STUDIES ON THE ANASTOMOSIS GROUPS OF BINUCLEATE *RHIZOCTONIA* AND THEIR PERFECT STATES

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Introduction

Binucleate *Rhizoctonia* have the characteristic mycelium of the genus *Rhizoctonia* DC[6], their vegetative mycelial cell is binucleate and the perfect state corresponds to the genus *Ceratobasidium* ROGERS[15]. According to this definition, there are a large number of binucleate *Rhizoctonia* within *Rhizoctonia* spp. and *Sclerotium* spp. which have been reported in the literature up to now[17,23]. These binucleate *Rhizoctonia* include several important plant pathogenic fungi as well as fungi associated with minor disease recently described[1,18,19].

OGOSHI *et al.*[17] indicated that the binucleate *Rhizoctonia* include various fungi and that they can be divided into groups with hyphal anastomosis like *R. solani*. They also described the anastomosis groups (AG-A-AG-O) of binucleate *Rhizoctonia* isolated in Japan. Meanwhile, BURPEE *et al.*[3] described the anastomosis groups (CAG-1-CAG-7) of binucleate *Rhizoctonia* isolated mainly in North America. As a result, it has become important to clarify the relation between both groups.

The premise that the perfect state of binucleate *Rhizoctonia* corresponds to the genus *Ceratobasidium*[17,24] can not always be validated on the basis of the observation of many isolates (or groups). Since it became evident that there are many anastomosis groups within binucleate *Rhizoctonia*, it should also be possible to identify the perfect state of the respective anastomosis groups. OGOSHI *et al.*[17] have already briefly reported that a number of isolates of Japanese binucleate *Rhizoctonia* formed a perfect state.

This study was undertaken to 1) determine which species among *Rhizoctonia* and related genera are binucleate, 2) clarify the relation between the Japanese and North American anastomosis groups of the binucleate *Rhizoctonia,* 3) observe the perfect state of the respective anastomosis groups, and 4) define the species name of fungi that belong to the respective anastomosis groups.

Materials and Methods

Isolates tested *Rhizoctonia* spp. were supplied by ATCC (American Type Culture Collection), CBS (Centraalbureau voor Schimmelcultures), and G. C. ADAMS, Jr., Department of Plant Pathology, University of California, Davis, U. S. A. (Table 1). Japanese binucleate *Rhizoctonia* used were the

TABLE 1. Binucleate *Rhizoctonia* among *Rhizoctonia* and related genera

Species	Accession*	BR or NBR**	BURPEE *et al.*[3]
R. alpina	CBS 309.35	BR	
R. anomala	CBS 116.12	BR	
R. crocorum	Adams' 710 (ATCC 10170)	NBR	
R. dichotoma	Adams' 715	NBR	
R. endophytica	ATCC 14013	BR	BR
R. endophytica var. *filicata*	ATCC 14014	NBR	
R. endophytica var. *filicata*	Adams' 714	NBR	
R. floccosa	Adams' 615	BR	BR
R. floccosa	CBS 337.36	BR	
R. fragariae	ATCC 14691	BR (AG-A)	BR (CAG-2)
R. fraxini	CBS 311.35	BR	BR
R. globularis	ATCC 14015	BR (AG-C)	
R. globularis	Adams' 713	BR (AG-C)	
R. lanuginosa	ATCC 11875	NBR	
R. mucoroides	ATCC 24974	NBR	NBR
R. mucoroides	Adams' 616	NBR	
R. muneratii	ATCC 13247	BR (AG-E)	BR (CAG-6)
R. oryzae	Adams' 541	NBR	NBR
R. pini-insignis	CBS 312.35	?	BR
R. quercus	CBS 313.35	?	NBR

Species	Accession*	BR or NBR**	BURPEE *et al.*[3]
R. ramicola	C B S 400.51	B R	
R. repens	A T C C 04975	N B R	
R. repens	Adams' 614	N B R	
R. rubi	A T C C 13342	?	
R. solani var. *fuchsiae*	C B S 343.36	B R	
R. stahlii	C B S 119.12	B R	
R. versicolor	Adams' 617	N B R	
R. zeae	C B S 384.34	N B R	
R. zeae	Adams' 590	N B R	
Corticium anceps	C B S 152.32	B R	
Ceratobasidium ramicola	Adams' 678	B R	B R (C A G-2)
Ceratobasidium stevensii	Adams' 681	?	
Waitea circinata	Adams' 241	N B R	

* *Rhizoctonia* spp. supplied by CBS (Centraalbureau voor Schimmelcultures), ATCC (American Type Culture Collection), and ADAMS, G. C.

