudoschimicola* sp. nov.

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Twenty strains previously assigned to the species *Bullera variabilis* Nakase & Suzuki were reclassified using a molecular taxonomic approach. The strains were regrouped first by nucleotide sequence comparison of the rDNA internal transcribed spacer (ITS) regions, including the 5.8S gene. Phylogenetic positions of *B. variabilis* strains with different ITS region sequences were then analysed based on their 18S rDNA sequences. The taxonomic status of the original *Bullera variabilis* strains was clarified further by DNA–DNA hybridization experiments. Of the 20 strains studied, five remained in the species *B. variabilis*, six strains were reassigned to the species *Bullera mrakii* and three novel species were proposed for eight of the nine remaining strains, namely *Bullera pseudohuiaensis* sp. nov. (one strain; type strain JCM 5984T = AS 2.2203T), *Bullera komagatae* sp. nov. (one strain; type strain JCM 5983T = AS 2.2202T) and *Bullera pseudoschimicola* sp. nov. (six strains; type strain JCM 3915T = AS 2.2201T). The remaining strain, JCM 6140, was closely related to *B. pseudoschimicola*. However, differences in ITS region sequences between strain JCM 6140 and strains of *B. pseudoschimicola*, and the intermediate DNA–DNA relatedness to representative strains of *B. pseudoschimicola* did not allow a definite taxonomic decision to be made for strain JCM 6140.

**Keywords:** *Bullera variabilis, Bullera pseudohuiaensis* sp. nov., *Bullera komagatae* sp. nov., *Bullera pseudoschimicola* sp. nov., phylogeny

INTRODUCTION

*Bullera variabilis* Nakase & Suzuki (1987) was initially described to accommodate a group of yeast strains that formed ballistoconidia of various shapes. Heterogeneity of the species has been shown by markedly different electrophoretic enzyme patterns among strains studied. However, it has been difficult to separate clear-cut groups based on enzyme patterns or any other phenotypic characteristic.

The yeasts of this group are common inhabitants of plant materials. Since *B. variabilis* was established in 1987, a considerable number of ballistoconidium-forming yeast strains phenotypically similar or phylogenetically closely related to this species have been isolated from various countries, including China, Japan, New Zealand, Thailand and Vietnam (Nakase, 2000). Before novel strains can be accurately classified, it is necessary to redefine the species concept of *B. variabilis* and clarify the taxonomic status of the strains previously assigned to this species. Since it is difficult to reclassify *B. variabilis* strains by conventional yeast taxonomy, molecular phylogenetic approaches were used to resolve the problem.

Abbreviation: ITS, internal transcribed spacer.

The GenBank accession numbers for the ITS region and 18S rDNA sequences of the strains determined in the present study are AF314965–AF314989 and AF314990–AF314999, respectively.

METHODS

Yeast strains. The strains used are listed in Table 1. In addition to the 17 strains originally described as *B. variabilis* (Nakase & Suzuki, 1987), all other strains listed under this
name in the last edition of JCM Catalogue of Strains (Nakase, 1999) were included.

18S rDNA and internal transcribed spacer (ITS) region sequencing. Nucleotide sequences of small-subunit rDNA (18S rDNA) and internal transcribed spacer (ITS1 and ITS2) regions, including 5.8S rDNA, were determined according to Sugita & Nakase (1999) with the following modifications: cycle sequencing was performed using the ABI BigDye cycle sequencing kit and samples were electrophoresed on an ABI PRISM 310 Genetic Analyzer.

Molecular phylogenetic analysis. Sequences of the 18S rDNA and ITS regions determined in this study and reference sequences were aligned with the clustal w program (Thompson et al., 1994) and adjusted manually. The reference sequences were obtained from DDBJ, EMBL and GenBank, where they had been deposited by other authors (Sugita et al., 1999a; Suh & Sugiyma, 1993; Suh et al., 1996a; b; Swann & Taylor, 1993; Takashima & Nakase, 1998, 1999; Van de Peer et al., 1992). The phylogenetic tree was constructed from the evolutionary distance data calculated from Kimura’s two-parameter model (Kimura, 1980) using the neighbour-joining method (Saitou & Nei, 1987). Sites where gaps existed in any of the aligned sequences were excluded. Bootstrap analyses (Felsenstein, 1985) were performed from 1000 random resamplings.

