Journal of Pharmacognosy and Phytochemistry
Available online at www.phytojournal.com

E-ISSN: 2278-4136
P-ISSN: 2349-8234
www.phytojournal.com
JPP 2021; 10(2): 461-466
Received: 20-12-2020
Accepted: 08-02-2021

Nandeesha CV
Department of Plant Pathology, College of Agriculture, JAU, Junagadh, Gujarat, India

Nandeesha KL
Department of Plant Pathology, College of Agriculture, JAU, Junagadh, Gujarat, India

CM Bhaliya
Department of Plant Pathology, College of Agriculture, UAHS, Shivamogga, Karnataka, India

Corresponding Author:
Nandeesha CV
Department of Plant Pathology, College of Agriculture, JAU, Junagadh, Gujarat, India

Evolutionary biology and interaction among the anastomosis groups of *Rhizoctonia* spp.

Nandeesha CV, Nandeesha KL and CM Bhaliya

DOI: https://doi.org/10.22271/phyto.2021.v10.i2f.13840

Abstract
Rhizoctonia solani Kuhn and other *Rhizoctonia* spp. are the plant pathogenic fungi widespread in the world and in both cultivated and noncultivated soils. *Rhizoctonia* spp. are readily isolated from diseased plants and soils, which differ in their pathogenicity, cultural, morphological and physiological characteristics. Identification of species and intraspecific groups (ISGs) is sometimes very difficult, due to the absence of the authentic cultures, which hinders mycological and pathological studies. The genus *Rhizoctonia* can be identified using various techniques such as, sequence analysis of ITS regions, DNA fingerprinting and the rDNA coding sequence. The introduction of the concept of anastomosis groups (AGs) or intraspecific groups has also aided species and subspecies identification. There are 13 different anastomosis groups exists in *Rhizoctonia solani* of which AG 1-4 were strong pathogenic on many plants and AG 6-10 were orchid mycorrhizae. Analysis of restriction fragment length polymorphisms (RFLPs) and the sequences within ribosomal RNA genes (rDNA) among different anastomosis groups of *R. solani* isolates exhibited DNA base sequence homology and diverging evolutionary affinities for hyphal anastomosis. More recently, ribosomal DNA (rDNA) sequences have been used to study the genetic relationships between AG of *R. solani*. The ecology and epidemiology of each ISG of *R. solani* must be investigated in order to gain a better understanding of this important group of fungi.

Keywords: Anastomosis groups, Identification, *Rhizoctonia solani*, *Rhizoctonia* spp.

Introduction
Rhizoctonia solani Kuhn and other *Rhizoctonia* spp. are the plant pathogenic fungi widespread in the world and in both cultivated and noncultivated soils. Many isolates of *Rhizoctonia* spp. are readily isolated from diseased plants and soils, which differ in pathogenicity and morphology, as well as cultural and physiological characteristics. Based on these differences, many species and intraspecific groups (ISGs) have been described; however, identification of species and ISGs is sometimes very difficult, owing to the absence of the authentic cultures, which hinders mycological and pathological studies. Fortunately, this situation has been put in order through the efforts of many researchers through characterization of the genus Rhizoctonia using various techniques as sequence analysis of ITS regions, DNA fingerprinting and the rDNA coding sequence. The introduction of the concept of anastomosis groups (AGs) or intraspecific groups has also aided species and subspecies identification.