** BR: Binucleate *Rhizoctonia*, NBR: Not binucleate *Rhizoctonia*, ?: Could not determine whether binucleate *Rhizoctonia* or not.

isolates of AG-A-AG-O (stock cultures of the Department of Plant Pathology, National Institute of Agricultural Sciences, and Laboratory of Plant Pathology, Faculty of Agriculture, Hokkaido University) described by OGOSHI *et al.*[17] However, AG-J and AG-M were excluded because these groups require further identification. North American isolates used were the isolates of CAG-1-CAG-7 supplied by L. L. BURPEE, Department of Agriculture and Fisheries, Botanical Garden, BERMUDA, and G. C. ADAMS, Jr. (Table 2). The isolates of *Rhizoctonia* spp. were examined to determine whether they were binucleate *Rhizoctonia*[17].

Observation of hyphal anastomosis Hyphal anastomosis between Japanese and North American isolates was observed, and *Rhizoctonia* spp. were fused with the representative isolates of AG-A-AG-O. The methods for the observation of hyphal anastomosis and determination of anastomosis groups were those described by OGOSHI[16].

Formation of perfect state The methods for obtaining the perfect state (the soil method) and for observing it were those described by STRETTON *et al.*[29] and OGOSHI[16]. The morphology and dimensions of the basidium, sterigma and basidiospore formed on soil were studied.

TABLE 2. Main isolates of binucleate *Rhizoctonia* used in anastomosis study

Anastomosis group	Isolate	Host or source	Geographic origin	Note
		Japanese isolates		
AG-A	AH-1	Peanut	Chiba	ATCC 38670
	SN-2	Soil	Nagano	
AG-Ba	C-314	Rice	Fukuoka	*Sclerotium fumigatum*
	C-484	Rice	Fukuoka	*Sclerotium fumigatum* ATCC 38673
AG-Bb	C-157	Rice	Fukuoka	*Sclerotium oryzae-sativae* ATCC 38472
	C-348	Rice	Fukuoka	*Sclerotium oryzae-sativae*
AG-B(others)	POER-2	Sweet potato	Tokushima	
	SIR-2	Sweet potato	Tokushima	
AG-C	GS-1	*Goodyera Schlechtendaliana*	Kyoto	
	STc-1	Soil	Tochigi	ATCC 38677
AG-D	C-46	Mat rush	Fukuoka	*Corticium gramineum*
	C-57	Mat rush	Fukuoka	*Corticium gramineum*
AG-E	F-18	Flax	Hokkaido	
	TM-1-1	Soil	Hokkaido	
AG-F	GJ-1	*Gerbera jamesonii*	Shizuoka	
	SIR-1	Sweet potato	Tokushima	
AG-G	CY-1-1	Soil	Hokkaido	
	OB-1-1	Soil	Hokkaido	
AG-H	STc-10	Soil	Tochigi	
	STc-12	Soil	Tochigi	
AG-I	AV-2	*Artemisia vulgaris* var. *indica*	Tokyo	
	54D09	Sugar beet	Hokkaido	
AG-K	AC-1	Onion	Hokkaido	
	SN-6	Soil	Nagano	
AG-L	EA-1	*Eleocharis acicularis*	Tokyo	
	FKo2-1	Soil	Fukuoka	
AG-N	SSh-2	Soil	Fukuoka	
AG-O	FKo2-24	Soil	Fukuoka	
	FKo6-2	Soil	Fukuoka	

Anastomosis group	Isolate	Host or source	Geographic origin	Note
		North American isolates*		
CAG-1	Bn 1	*Agrostis*	Pennsylvania	
CAG-2	Bn 4			ATCC 34969
CAG-3	Bn 31	*Arachis*	Georgia	
CAG-4	Bn 38	*Glycine*	Georgia	
CAG-5	Bn 37	*Cucumis*	Georgia	
CAG-6	Bn 74	*Erigeron*		ATCC 13247 *Rhizoctonia muneratii*
CAG-7	Bn 22	*Pittosporum*	Florida	FTCC 585**

* BURPEE *et al.*[3]
** Florida Type Culture Collection.