DNA–DNA reassociation. Crude DNA was extracted from ground freeze-dried cells using the methods of Raeder & Broda (1985). DNA purification, DNA base composition determination and DNA–DNA reassociation were performed according to Takashima & Nakase (2000).

RESULTS AND DISCUSSION

Grouping of the B. variabilis strains by ITS region sequence comparison

The complete ITS region (including 5.8S rDNA) sequences of all the B. variabilis strains used were determined first. A dendrogram was drawn by neighbour-joining analysis based on alignment of the ITS region sequences. The 20 B. variabilis strains clearly separated into three groups corresponding to the three main clusters of the dendrogram (Fig. 1). Five strains, including B. variabilis JCM 5275T, clustered into group I, seven into group II and the other eight were in group III. Groups II and III were further subdivided as depicted in Fig. 1.

The total lengths of ITS1–5.8S rDNA–ITS2 regions of the strains were as follows: group I, 389 nt; group IIa, 470 nt; group IIb, 488–490 nt; group IIIa, 493 nt; and group IIIb, 496–498 nt. The dramatic differences in ITS region length of group I from those of groups II and III indicated that the strains in group I were remarkably different from those in groups II and III. According to ITS region sequence similarity, group I

<table>
<thead>
<tr>
<th>Group</th>
<th>Strain</th>
<th>Source</th>
<th>Assimilation of:</th>
<th>Starch formation</th>
<th>$T_{max}$ (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Lactose</td>
<td>Erythritol</td>
<td>Glucitol</td>
</tr>
<tr>
<td>I</td>
<td>JCM 5275T</td>
<td>Dead leaf of Oryza sativa, Japan</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>JCM 5276</td>
<td>Dead leaf of Oryza sativa, Japan</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>JCM 5277</td>
<td>Dead leaf of Oryza sativa, Japan</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>JCM 6137</td>
<td>Straw of Oryza sativa, Japan</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>IIa</td>
<td>JCM 7267</td>
<td>Dead leaf of Miscanthus sinensis, Japan</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>JCM 7584T</td>
<td>Dead leaf of Sasa sp., Japan</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>IIb</td>
<td>JCM 5986</td>
<td>Dead leaf of Sasa sp., Japan</td>
<td>l</td>
<td>L</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>JCM 7265</td>
<td>Dead leaf of Miscanthus sinensis, Japan</td>
<td>L</td>
<td>L</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>JCM 7266</td>
<td>Dead leaf of Miscanthus sinensis, Japan</td>
<td>L</td>
<td>L</td>
<td>-</td>
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<tr>
<td></td>
<td>JCM 7491</td>
<td>Sooty moulds on Pseudananas arboreum, New Zealand</td>
<td>l</td>
<td>L</td>
<td>-</td>
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<tr>
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<td>NB-54</td>
<td>Dead leaf of Miscanthus sinensis, Japan</td>
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<td>l</td>
<td>-</td>
</tr>
<tr>
<td>IIla</td>
<td>JCM 5983T</td>
<td>Dead leaf of Sasa sp., Japan</td>
<td>-</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>JCM 3914</td>
<td>Dead base of bamboo culm, Canada</td>
<td>-</td>
<td>l</td>
<td>L</td>
</tr>
<tr>
<td></td>
<td>JCM 3915T</td>
<td>Dead base of bamboo culm, Canada</td>
<td>-</td>
<td>w</td>
<td>+</td>
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<tr>
<td></td>
<td>JCM 5985</td>
<td>Dead leaf of Sasa sp., Japan</td>
<td>-</td>
<td>w</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>JCM 7406</td>
<td>Dead leaf of Vitis incisa var. lobata, Japan</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td>NB-143</td>
<td>Dead leaf of Miscanthus sinensis, Japan</td>
<td>-</td>
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<tr>
<td></td>
<td>NB-239</td>
<td>Dead leaf of Mueantheum bifolium var. dilatatum, Japan</td>
<td>-</td>
<td>-</td>
<td>l</td>
</tr>
<tr>
<td></td>
<td>JCM 6140</td>
<td>Dead leaf of Magnolia grandiflora, Japan</td>
<td>-</td>
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<td>-</td>
</tr>
</tbody>
</table>