Rhizoctonia spp. and *Rhizoctonia solani*
Rhizoctonia spp.
The genus concept of *Rhizoctonia* spp. was first established by de Candolle (1815) [14] after which, more than one hundred species of it have been described. Based on morphology, dimension of sclerotia and monilioid cells and their pathogenicity these species are distinguished from one another. According to available information, Rhizoctonia is considered a genus of basidiomycetous imperfect fungi, characterized as follows (Ogoshi 1975a) [46] branching near the distal septum of cells in young, vegetative hyphae; (b) formation of a septum in the branch near the point of origin; (c) construction of the branch; (d) dolipore septum; (e) no clamp connection; (j) no conidium, except monilioid cells; (g) sclerotium not differentiated into rind and medulla; and (h) no rhizomorph. In terms of these characteristics, only forty-nine of one hundred species of *Rhizoctonia* reported up to now are true *Rhizoctonia* spp., eleven are not, and forty are dubious (Ogoshi 1984 and 1987) [47, 48].
Rhizoctonia isolates are divided into three groups, if the above concept is adopted: One is the multinucleate Rhizoctonia, which has three or more nuclei per cell, larger hyphae and teleomorph in the genus *Thanatephorus* Donk. Another is the binucleate Rhizoctonia, which has only two nuclei per cell (rarely one or three), smaller hyphae (4-7 µm), and teleomorph in the genus *Ceratobasidium* Rogers.

The third includes *R. oryzae* and *R. zeae*, which are multinucleate and have teleomorphs in the genus *Waitea* Warcup and Talbot.

Rhizoctonia solani

R. solani (*Thanatephorus cucumeris*) is the representative of *Thanatephorus* which is multinucleate having three other species, *Thanatephorus sterigmaticus* (Talbot 1965) [66], *Thanatephorus orchidicola* (Warcup *et al*. 1966) [69] and *Thanatephorus corchorus* (Tu *et al*. 1977) [67]. However, these three species are not frequently isolated and are thought to have limited distribution.

In the last two decades some important developments were made in the study of *R. solani*: (a) the concept of *R. solani* as a species became clearer; (b) the concept of intraspecific groups of *R. solani* was introduced and became well established; and (c) studies on the teleomorph of *R. solani* were developed, and the taxonomic classification was determined (Ogoshi 1987) [48]. Parmeter and Whitney (1970) [52] gave a detailed description of the characteristics specific to *R. solani*: Teleomorph is *Thanatephorus cucumeris* (Frank) Donk, hyphae are multinucleate, and hyphae and sclerotia have characteristics typical of *Rhizoctonia*.

Intraspecific grouping of *R. solani*

Observations show that *R. solani* is varied in its pathogenicity, sclerotial morphology, cultural appearance on media, physiological characteristics, etc, this fungus has long been thought to have many ISGs, and indeed there have been many attempts to divide *R. solani* into logical groups. These attempts fall basically into two categories: those based on the differences in pathogenicity, cultural appearance, morphology, physiology, or ecology; and those based on hyphal anastomosis on culture media (Ogoshi 1987) [48].

Morphological and Pathological Grouping was given by Exner (1953) [17] where she recognized four formae speciales, namely, solani, microsclerotia, sasakii, and timsii, in *Pellicularia filamentosa* (*T. cucumeris*). Takahashi & Matsuura (1954) [65] divided *R. solani* into six groups by morphology (mainly of sclerotia) and pathogenicity, resulting in the addition of formae specials betae and compacta to Exner's groups.

Hyphal Anastomosis Grouping are observed when isolates of *R. solani* are paired 2-3 cm apart on a medium (usually 2% water agar) in a petri dish, their mycelia grow and overlap, which can be observed under a light microscope at low magnification. If hyphal fusion occurs, these isolates belong to the same anastomosis group, and often, attraction of hyphae and death of fused cells are observed (McCoy and Kraft 1984 [38]; Yokoyama and Ogoshi 1984 [47]). If fusion, attraction, and hyphal death do not occur, the isolates belong to different AGs. Accordingly, attraction and hyphal death are reliable clues for detecting hyphal fusion.