Results and Discussion

Binucleate *Rhizoctonia* Of the twenty-seven species of *Rhizoctonia* and related genera (33 isolates) examined, 13 species were binucleate *Rhizoctonia* (Table 1). *R. fragariae* ATCC 14691 corresponded to AG-A, two isolates of *R. globularis* to AG-C, and *R. muneratii* ATCC 13247 to AG-E. PARMETER and WHITNEY[23] reported that *R. endophytica, R. fragariae, R. fraxini, R. globularis, R. muneratii, R. pini-insignis,* and *R. quercus* were binucleate. BURPEE *et al.*[3] also reported that *R. endophytica, R. floccosa, R. fragariae, R. flaxini, R. muneratii, R. pini-insignis,* and *Ceratobasidium ramicola* were binucleate *Rhizoctonia.*

Hyphal anastomosis between Japanese and North American isolates Five of the 7 anastomosis groups of North American binucleate *Rhizoctonia* were identical with the Japanese groups for the following reasons : 2 isolates of AG-A had fused with the isolate Bn 4 of CAG-2 ; 2 isolates of AG-D had fused with the isolate Bn 1 of CAG-1 as reported by ONIKI *et al.*[19] ; 2 isolates of AG-E had fused with the isolate Bn 31 of CAG-3 ; and 2 isolates of AG-F had fused with the isolate Bn 38 of CAG-4 (Table 3). Since 2 isolates of AG-E had also fused with Bn 74 of CAG-6 which in turn had fused with Bn 31, CAG-3 and CAG-6 were considered to be identical. However, further studies on other isolates of both groups should be carried out in the future. Isolates of CAG-5 and CAG-7 had not fused with any of the isolates of the Japanese anastomosis groups and these two groups were thought to be different from the others.

Perfect state of binucleate *Rhizoctonia* Sixty-eight isolates among

TABLE 3. Hyphal anastomosis between Japanese and North American isolates of binucleate *Rhizoctonia*

Japanese		North American Isolates						
Group	Isolate	CAG-1 Bn 1	CAG-2 Bn 4	CAG-3 Bn 31	CAG-4 Bn 38	CAG-5 Bn 37	CAG-6 Bn 74	CAG-7 Bn 22
A	AH-1	−*	+	−	−	−	−	−
	SN-2	−	+	−	−	−	−	−
Ba	C-314	−	−	−	−	−	−	−
	C-484	−	−	−	−	−	−	−
Bb	C-157	−	−	−	−	−	−	−
	C-348	−	−	−	−	−	−	−
B (others)	POER-2	−	−	−	−	−	−	−
	SIR-2	−	−	−	−	−	−	−
C	GS-1	−	−	−	−	−	−	−
	STc-1	−	−	−	−	−	−	−
D	C-46	+	−	−	−	−	−	−
	C-57	+	−	−	−	−	−	−
E	F-18	−	−	+	−	−	+	−
	TM-1-1	−	−	+	−	−	+	−
F	GJ-1	−	−	−	+	−	−	−
	SIR-1	−	−	−	+	−	−	−
G	CY-1-1	−	−	−	−	−	−	−
	OB-1-1	−	−	−	−	−	−	−
H	STc-10	−	−	−	−	−	−	−
	STc-12	−	−	−	−	−	−	−
I	AV-2	−	−	−	−	−	−	−
	54D09	−	−	−	−	−	−	−
K	AC-1	−	−	−	−	−	−	−
	SN-6	−	−	−	−	−	−	−
L	EA-1	−	−	−	−	−	−	−
	FKo2-1	−	−	−	−	−	−	−
N	SSh-2	−	−	−	−	−	−	−
O	FKo2-24	−	−	−	−	−	−	−
	FKo6-2	−	−	−	−	−	−	−

* −: no anastomosis, +: anastomosis.