Fig. 1. Dendrogram drawn from neighbour-joining analysis based on ITS region sequences showing the grouping of the B. variabilis strains.
Reclassification of *Bullera variabilis*

Among the five strains in this group, four strains, including the type strain of *B. variabilis*, had identical ITS region sequences which differed from the fifth strain (JCM 5277) in only 1 nt. However, both groups II and III seemed to be heterogeneous. The two subgroups in each of these two groups differed from each other significantly in their ITS region sequences. Even within the same subgroups, especially in group IIIb, the ITS region sequences of the strains differed from each other to varying degrees, as indicated in Fig. 1.

Physiological profiles of the three groups recognized by ITS region sequence analysis were compared and differences were found in assimilation reactions of lactose, erythritol, glucitol and ethylamine, starch formation and maximum growth temperatures (Table 1). Strains in group I had almost identical assimilation patterns and similar maximum growth temperatures and could easily be distinguished from strains in the other two groups. In group II, strains in group IIb also had identical physiological characters, enabling them to be differentiated from the strain in group IIa. Strains in group III could be distinguished from strains in the other two groups, but were less homogeneous in their physiological characters. Their erythritol and glucitol assimilation reactions and maximum growth temperatures were divergent. The two subgroups IIIa and IIIb were indistinguishable in their physiological characters.

**Phylogenetic positions of the *B. variabilis* strains inferred from 18S rDNA sequencing**

Heterogeneity of the *B. variabilis* strains was clearly demonstrated by their remarkable differences in ITS region sequences as mentioned above. To elucidate the phylogenetic relationships of the *B. variabilis* strains with one another and with other species in the genus *Bullera* and related xylose-containing basidiomycetous yeast taxa, 18S rDNA sequences of representative *B. variabilis* strains were determined, namely those belonging to groups II and III which differ from each other in more than one nucleotide in ITS region.
sequences. A phylogenetic tree was constructed based on 18S rDNA sequence alignment using neighbour-joining analysis (Fig. 2).

The 18S rDNA sequence of the type strain of *B. variabilis* (JCM 5275\textsuperscript{T}), which represents group I, has already been determined (Suh & Nakase, 1995). The similarities in ITS region sequences and in physiological characters among the strains in group I as discussed above suggest that this group is homogeneous and can thus be assigned to the species *B. variabilis*. Therefore, no other strain was selected from group I for 18S rDNA sequencing.

The groupings of the *B. variabilis* strains based on ITS region sequences were correspondingly separated in the phylogenetic tree based on 18S rDNA sequences (Fig. 2), which shows the species of *Bullera* separated into two main clades as already indicated by Suh et al. (1996a) and Takashima & Nakase (1999). The representative strains of the three groups in this study are limited to one of the clades, which coincides with the ‘Cryptococcus luteolus lineage’ of Takashima & Nakase (1999). *B. variabilis* JCM 5275\textsuperscript{T}, representing group I, is basal to the clade and thus only distantly related to the others. Strains of group II clustered with *Bullera mraigii*, *Bullera boninensis*, *Bullera waltii* and *Bullera huiaensis*. The four strains of group IIb had identical 18S rDNA sequences and were closest to *B. mraigii*, whereas strain JCM 5984\textsuperscript{T} had a unique sequence. All strains in group III had identical 18S rDNA sequences and clustered with *Bullera schimicola*.

**Phylogenetic relationships of the *B. variabilis* strains with closely related *Bullera* species demonstrated by ITS region sequence analysis**

The ITS region sequences of the *Bullera* species in the clade containing the representative *B. variabilis* strains in the tree drawn from 18S rDNA sequences (Fig. 2) were then determined and aligned with those of all the other sequences. A phylogenetic tree was constructed based on ITS region (including 5-8S rDNA) sequence alignment showing the relationships of the *B. variabilis* strains with closely related *Bullera* species. Bootstrap percentages over 50% from 1000 bootstrap replicates are shown. The GenBank/EMBL/DDBJ accession numbers are indicated.