Mechanism of Hyphal Fusion

The process of perfect fusion of hyphae of *R. solani* is summarized as follows: hyphal growth, secretion of one or more attracting substances, attraction to the substances, contact of hyphae, cessation of hyphal growth, formation of branchlike projections, dissolution of cell walls, and connection of protoplasms (Yokoyama *et al.* 1983, 1985, 1985a) [73, 72, 74]. Imperfect fusion differs in that dissolution of cell walls is followed by death of cells (Yokoyama and Ogoshi 1984) [47]. An isolate of an AG can recognize and fuse only with members of the same AG. At present, four categories of anastomosis (C3 to C0) defined by Carling *et al*. (1996) [7] have been accepted by many researchers. These are useful for a better understanding of the genetic diversity of *R. solani* populations, because of the background genetically supported by vegetative or somatic compatibility (VC or SC) of confronted isolates (MacNish *et al*. 1997) [34]. Each of categories is as follows:

C3: walls fuse; membranes fuse, accompanied with protoplasm connection; anastomosis point frequently is not obvious; diameter of anastomosis point is equal or nearly equal hyphal diameter; anastomosing cells and adjacent cells may die, but generally do not. This category occurs for the same anastomosis group, same vegetative compatibility population (VCP) and the same isolate.

C2: wall connection is obvious, but membrane contact is uncertain; anastomosing and adjacent cells always die. This category occurs in same AG, but not between different VCPs.

C1: wall contact between hyphae is apparent, but both wall penetration and membranemembrane contact do not occur; occasionally one or both anastomosing cells and adjacent cells die. This category occurs between different AGs or in the same AG.

C0: no reaction. This category occurs between different AGs.

In general, hyphal fusion occurs at a high frequency (50%≥) within members of the same AG, with the exception of non-self-anastomosing isolates (Hyakumachi and Ui, 1988) [24]. On the other hand, hyphal fusion among members of different AGs occurs at either a low frequency (≤30%) or no fusion occurs. *Rhizoctonia* isolates giving C3 to C1 reactions in anastomosing test have been taken to be the same AG.

Anastomosis Groups

Martin *et al.* (1983) [35] found AG1 on tall fescue (*Festuca arundinaceae* Schreb). Martin and Lucas (1984) [36] found AG1-IA on turfgrass, and AG5 causing brown patch on turfgrass. Hurd and Grisham (1983) [23] found AG2-2IIIB causing brown patch of turfgrass. Oniki *et al.* (1986) [50] found AG2-2IV causing large patch on turfgrass. Hyakumachi *et al.* (1998) [1] found *R. solani* AG2-2 IIIB for all their isolates from *Agrostis palustris* Huds. in Japan. Herr and Fulton (1995) [20] found AG2-2 IIIB from *A. palustris* in Ohio, as well as AG1-IA from tall fescue. Sneh *et al.* (1991) reported AG1 and AG2-2 associated with turfgrasses. Burpee and Martin (1992) [5] in their review of *Rhizoctonia* species associated with turfgrasses, listed AG1, AG2-2, AG4 and AG5. Zhang and Dernoeden (1995) [75] cite studies which list six AG on both warm and cool season turfgrasses including: AG1, AG2-2, AG3, AG4, AG5 and AG6. Parmeter *et al.* (1969) [53] reported that *R. solani* should be divided into AGs 1,-2, 3, and 4, based on hyphal fusion. They also discussed the possibility of the existence of additional anastomosis groups and the possibility of "bridging" isolates, *i.e.* those capable of anastomosis with members of two or more' groups. This speculation has now been verified (Homma *et al.* 1983 [22], Kuninaga *et al*. 1979 [31], Neate and Warcup 1985 [43], Ogoshi 1975 [45], Rovira *et al*. 1986 [58]). Ogoshi (1975) [45] attempted to divide the Japanese isolates of *R. solani* into groups by hyphal fusion. Tests of hyphal fusions among 255 isolates indicated that 242 could be assigned to one of five AGs (AG-I-AG-5). The remaining 13 isolates were 'not assigned to any AG. AG-2 was further divided into type-l and type-2 (AG-2-1 and AG-2-2) based on the relative frequency of hyphal fusion, with fusion between two isolates from the same type in AG-2 being frequent, but that of frequency between two isolates from different types in AG-2 being rare (Ogoshi 1975) [45].