TABLE 4. Anastomosis groups and isolates of binucleate *Rhizoctonia* that developed the perfect state

Anastomosis Group	No. of Isolates tested	No. of Isolates that fruited	Anastomosis Group	No. of Isolates tested	No. of Isolates that fruited
A	64	7	G	8	5
Ba	20	0	H	9	5
Bb	15	4*	I	37	0
B (others)	23	4	K	6	0
C	27	11	L	20	15
D	57	9**	N	2	0
E	12	4	O	6	2
F	14	2	Total	320	68

* ONIKI *et al.*[20)]
** ONIKI *et al.*[21)]

11 of the 15 anastomosis groups of the Japanese binucleate *Rhizoctonia* developed their perfect states when the soil method was applied (Table 4), whereas the isolates of AG-Ba, AG-I, AG-K, and AG-N did not develope the perfect state. Data on the perfect state of AG-Bb and AG-D have already been reported by ONIKI *et al.*[20,21)]

Basidia formed were spherical or subglobose, differing from the clavate basidia of *Thanatephorus*. The dimensions of the basidia and basidiospores varied not only with the anastomosis groups but also with the isolates of the same group. Moreover, the dimensions of the isolates also varied widely (Table 5). Usually there were 4 sterigmata, rarely 3, except for AG-Bb that had only 2 sterigmata per basidium[20)].

On the basis of the characteristics of the basidium it was demonstrated that the isolates fruited corresponded to the genus *Ceratobasidium*. However, it was difficult to determine the name of a species from the morphology and dimensions of the basidium, basidiospore, and sterigma. PARMETER *et al.*[24)] also pointed out that the identification of the species name of *Ceratobasidium* was very difficult. However, many isolates appeared to be similar to *C. cornigerum* ROGERS[25)] and some were similar to *C. anceps* JACKSON[9)] (Table 6). It is evident that AG-Bb is different from *Ceratobasidium* spp. previously reported in the literature.

The dimensions of the components of the perfect states of *Ceratobasidium* spp. similar to those of *C. cornigerum* are shown in Table 6. As the dimensions of the basidium or basidiospore vary with the reports, it was

TABLE 5. Dimensions of the components of the perfect state of binucleate *Rhizoctonia* that fruited on soil

Anastomosis Group	Isolate	Basidia		Basidiospores		Sterigmata		
		Length (μm)	Width (μm)	Length (μm)	Width (μm)	Length (μm)	Width (μm)	Number
A	F C-2	10–15.5	8–10	8–9	5–6.5	6.5–8		4
	I B-1	10–14–20	8–9–10	8–9–10	5–5.5–6	10–12		4
B (others)	S T c-18	10–12–13	8–8.5–9	8–9	5–6.5	9–10		4
C	S T c-1	11–15–23	9–12–19	9–12–17	5–8–10	2–7–11	2–3–4	4
	S T c-2	16–18–21	13–14–16	10–11–13	5–7–8	8–13		(3–) 4
	S T c-3	16–19–23	10–13–16	10–13–16	6–7–8	16–23		(3–) 4
	S T c-4	13–16–21	10–12–13	8–10–16	6–7–8	8–13		4
	S T c-7	18–19–26	10–12–13	10–14–16	8–8–9	8–10		(2–) 4
E	F-7	16–26	10–11.5	9–13	5–8			4
G	S U-1	10–13	8	8	5	10		4
H	S T c-17	8–17–25	6–9–12	5–8–10	3–5–6	2–6–12	1–2–3	4
B b*		13.4–18.8	12.3–15.9	11.6–20.0	8.5–17.5	8.7–24.7	5	2
D**		11.3	9.2	8.7	5.2			4

* ONIKI *et al.*[20]
** ONIKI *et al.*[21]

TABLE 6. Dimensions of the components of the perfect state of *Ceratobasidium* and related species described in the literature