![Phylogenetic tree](image)

**Fig. 3.** Phylogenetic tree drawn from neighbour-joining analysis based on ITS region (including 5-8S rDNA) sequence alignment showing the relationships of the *B. variabilis* strains with closely related *Bullera* species. Bootstrap percentages over 50% from 1000 bootstrap replicates are shown. The GenBank/EMBL/DDBJ accession numbers are indicated.
B. variabilis strains used in the present study. A phylogenetic tree was drawn, with group I as the outgroup, according to the topology of the phylogenetic tree constructed from 18S rDNA sequences. Four main clades were recognized in the phylogenetic tree drawn from the ITS region sequences and the original B. variabilis strains were distributed in three of them (Fig. 3).

**Taxonomic status of the strains in group II**

The strains in group II were included in the clade represented by B. mrakii (Fig. 3). The single strain in group IIA, JCM 5984T, clustered close to B. huiaensis and the five strains in group IIB were located together with B. mrakii. The numbers of nucleotide differences in ITS region sequences among all the strains in this clade were calculated by pairwise comparison. The strains in group IIB differed from each other in 1–6 nt and differed from the type strain of B. mrakii in 0–3 nt. Data predict that the group IIB strains belong to B. mrakii. Strain JCM 5984T differed from the type strain of the closely related species B. huiaensis in 18 nt (3-8%), implying that JCM 5984T represents a distinct species.

DNA–DNA reassociation was performed between the type strain of B. mrakii and selected group IIB strains (Table 2). Strains JCM 5986 and JCM 7491 were clearly conspecific with B. mrakii because DNA homology values with the type strain of this species were 77–93%. The other two strains, JCM 7265 and JCM 7266, had 82–87% DNA similarity, though they differed in 5 nt in ITS region sequences, but only had relatively low (56–68%) DNA homology with the type strain of B. mrakii, JCM 5986 and JCM 7491. Data indicate that strains JCM 7265 and JCM 7266 represent a somewhat different population from that represented by the type strain of B. mrakii. Considering that the two strains differed from the type strain of B. mrakii in only 2–3 nt in the ITS region and that their DNA relatedness with B. mrakii was still within the range of the same species, it is thought that they should be assigned to the species B. mrakii. The morphological and physiological characters of the group IIB strains corresponded to those in the description of B. mrakii (Hamamoto & Nakase, 1996).

As well as marked ITS region sequence differences, DNA homology of strain JCM 5984T with closely related species in the same clade was 17–31% (Table 3), which suggested that this strain represents an undescribed species, for which the name Bullera pseudohuiaensis sp. nov. is proposed.

**Taxonomic status of the strains in group III**

The B. variabilis strains in group III were located in a clade containing only one recently described species, B. schimicola (Sugita et al., 1999a) (Fig. 3). Group III strains differed from the type strain of B. schimicola in more than 18 nt (3-6%) in the ITS region, implying

### Table 2. DNA–DNA relatedness of selected group IIB strains of B. variabilis with the type strain of Bullera mrakii

<table>
<thead>
<tr>
<th>Species/strain</th>
<th>G + C (mol%)</th>
<th>8934T</th>
<th>7491</th>
<th>5986</th>
<th>7266</th>
<th>7265</th>
</tr>
</thead>
<tbody>
<tr>
<td>B. mrakii JCM 8934T</td>
<td>43.0</td>
<td>100</td>
<td>93</td>
<td>82</td>
<td>64</td>
<td>65</td>
</tr>
<tr>
<td>Strain JCM 7491</td>
<td>42.6</td>
<td>91</td>
<td>100</td>
<td>77</td>
<td>56</td>
<td>57</td>
</tr>
<tr>
<td>Strain JCM 5986</td>
<td>42.7</td>
<td>91</td>
<td>92</td>
<td>100</td>
<td>61</td>
<td>67</td>
</tr>
<tr>
<td>Strain JCM 7266</td>
<td>42.9</td>
<td>61</td>
<td>63</td>
<td>58</td>
<td>100</td>
<td>87</td>
</tr>
<tr>
<td>Strain JCM 7265</td>
<td>43.0</td>
<td>60</td>
<td>68</td>
<td>57</td>
<td>82</td>
<td>100</td>
</tr>
</tbody>
</table>