Kuninaga *et al.* (1978) added AG-6 and AG-BI (bridging isolates) to Ogoshi's six groups.

Furthermore, Homma *et al.* (1983) [22] reported an eighth group, AG-7. Recently, Neate & Warcup (1985) [43] reported a ninth group, AG-8, which is thought to be the primary pathogen responsible for "bare patch" of cereals. To date, isolates of *R. solani* have been assigned to 13 anastomosis groups (AG) and some of which include several subgroups and isolates of *R. zeae* and *R. oryzae* have been assigned to WAG-Z and WAG-O, respectively (Sneh *et al.* 1991; Carling *et al.* 1999, 2002a [13, 10]). Furthermore, AG-8 is also a "bridging" isolate, as it can fuse with AG-2 and AG-BI, though frequency of fusion depends on isolates and related groups (Rovira *et al.* 1986) [58]. AG-8 and AG-BI differ in their thiamine requirement; the former is thiamine autotrophic and the latter, auxotrophic (discussed in a later section). The behavior of bridging isolates is interesting from the viewpoint of the phylogeny of *R. solani*.

In general, there is no contradiction in the conventional anastomosis grouping system by taking anastomosis frequency into consideration. However, two exceptional cases where anastomosis frequency mismatched with morphological, physiological and pathogenic characteristics have been reported from tobacco (Nicoletti *et al.* 1999) [44] and soybean (Naito and Kanematsu 1994) [41]. These demonstrate the limitations of using hyphal anastomosis as the sole criteria for characterization and identification of closely related fungi. In addition, it is not easy to determine the subgroup of isolates within the same AG because no differences occur in their anastomosis reaction. Thus, in order to determine AGs or subgroups in *R. solani*, genetic analysis using molecular approaches that employ multiple genetic loci is needed.

Isolates of *R. solani* that exhibits DNA base sequence homology and affinities for hyphal anastomosis may represent a diverging evolutionary unit (Kuninaga and Yokosawa 1980) [29]. This hypothesis is supported by analysis of restriction fragment length polymorphisms (RFLPs) and the sequences with in ribosomal RNA genes (rDNA) among different anastomosis groups of *R. solani* (Vilgalys and Gonzalez 1990 [68]; Gonzalez *et al.* 2001 [19]; Carling *et al.* 2002 [12]). More recently, ribosomal DNA (rDNA) sequences have been used to study the genetic relationships between AG of *R. solani*. Boysen *et al.* (1996) [4] studied the relatedness of *R. solani* AG4 isolates based on sequences of the rDNA internal transcribed spacer region (ITS, composed of ITS1, 5.8S, ITS2 regions). Kuninaga *et al.* (1997) sequenced the ITS of 45 Japanese isolates of *R. solani* from different anastomosis groups, and found that isolates of each AG clustered together. Salazar *et al.* (1999 and 2000) [59, 60] sequenced the ITS of *R. solani* AG2 isolates and used these data to examine the relationships between and within AG2 subgroups. These results suggested that sequence analysis of the ITS region could be used to identify AG subgroups.

Characteristics of anastomosis groups and subgroups of *Rhizoctonia solani*

1. AG-1: IA, IB, IC, ID

AG-1 IA (Li and Yan 1990 [32]; Sneh *et al.*, 1991; Fenille *et al.*, 2002 [18]; Naito, 2004 [40]).

Symptoms: sheath blight, foliar blight, leaf blight, web-blight, head rot, bottom rot, and brown patch.

Host: rice, corn, barley, sorghum, potato, barnyard millet, common millet, soybean, peanut, lima bean, cabbage, leaf lettuce, Stevia, turfgrass, etc.

There is a general tendency to attack aerial parts of the plants by this group of pathogens. Basidiospore infection of rice has been reported, but sclerotia are more important as an infection source. The optimum growth temperature is higher than those of AG-1 IB.