Species	Basidia		Basidiospores		Sterigmata			Author
	Length (μm)	Width (μm)	Length (μm)	Width (μm)	Length (μm)	Width (μm)	Number	
C. cornigerum	12–14	7.5–11	7.5–9.5	4–4.5–6	9–12	2–3	4	ROGERS[25]
	11–13	6.5–9	7.5–10	4–5.5	8.5	1.8–2	4	CHRISTIANSEN[5]
	13–17	9–12	6.5–9.3	4.5–6	–7		(3–) 4 (–6)	WARCUP and TALBOT[33]
C. obsculum	19–24	9–11	7.5–8	6	10–20	3.5–4.5	4	ROGERS[25]
	18–22	11.5–13	7.5–10	9–13	–20	3.5	4 (–6)	WARCUP and TALBOT[34]
C. anceps	10–18	8–12	9–12	4.5–7	10–16		(3–) 4	JACKSON[9]
C. pseudocornigerum	14–15	8–10	8–11.5	3.5–4	10	2.5	4	CHRISTIANSEN[5]
C. ramicola	8.0–11.1–15.6	5.2–7.8–10.8	5.2–8.5–10.5	3.5–5.2–6.9			4	TU *et al.*[30]
C. sphaerosporum	11–14.5	8–10		6.5–9	–6		4	WARCUP and TALBOT[35]
C. angustisporum	10–18	7–11	(7–) 11–14		6–9	2.5	4	WARCUP and TALBOT[36]
C. globisporum	15–22	13–16	10–12 (–14)	10–12	6–11 (–20)	2–3	4	WARCUP and TALBOT[36]
Hypochnus setariae	10–14	12–13	11–15	10–12	11–12	3–3.5	2	SAWADA[27]
Corticium gramineum	9.9–21.6	8.3–9.9	3.3–6.6	3.3–3.9				MATSUURA[12]

difficult to differentiate one species from another. In taking into account the fact that binucleate *Rhizoctonia* can be divided into several groups with hyphal anastomosis, it was deemed practical to divide *Ceratobasidium* spp. into groups with hyphal anastomosis, although some *Ceratobasidium* species have characteristic morphology and can be identified without difficulty.

Conclusions and General Remarks

From the results of the present study and other reports on the binucleate *Rhizoctonia*, the pathogenicity of each anastomosis group and its relationship to *Rhizoctonia* spp. and *Ceratobasidium* spp. can be described as follows:

AG-A

Rhizoctonia candida YAMAMOTO Pathogen of strawberry root rot[39], Pathogen of damping-off of sugar beet seedlings[40]
R. fragariae HUSAIN et MCKEEN Pathogen of strawberry root rot[7,17]
R. endophytica var. *endophytica* SAKSENA et VAARTAJA[26]
Pathogen of strawberry root rot[10]
Pathogen of tortoise shell-like symptoms of potato tubers[1]
Pathogen of browning of peanut pods[18,19]
Ceratobasidium cornigerum ROGERS[14,25]
CAG-2 (*C. cornigerum*)[3]
R. ramicola WEBER et ROBERTS[3,37]
C. ramicola TU *et al.*[30]
G-3 Isolates from diseased seedlings of sugar beets[31]
Ceratobasidium sp. (based on the results of the present study)

Rhizoctonia candida, which was reported as the pathogen of strawberry root rot and damping-off of sugar beet seedlings, was found to belong to AG-A. Some isolates of *R. fragariae*, which had been reported as being the pathogen of strawberry root rot, also belonged to this group. However, as some isolates that were identified as *R. fragariae* also belonged to AG-G or AG-I, *R. candida* could not always be identified as *R. fragariae*[17]. One isolate of *R. endophytica* var. *endophytica* and the causal fungus of strawberry root rot reported by KODAMA *et al.*[10] also belonged to this group. The pathogen causing tortoise shell-like symptoms of potato tubers and the main pathogen causing browning on peanut pods were reported to belong to AG-A. The latter disease is caused also by AG-G and *R. solani* AG-2-2 in some cases[19]. NISIKAWA and UI[14] reported that the isolate from *Spiranthes sinensis* (PERS.) AMES corresponded to *Ceratobasidium cornigerum* ROGERS, which also belongs to AG-A.

From the present study, it was concluded that AG-A and CAG-2 are identical. BURPEE *et al.*[3] reported that *R. fragariae* and *R. ramicola* belonged to this group and that the perfect state of CAG-2 isolates corresponded to *C. cornigerum*. Also TU *et al.*[30] reported that the perfect state of *R. ramicola* corresponded to *C. ramicola*. Although BURPEE *et al.*[3] reported that the isolate FTCC 169 A (Bn 57 by BURPEE *et al.*) of *C. ramicola* corresponded to CAG-2, this isolate supplied by ADAMS did not fuse with AG-A isolates and isolates Bn 4 of CAG-2 for undetermined reasons. UCHINO *et al.*[31] divided the isolates of binucleate *Rhizoctonia* recovered from diseased seedlings of sugar beets into five anastomosis groups (G-1-G-5) and reported that G-3 was similar to AG-A.