### Table 3. DNA–DNA relatedness of strain JCM 5984T with closely related species

<table>
<thead>
<tr>
<th>Species/strain</th>
<th>G + C (mol%)</th>
<th>5984T</th>
<th>8933T</th>
<th>934T</th>
<th>10570T</th>
<th>10575T</th>
</tr>
</thead>
<tbody>
<tr>
<td>B. pseudohuiaensis JCM 5984T</td>
<td>43.9</td>
<td>100</td>
<td>18</td>
<td>17</td>
<td>17</td>
<td>17</td>
</tr>
<tr>
<td>B. huiaensis JCM 8933T</td>
<td>44.5</td>
<td>31</td>
<td>100</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>B. mrakii JCM 8934T</td>
<td>43.0</td>
<td>23</td>
<td>ND</td>
<td>100</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>B. boninensis JCM 10570T</td>
<td>43.3</td>
<td>22</td>
<td>ND</td>
<td>ND</td>
<td>100</td>
<td>ND</td>
</tr>
<tr>
<td>B. waltii JCM 10575T</td>
<td>43.1</td>
<td>31</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>100</td>
</tr>
</tbody>
</table>

ND, Not done.
that the former can be genetically differentiated from *B. schimicola*. Although the representative strains in group III all had identical 18S rDNA sequences, strain JCM 5983<sup>T</sup> in group IIIa differed from the strains in group IIIb by 18–22 nt (3.6–4.4%) in the ITS region, suggesting that it represents a separate species. The taxonomic relationships of the seven strains in group IIIb showed by ITS region sequencing are not clear. Strain JCM 6140 differed from the other strains in the same subgroup by 7–11 nt in the ITS region and was on a separate branch in the neighbour-joining tree drawn from ITS region sequences (Fig. 3). However, its intermediate DNA–DNA homology values (52–62%) with, and its unclear ITS region sequence divergences from, other strains of group IIIb make it difficult to make a definite taxonomic decision for JCM 6140. Therefore, JCM 6140 should be treated as *Bullera* sp. at present.

**The taxonomic significance of the ITS region sequences, electrophoretic patterns of enzymes and mycocins**

Because of its relatively higher rate of divergence compared to small-subunit or large-subunit rDNA, ITS region sequences have been considered to be a useful tool in resolving relationships among closely related taxa (Berbee et al., 1995; Fell et al., 2000; James et al., 1996; Oda et al., 1997; Waalwijk et al., 1996). Recent studies involving yeasts have found that ITS region sequence similarity is generally consistent with DNA–DNA relatedness and conspecific strains usually have fewer than 1% nt differences in the ITS1 and ITS2 regions overall (Nagahama et al., 1996). The coincidence of the ITS region sequence similarity and DNA–DNA relatedness was observed among yeast strains used in the present study. However, up to approximately 2% nt divergences in the ITS1 and ITS2 regions overall exist among some strains within each species *B. mrakii* and *B. pseudoschimicola* sp. nov.

Boekhout et al. (1991) used six original *B. variabilis* strains in mating experiments. They found that mating only occurred between CBS 7347<sup>T</sup> (= JCM 5275<sup>T</sup>) and CBS 7367 (= JCM 7267). The former is the type strain of *B. variabilis* and the latter is retained in this species because of its identical ITS region sequence with the former. In the present study, the remaining four *B. variabilis* strains used by Boekhout et al. (1991) were

**Table 4. DNA–DNA relatedness of representative group III strains of *B. variabilis* with closely related species**

<table>
<thead>
<tr>
<th>Species/strain</th>
<th>G + C (mol%)</th>
<th>Relative binding (%) of DNA with JCM strain:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>3915&lt;sup&gt;T&lt;/sup&gt;</td>
</tr>
<tr>
<td><em>B. pseudoschimicola JCM 3915&lt;sup&gt;T&lt;/sup&gt;</em></td>
<td>44-4</td>
<td>100</td>
</tr>
<tr>
<td>Strain JCM 5985</td>
<td>44-3</td>
<td>66</td>
</tr>
<tr>
<td>Strain JCM 7486</td>
<td>43-9</td>
<td>67</td>
</tr>
<tr>
<td><em>Bullera sp. JCM 6140</em></td>
<td>44-7</td>
<td>54</td>
</tr>
<tr>
<td><em>B. schimicola JCM 10582&lt;sup&gt;T&lt;/sup&gt;</em></td>
<td>43-1</td>
<td>50</td>
</tr>
<tr>
<td><em>B. komagatae JCM 5983&lt;sup&gt;T&lt;/sup&gt;</em></td>
<td>44-5</td>
<td>35</td>
</tr>
</tbody>
</table>

ND, Not done.