AG-1 IB (Sneh *et al.*, 1991; Naito, 2004 [40]; Yang *et al.*, 2005b [70]).

Symptoms: sheath blight, leaf blight, foliar blight, web-blight, root rot, damping off, head rot, and bottom rot.

Host: corn, sugar beet, common bean, fig, soybean, cabbage, lettuce, apple, pear, marigold.

AG-1 IC (Sneh *et al.*, 1991; Naito, 2004) [40].

Symptoms: damping-off, summer blight, foot rot, crown rot canker, and root rot.

Host: sugar beet, carrot, buckwheat, flax, soybean, bean, cabbage, pineapple and radish.

AG-1 ID (Priyatmojo *et al.*, 2001) [55].

Symptom: leaf spot.

Host: coffee.

This subgroup was recently reported in the Philippines (Priyatmojo *et al.*, 2001) [55]

2. AG-2: 2-1, 2-2 IIIB, 2-2 IV, 2-2 Lp, 2-3, 2-4, 2-BI.

AG-2-1 (Satoh *et al.*, 1997 [61]; Camporota and Perrin, 1998 [6]; Sneh *et al.*, 1991; Rollins *et al.*, 1999 [57]; Khan and Kolte, 2000 [26]; Naito, 2004 [40])

Symptoms: damping-off, leaf rot, leaf blight, root rot, foot rot, bottom rot, and bud rot.

Host: sugar beet, wheat, potato, cowpea, canola, rape, cauliflower, mustard, turnip, pepper, spinach, lettuce, strawberry, tulip, tobacco and clover.

AG-2-2 III B (Sneh *et al.*, 1991; Priyatmojo *et al.*, 2001 [55]; Naito, 2004 [40]).

Symptoms: brown sheath blight, dry root rot, root rot, brown patch, large patch, black scurf, stem rot, stem blight, *Rhizoctonia* rot, damping-off, stem rot, collar rot, and crown brace rot.

Host: rice, soybean, corn, sugar beet, elephant foot yam, saffron, turfgrass, *gladiolus* and ginger.

AG-2-2 IV: (Sneh *et al.*, 1991; Naito, 2004 [40]).

Symptoms: leaf blight, foliage rot, root rot, and stem rot.

Host: sugar beet, carrot, eggplant (*Solanum* Linn), pepper, spinach and turfgrass.

AG-2-2 LP: (Aoyagi *et al.*, 1998) [1].

Symptoms: large patch.

Host: Zoysia grass.

AG 2-3: (Naito and Kanematsu, 1994 [41]; Sumner *et al.*, 2003 [64]).

Symptoms: leaf blight and root rot.

Host: soybean.

AG-2-4: (Sumner, 1985) [63].

Symptoms: crown rot, brace rot, and damping-off.

Host: corn and carrot.

AG-2-BI: (Carling *et al.*, 2002b).

Symptoms: nonpathogenic.

Host: isolates, obtained only from soils and plants in forests. (Formerly known as AG-BI.)

3. AG 3: PT, TB (Sneh *et al.*, 1991; Kuninaga *et al.*, 2000 [30]).

Symptoms: black scurf, leaf spot, target leaf spot, and damping-off.

Host: potato with black scurf symptoms, tobacco with target leaf spot symptoms.

4. AG-4: HG-I, HG-II, HG-III (Baird, 1996 [3]; Holtz *et al*., 1996 [21]; Sneh *et al.*, 1991; Fenille *et al*., 2002 [18]; Ravanlou and Banihashemi, 2002 [56]; Kuramae *et al*., 2002 [18]; Naito, 2004 [40]).
Symptoms: damping-off, root rot, stem canker, fruit rot, and stem rot.
Host: pea, sugar beet, melon, soybean, common bean, snap bean, lima bean, carrot, spinach, taro, tomato, potato, alfalfa, elephant foot, beans, barley, buckwheat, cabbage, canola, turnip, carnation, cauliflower, Chinese chive, chrysanthemum, corn, cotton, tobacco, turfgrass, wheat and cauliflower.