In the present study it was confirmed that the perfect state of AG-A also corresponded to *Ceratobasidium* spp. but the identification of the species requires further studies for the reasons mentioned above.

AG-Ba

Sclerotium fumigatum NAKATA Pathogen of "haiiro-kinkaku-byo" (gray sclerotium disease) of rice plant[13]

AG-Ba is identical with *Sclerotium fumigatum*. This fungus and *S. oryzae-sativae* are apparently binucleate *Rhizoctonia*, based on the morphology of the mycelium and sclerotium, and the number of nuclei in a cell[17]. The perfect state of this group has not been identified yet.

AG-Bb

Sclerotium oryzae-sativae SAWADA Pathogen of brown sclerotium disease of rice plant[28]

Ceratobasidium sp.

Hypochnus setariae SAWADA Pathogen of "haiiro-sirakinu-byo" (gray sclerotium disease) of foxtail millet[20,27]

AG-Bb is identical with *S. oryzae-sativae*, the causal fungus of brown sclerotium disease of rice plant. ONIKI *et al.*[20] observed the perfect state of this fungus, which had spherical basidia and two sterigmata per basidium. This fungus belongs to *Ceratobasidium* sp. but the identification of the species requires further studies because there are no species within *Ceratobasidium* spp. that correspond to this fungus. SAWADA[27] described *Hypochnus setariae* which had spherical basidia and two sterigmata per basidium. ONIKI *et al.*[20] suggested that these two fungi might be identical.

AG-B (others)

C. cornigerum Pathogen of sheath blight-like lesions of rice plant[22]

Ceratobasidium sp. (based on the results of the present study)

The perfect state of this group also corresponds to *Ceratobasidium* sp. (Table 5). ONIKI *et al.*[22] isolated a group of binucleate *Rhizoctonia* from sheath blight-like lesions on rice plant, which resembled *Sclerotium fumigatum* but differed from the latter in the colour of the colonies, and they identified it as *C. cornigerum*. This pathogen belongs to AG-B (others), but not to AG-Ba or AG-Bb.

AG-C

G-5 (*C. cornigerum*) Isolates from diseased seedlings of sugar beets[31]
R. globularis DOAM#138805A
Ceratobasidium sp. (based on the results of the present study)

Of the 5 groups of sugar beet seedling isolates described by UCHINO *et al.*[31], G-5 was found to belong to AG-C as *R. globularis* supplied by ADAMS. UCHINO *et al.*[31] observed the perfect state of an isolate of AG-C, and identified it as *C. cornigerum*. The isolates of AG-C formed the perfect state even on water agar[17]. The perfect state of AG-C corresponds to *Ceratobasidium* sp. (Table 5).

AG-D

Corticium gramineum IKATA et MATSUURA Pathogen of foot rot of cereals[12], Pathogen of winter stem rot of mat rush[8,11]
Ceratobasidium gramineum (IKATA et MATSUURA) ONIKI *et al.*[21]
CAG-1[3,21]
R. cerealis van der Hoeven Pathogen of sharp eyespot of cereals[2], Pathogen of yellow patch of turfgrass[3,4]

Corticium gramineum, the causal fungus of foot rot of cereals, is similar to this group. MATSUOKA[11] reported that the winter stem rot fungus of mat rush (*Junchus effusus* L. var. *decipiens* BUCHEN) reported by IKATA and YOSHIDA[8] could be identified as *C. gramineum*. On the other hand, ONIKI *et al.*[21] suggested that it could be identified as *Ceratobasidium gramineum* (IKATA et MATSUURA) ONIKI *et al.*, because *Corticium gramineum* was thought to belong to the genus *Ceratobasidium* on the basis of the observation of the perfect state of several isolates of this fungus.