The taxonomic status of the remaining strain in group IIIb, JCM 6140, is not easy to determine according to the data obtained so far. It does not seem reasonable to classify JCM 6140 as *B. pseudoschimicola* because this strain is located in a distinct branch, separated from the other strains of group IIIb by *B. schimicola* in the phylogenetic tree drawn from ITS region sequence comparison (Fig. 3). However, its intermediate DNA–DNA homology values (52–62%) with, and its unclear ITS region sequence divergences from, other strains of group IIIb make it difficult to make a definite taxonomic decision for JCM 6140. Therefore, JCM 6140 should be treated as *Bullera* sp. at present.
shown to belong to three other species: *B. pseudoschimicola* sp. nov. (CBS 7354 = JCM 3914), *B. pseudohiuiaensis* sp. nov. (CBS 7364T = JCM 5984T) and *B. mrakii* (CBS 7365 = JCM 7265; CBS 7366 = JCM 7266).

As mentioned previously, the heterogeneity of *B. variabilis* was first observed in the remarkable differences in electrophoretic patterns of enzymes among the strains originally assigned to this species (Nakase & Suzuki, 1987). However, it is difficult to clearly correlate enzyme pattern similarities with ITS region sequence similarities among these strains. The present study showed that strains showing similarities below 30% in enzyme electrophoretic patterns may certainly be expected to represent different species. However, conspecific strains may have as low as 36% similarity, whereas strains belonging to different species may have as high as 69% similarity in enzyme patterns. A previous study (Bai et al., 1999) also indicated that yeast strains with different enzyme patterns may have very high DNA–DNA complementarities.

Sensitivity to mycocins (killer toxins) has been considered to be a useful tool in yeast taxonomy (Golubev, 1998). Mycocinogeny studies (Golubev & Nakase, 1997, 1998) indicated that the killer-sensitive patterns of some strains originally classified as *B. variabilis* were different, implying that the species was heterogeneous. This observation has been confirmed here. However, the present study has shown that strains with different killer-sensitive patterns may be conspecific. For example, the two strains reclassified as *B. mrakii* in the present study, JCM 7479 and JCM 7491, have obviously different mycocin responses from each other and from the type strain of *B. mrakii* JCM 8934T (Golubev & Nakase, 1998). The type strain of *B. variabilis*, JCM 5275T, is insensitive to the *Bullera sinensis* mycocin, whereas strain JCM 6137, which has an ITS region sequence identical to that of JCM 5275T, is weakly sensitive to this mycocin.

**Latin diagnosis of *Bullera pseudohiuiaensis* Bai, Takashima & Nakase sp. nov.**


**Description of Bullera pseudohiuiaensis** Bai, Takashima & Nakase sp. nov.

*Bullera pseudohiuiaensis* (pseu.do.hui.a.en’sis. Gr. pseudes false; pseudohiuiaensis referring to the close relationship of the species to *Bullera huiiaensis*).