5. AG-5 (Li *et al*., 1998 [33]; Demirci, 1998 [15]; Sneh *et al*., 1991; Ravanlou and Banihashemi, 2002 [56]; Eken and Demirci, 2004 [16]; Naito, 2004 [40]).
Symptoms: root rot, damping-off, black scurf, brown patch, and symbiosis (orchids).
Host: soybean, apple, barley, chickpea, common bean, lima bean, potato, strawberry, sugar beet, tobacco, turfgrass and wheat.

6. AG-6: HG-I, GV (Mazzola, 1997 [37]; Meyer *et al*., 1998 [39]; Sneh *et al*., 1991; Carling *et al*., 1999 [13]; Pope and Carter, 2001 [54]; Naito, 2004 [40])
Symptom: root rot, crater rot, and symbiosis (orchids).
Host: apple, wheat, carrot, and carnation.

7. AG-7: (Naito *et al.*, 1993 [43]; Baird and Carling, 1995 [2]; Carling, 1997, 2000 [8, 9]; Carling *et al.*, 1998) [11]
Symptoms: damping-off, root rot, and black scurf.
Host: carnation, cotton, soybean, watermelon and potato.

8. AG-8: (Sneh *et al.*, 1991; Naito, 2004 [40]).
Symptoms: bare patch.
Host: barley, potato and wheat.

9. AG-9: (Sneh *et al*., 1991; Naito, 2004 [40]).
Symptoms: black scurf.
Host: potato, crucifers, wheat and barley.

10. AG-10: (Sneh *et al*., 1991).
Symptoms: weak pathogenic.
Host: barley and wheat.

11. AG-11: (Kumar *et al*., 2002).
Symptoms: damping-off and hypocotyls rot.
Host: barley, lupine, soybean, and wheat.
This group is considered as bridging isolates (anastomose with each members of AG-2-1, AG-2 BI, AG-8) (Carling *et al*., 1996).

12. AG-12: (Kumar *et al.*, 2002) [28].
Symptoms: symbiosis (orchids).
Host: *Dactylorhiza aristata* (Orchidaceae).

13. AG-13: (Carling *et al*., 2002a) [10].
Symptoms: none.
Host: cotton.

Summary
Taxonomic and epidemiological studies of Rhizoctonia are important at the level of both species and intraspecific group in the same way that studies of intraspecific groups (formae speciales) of *Fusarium* have proven vital to our understanding of that important genus of fungi. Taxonomic differences among ISGs of *R. solani* are often closely related to ecological and epidemiological differences. For example, leaf blight of sugar beet in Japan is caused by *R. solani* AG-I IB and AG-2-2 IV, two epidemiologically distinct fungi. The former spreads only by mycelia, and the latter disseminates by both mycelia and basidiospores. Measures to control these two intraspecific groups must be considered accordingly. Life cycles and disease cycles of some ISGs of *R. solani* have been well studied; however, those of most have not.
Rhizoctonia solani includes 13 anastomosis groups, of which AG 1-4 were strong pathogenic on many plants and AG 6-10 were orchid mycorrhizae, new groups are still being identified. Field survival of sclerotia of the sheath-blight fungus of rice (*R. solani* AG-l IA), for example, has been studied for some time, yet the role of basidiospores in the disease cycle was not understood until recently, although spore formation in paddy fields had been frequently observed. A similar situation exists with *R. solani* AG-3 on potatoes, where spore formation on plant stems has been observed, yet their role in the disease cycle is obscure. Interestingly, however, it was reported that spores of AG-3 infected and caused leaf spots on tomato and eggplant (Kodama *et al.* 1982) [27].
The ecology and epidemiology of each ISG of *R. solani* must be investigated in order to gain a better understanding of this important group of fungi. Descriptions of binucleate Rhizoctonia and multinucleate Rhizoctonia other than *R. solani* are absent from this report. These fungi are frequently isolated alone or in association with *R. solani*, and many are important plant pathogens. AGs, and possibly ISGs, are contained in other species of Rhizoctonia (Ogoshi *et al*. 1979, Oniki *et al.* 1985) [31, 51], although they are less studied. Further taxonomic and epidemiological examinations of Rhizoctonia species are needed, and are anxiously anticipated.