It has been reported that AG-D is similar to CAG-1[21]. According to BURPEE *et al.*[3,4], CAG-1 is the main causal fungus of yellow patch of turfgrass and is similar to *R. cerealis*, the causal fungus of sharp eyespot of cereals.

AG-E

The summer strain of flax[32]
G-1 Isolates of diseased seedlings of sugar beets[31]
CAG-3[3]
CAG-6[3]
R. muneratii CASTELLANI[3]
Ceratobasidium sp. (based on the results of the present study)

A part of the summer strain described by UI *et al.*[32], which is pathogenic to flax, belonged to this group. The G-1 by UCHINO *et al.*[31] is similar to this group and is the most pathogenic to sugar beet seedlings among the 5 anastomosis groups of sugar beets (UCHINO *et al.*, unpublished). AG-E also corresponds to *Ceratobasidium* sp. (Table 5).

This group is similar to CAG-3, and also to CAG-6. Accordingly, since CAG-3 and CAG-6 were thought to be identical, anastomosis between the two groups was observed. As a result, it was certified that the isolate Bn 31 of CAG-3 fused with the isolate Bn 74 of CAG-6. Bn 74 has been reported to be *R. muneratii*[3].

AG-F

CAG-4[3]
Ceratobasidium sp. (based on the results of the present study)

CAG-4 is identical with this group. The perfect state of AG-F also corresponds to *Ceratobasidium* sp.

AG-G

Pathogen of browning on peanut pods[19]
R. fragariae[17]
Ceratobasidium sp. (based on the results of the present study)

Although the main pathogen of browning on peanut pods is AG-A, the disease can also be caused by AG-G in some cases[19]. A part of *R. fragariae* belongs to this group. The perfect state of AG-G corresponds to *Ceratobasidium* sp. (Table 5). Although it has also been reported that the perfect state of *R. fragariae* corresponds to *Ceratobasidium* sp.[38], it would thus be important to determine which anastomosis group the isolates of *R. fragariae* belong to, namely AG-A, AG-G, or AG-I. Of the four isolates from strawberries supplied by ADAMS one belonged to AG-A, two to AG-G, and one to AG-I.

AG–H

Ceratobasidium sp. (based on the results of the present study)

AG–I

G–2 Isolates of diseased seedlings of sugar beets[31]
R. fragariae[17]

A part of *R. fragariae* belongs to this group, as mentioned above. G–2 is similar to this group. The perfect state of this group has not yet been identified.

AG–K

G–4 Isolates of diseased seedlings of sugar beets[31]
Ceratobasidium sp. (based on the results of the present study)

G–4 is similar to AG–K. The perfect state of this group also corresponds to *Ceratobasidium* sp.

AG–L

Ceratobasidium sp. (based on the results of the present study)

AG–N

The perfect state of this group has not yet been identified.

AG–O

Ceratobasidium sp. (based on the results of the present study)

Summary

Thirteen species among 27 species of *Rhizoctonia* and related genera examined were found to be binucleate *Rhizoctonia* as follows: *R. alpina, R. anomala, R. endophytica, R. floccosa, R. fragariae, R. fraxini, R. globularis, R. muneratii, R. ramicola, R. solani* var. *fuchsiae, R. stahlii, Corticium anceps,* and *Ceratobasidium ramicola.* Hyphal anastomoses between 15 Japanese anastomosis groups (AG–A–AG–O) and 7 North American anastomosis groups (CAG–1–CAG–7) of binucleate *Rhizoctonia* were examined. The results indicated that AG–A, AG–D, and AG–F corresponded to CAG–2, CAG–1, and CAG–4, respectively. AG–E corresponded to CAG–3 and CAG–6. Since one isolate of CAG–3 and one isolate of CAG–6 had fused, it was concluded that these two groups were identical. On the other hand, CAG–5 and CAG–7 had not fused with any of the Japanese groups. Among the Japanese anastomosis groups, 11 groups developed their perfect states on soil and all the perfect states corresponded to *Ceratobasidium* spp. However,

the identification of the species could not be determined, except in the case of AG-B (others) and AG-D. The remaining 4 groups have not yet developed their perfect states. The difficulties in identifying the species of *Ceratobasidium*, and the species names or fungal groups belonging to the respective anastomosis groups are discussed.

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