In YM broth, after 5 d at 17 °C, cells are oval, ellipsoidal or long ellipsoidal, 2–4 × 5–8 μm. They occur singly or in clusters (Fig. 4, left). True mycelia are also present. An incomplete ring and a sediment are formed. After 1 month at 17 °C, an incomplete ring, a fragile sediment and islets are present. On YM agar, after 1 month at 17 °C, the streak culture is light yellow, butyrous, wrinkled, semi-shining to dull and has an entire margin. In Dalmau plate culture on corn meal agar, pseudomycelia and true mycelia are produced. Ballistroconidia are produced on corn meal agar after 7 d at 20 °C. Bars, 10 μm.
soluble starch, D-xylose, L-arabinose, D-arabinose (delayed), D-ribose (delayed and weak), L-rhamnose (delayed), galactitol (weak), glucitol (delayed), methyl α-D-glucoside (delayed and weak), salicin (delayed), glucono-δ-lactone, 2-ketogluconic acid, 5-ketogluconic acid, succinic acid (delayed and weak) and inositol (delayed and weak) are assimilated. L-sorbose, lactose, inulin, ethanol, glycerol, erythritol, ribitol, D-mannitol, DL-lactic acid and citric acid are not assimilated. Ammonium sulfate, ethylamine hydrochloride (delayed) and L-lysine are assimilated. Potassium nitrate, sodium nitrate and cadaverine dihydrochloride are not assimilated. Thiamin is required for growth. Maximum growth temperature is 23–24 °C. Starch-like substances are produced. Urease activity is positive. Diazonium blue B reaction is positive. The G+C content of nuclear DNA is 43.9 mol% as determined by HPLC. The major ubiquinone is Q-10. Xylose is present in the whole cell hydrolysate. The type strain, JCM 5984T (originally NB-192T), was isolated from a dead leaf of Sasa sp. collected from Suga-daira, Nagano Prefecture, Japan in May, 1985. This strain has also been deposited in the China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, as AS 2.2203T.

As shown in Table 1, B. pseudoautosaprobica, represented by strain JCM 5984T, is physiologically distinct from the other taxa represented by the remaining strains originally assigned to the species B. variabilis. In practice, Bullera pseudoautosaprobica can be distinguished from its closely related species B. huiensis by its inability to assimilate mannitol and cadaverine.

Latin diagnosis of Bullera komagatae Bai, Takashima & Nakase sp. nov.


Description of Bullera komagatae Bai, Takashima & Nakase sp. nov.

Bullera komagatae (ko.ma.ga.tae. M.L. komagatae in honour of Professor K. Komagata, Japan).

In YM broth, after 5 d at 17 °C, cells are long oval to long ellipsoidal, 2–4 x 4–8 μm. They occur singly or in clusters (Fig. 5, left). True mycelia are also present. A ring and a sediment are formed. After 1 month at 17 °C, a ring, a fragile sediment and islets are present. On YM agar, after 1 month at 17 °C, the streak culture is orange-yellow, butyrous, smooth, semi-shining and has an entire margin. In Dalmau plate culture on corn meal agar, pseudomycelium and true mycelia are produced. Ballistoconidia are produced on corn meal agar. They are napticform, turbinate, trigonal or tetragonal, 3–4 x 4–6 μm (Fig. 5, right). Fermentation is absent. Glucose, galactose, sucrose, maltose, cellobiose (delayed), trehalose, melibiose, raffinose, melezitose, soluble starch, D-xylose, L-arabinose, D-arabinose (delayed), D-ribose (delayed), L-rhamnose (delayed), galactitol, D-mannitol (delayed), glucitol, methyl α-D-glucoside (weak), salicin, glucono-δ-lactone, 2-ketogluconic acid, 5-ketogluconic acid, succinic acid (delayed), citric acid (delayed and weak) and inositol (delayed) are assimilated. L-Sorbose, lactose, inulin, ethanol, glycerol, erythritol, ribitol and DL-
lactic acid are not assimilated. Ammonium sulfate and l-lysine are assimilated. Potassium nitrate, sodium nitrite, ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Thiamin is required for growth. Maximum growth temperature is 24–25°C. Starch-like substances are not produced. Urease activity is positive. Diazonium blue B reaction is positive. The G + C content of nuclear DNA is 44.5 mol% as determined by HPLC. The major ubiquinone is Q-10. Xylose is present in the whole cell hydrolysate. The type strain, JCM 5983T (originally NB-190T), was isolated from a dead leaf of Sasa sp. collected from Suga-daира, Nagano Prefecture, Japan, in May 1985. This strain has also been deposited in the China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China as AS 2.2202T.

**Latin diagnosis of *Bullera pseudoschimicola* Bai, Takashima & Nakase sp. nov.**


**Description of *Bullera pseudoschimicola* Bai, Takashima & Nakase sp. nov.**

*Bullera pseudoschimicola* (pseu.do.schi.mi.co’la. Gr. pseudo=false; pseudoschimicola referring to the close relationship of the species to *Bullera schimicola*).