References
1. Aoyagi T, Kageyama K, Hyakumachi M. Characterization and survival of *Rhizoctonia solani* AG2-2 LP associated with large patch disease of zoysia grass. Plant Dis 1998;82:857-863.
2. Baird RE, Carling DE. First report of *Rhizoctonia solani* AG-7 in Indiana. Plant Dis 1995;79(3):321.
3. Baird RE. First report of *Rhizoctonia solani* AG-4 on canola in Georgia. Plant Dis 1996;80(1):104.
4. Boysen M, Borja M, del Moral C, Salazar O, Rubio V. Identification at strain level of *Rhizoctonia solani* AG4 isolates by direct sequence of asymmetric PCR products of the ITS regions. Curr. Genet 1996;29:174-181.
5. Burpee L, Martin B. Biology of *Rhizoctonia* species associated with turfgrasses. Plant Dis 1992;76:112-117.
6. Camporota P, Perrin R. Characterization of *Rhizoctonia* species involved in tree seedling damping-off in French forest nurseries. Appl. Soil Ecol 1998;10:65-71.
7. Carling DE. Grouping in *Rhizoctonia solani* by hyphal anastomosis reaction. In: Sneh, B., Jabaji-Hare, S., Neat, S. and Dijst, G. *et al*., (eds). *Rhizoctonia* species: Taxonomy, Molecular Biology, Ecology, Pathology and Disease Control. Kluwer Academic Publishers, Dordecht, The Netherlands 1996,37-47p.
8. Carling DE. First report of *Rhizoctonia solani* AG-7 in Georgia. Plant Dis 1997;82(1):127.