In YM broth, after 5 d at 17 °C, cells are long oval, long ellipsoidal to club-shaped, 2–4 x 5–13 μm. They occur singly or in clusters (Fig. 6, left). True mycelia are also present. Usually a ring and a sediment are formed. After 1 month at 17 °C, a ring, a fragile sediment and islets are present. On YM agar, after 1 month at 17 °C, the streak culture is light yellow, orange-yellow or reddish-yellow, butyrous, smooth or wrinkled, shining or semi-shining and has an entire margin. In Dalmau plate culture on corn meal agar, pseudomycelia and true mycelia are produced. Ballistoconidia are produced on corn meal agar. Usually they are napiiform or turbinate. Polygonal, including trigonal, tetragonal or pentagonal, ballistoconidia are also produced, 40–50 x 6.0–7.5 μm (Fig. 6, right). Fermentation is absent. Glucose, galactose, sucrose (or delayed), maltose (or delayed), celllobiose (or delayed), trehalose (or delayed), melibiose, raffinose, melezitose, soluble starch, D-xylose (or delayed), L-arabinose (or delayed), D-arabinose (or delayed), D-ribose (delayed), L-rhamnose (or delayed), galactitol (variable), D-mannitol (or delayed), glucitol (variable), methyl z-D-glucoside (delayed or weak), salicin (or delayed or weak), glucono-δ-lactone (or delayed), 2-ketogluconic acid, 5-ketogluconic acid, succinic acid (or delayed or weak), citric acid (delayed and weak) and inositol (or delayed or weak) are assimilated. L-Sorbose, lactose, inulin, ethanol, glycerol, erythritol (or weak), ribitol (or weak) and DL-lactic acid (or weak) are not assimilated. Ammonium nitrate, sodium ni-
trite (or delayed and weak), ethylamine hydrochloride and cadaverine dihydrochloride are not assimilated. Thiamin is required for growth. Maximum growth temperature is 23–27 °C. Starch-like substances are not produced. Urease activity is positive. Diazonium blue B reaction is positive. The G + C content of nuclear DNA is 43.9–44.4 mol% as determined by HPLC. The major ubiquinone is Q-10. Xylose is present in the whole cell hydrolysate. The type, JCM 3915T, was isolated from the dead base of bamboo culm collected from Vancouver, Canada, in January, 1985. This strain has also been deposited in the China General Microbiological Culture Collection Center, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China as AS 2.2201T.

Phenotypically, B. komagatae and B. pseudoschimicola, originally B. variabilis strains in group III, are distinguishable from the strains in groups I and II (Table 1). However, these two novel species are indistinguishable from each other by the morphological, physiological and biochemical characters examined in the present study. They differ slightly from their closely related species B. schimicola in L-sorbosé assimilation reactions: the two novel species give negative results, whereas B. schimicola is weakly positive. In morphology, a considerable proportion of the ballistoconidia produced by strains of B. komagatae and B. pseudoschimicola were polygonal or irregularly shaped, whereas the ballistoconidia produced by B. schimicola were globose to napiform and polygonal or irregularly shaped ones were rarely observed.

**Redeinition of Bullera variabilis Nakase & Suzuki**

The original description of B. variabilis was based on the 17 strains studied by Nakase & Suzuki (1987). After reclassification of these strains in the present study, the demarcation of B. variabilis needs to be revised. According to the phenotypic characters of the five strains retained in B. variabilis, some physiological characters in the original description of this species are revised as follows: lactose and erythritol are not assimilated; galactitol and D-glucitol are assimilated; maximum growth temperature is 27–31 °C; and starch-like substances are produced. B. variabilis was also originally described as forming variously shaped ballistoconidia. However, the strains forming polygonal ballistoconidia were limited to group III of the present study and were assigned to the species B. komagatae and B. pseudoschimicola. The strains remaining in the species B. variabilis usually form napiform, turbinate to subglobose ballistoconidia as shown in the original figure of the type strain of this species (Nakase & Suzuki, 1987). The G + C contents of the type strain (JCM 5275T) and two other strains (JCM 5276 and JCM 5277) of B. variabilis were reported to be 55.9–56.9 mol% (Nakase & Suzuki, 1987), which differ remarkably from those of the strains in groups II and III (42.7–44.7 mol%; Tables 2, 3 and 4) which have been reassigned to other species.

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**REFERENCES**


Reclassification of *Bullera variabilis*