9. Carling DE. Anastomosis groups and subsets of anastomosis groups of *Rhizoctonia solani*. Abstract in Proceedings of the Third International Symposium on *Rhizoctonia*. National Chung Hsing University, Taichung, Taiwan 2000,14p.
10. Carling DE, Baird RE, Gitaitis RD, Brainard KA, Kuninaga S. Characterization of AG-13, a newly reported anastomosis group of *Rhizoctonia solani*. Phytopathol 2002a;92:893-899.
11. Carling DE, Brainard KA, Virgen-Calleros G, Olalde-Portugal VF. First report of *Rhizoctonia solani* AG-7 on potato in Mexico. Plant Dis 1998;82(1):127.
12. Carling DE, Kuninaga S, Brainard KA. Hyphal anastomosis reactions, rDNA internal transcribed spacer sequences, and virulence levels among subsets of *Rhizoctonia solani* anastomosis group-2 (AG-2) and AG BI. Phytopathol 2002;92:43-50.
13. Carling DE, Pope EJ, Brainard KA, Carter DA. Characterization of mycorrhizal isolates of *Rhizoctonia solani* from an orchid, including AG-12, a new anastomosis group. Phytopathol 1999;89(10):942-946.
14. de Candolle A. Uredo rouille des cereals In Forafran caise, famille des champigons 1815,83p.
15. Demirci E. *Rhizoctonia* species and anastomosis groups isolated from barley and wheat in Erzurum, Turkey. Pl. Pathol 1998;47(1):10-15.
16. Eken C, Demirci E. Anastomosis groups and pathogenicity of *Rhizoctonia solani* and binucleate *Rhizoctonia* isolates from bean in Erzurum, Turkey J. Pl. Pathol 2004;86(1):49-52.
17. Exner B. Comparative studies of four rhizoctonias in Louisiana. Mycologia 1953;45:698-718.
18. Fenille RC, Luizde SN, Kuramae EE. Characterization of *Rhizoctonia solani* associated with soybean in Brazil. Eur. J. of Pl. Pathol 2002;108(8):783-792.
19. Gonzalez D, Carling DE, Kuninaga S, Vilgalys R, Cubeta MA. Ribosomal DNA systematics of *Ceratobasidium* and *Thanatephorus* with *Rhizoctonia* anamorphs. Mycologia 2001;93(6):1138-1150.
20. Herr LJ, Fulton MM. *Rhizoctonia solani* AG1-IA and AG2-2 IIB cause brown patch on tall fescue and creeping bentgrass in Ohio. Plant Dis 1995;79:1186.
21. Holtz BA, Michailides TJ, Feguson L, Hancock JG, Weinhold AR. First report of *Rhizoctonia solani* (AG-4) on pistachio rootstock seedlings. Plant Dis 1996;80(11):1303.
22. Homma Y, Yamashita Y, Ishii M. A new anastomosis group (AG-7) of *Rhizoctonia solani* Kuhn from Japanese radish fields. Ann. Phytopathol. Soc. Jpn 1983;49:184-90
23. Hurd B, Grisham MP. *Rhizoctonia* spp. associated with brown patch of St. Augustinegrass. Phytopathol 1983;73:1661-1665.
24. Hyakumachi M, Ui T. Development of the teleomorph of non-self-anastomosing isolates of *Rhizoctonia solani* by a buried-slide method. Pl. pathol 1988;37(3):438-440
25. Hyakumachi M, Mushika T, Ogiso Y, Toda T, Kageyama K, Tsuge T. Characterization of a new cultural type (LP) of *Rhizoctonia solani* AG2-2 isolated from warm-season turfgrasses, and its genetic differentiation from other cultural types. Pl. Pathol 1998;47:1-9.
26. Khan RU, Kolte SJ. Some seedling diseases of rapeseed-mustard and their control. Indian Phytopathol 2000;55(1):102-103.
27. Kodama T, Horimoto K, Ogoshi A. On the brown spot of eggplants by *Thanatephorus cucumeris* (Frank) Donk (*Rhizoctonia solani*) AG-3. Ann. Phytopathol. Soc. Jpn 1982;48:356
28. Kumar S, Sivasithamparam K, Sweetingham MW. Prolific production of sclerotia in soil by *Rhizoctonia solani* anastomosis group (AG) 11 pathogenic on lupin. Annal. Appl. Biol 2002;141(1):11-18.
29. Kuninaga S, Yokosawa R. A comparison of DNA compositions among anastomosis groups in *Rhizoctonia solani* Kühn. Ann. Phytopathol. Soc. Japan 1980;46:150-158.
30. Kuninaga S, Nicoletti R, Lahoz E, Naito S. Ascription of Nt-isolates of *Rhizoctonia solani* to anastomosis group 2-1 (AG-2-1) on account of rDNA-ITS sequence similarity. J. Plant Pathol 2000;82:61-64.
31. Kuninaga S, Yokosawa R, Ogoshi A. Some properties of anastomosis group 6 and BI in *Rhizoctonia solani* Kuhn. Ann. Phytopathol. Soc. Jpn 1979;45:207-17
32. Li HR, Yan SQ. Studies on the strains of pathogens of sheath blight of rice in the east and south of Sichuan Province. Acta Mycologica Sinica 1990;9:41-49. (Chinese with English abstract).
33. Li HR, Wu BC, Yan SQ. Aetiology of *Rhizoctonia* in sheath blight of maize in Sichuan. Pl. Pathol 1998;47(1):16-21.
34. MacNish GC, Carling DE, Brainard KA. Relationship of microscopic vegetative reactions in *Rhizoctonia solani* and the occurrence of vegetatively compatible populations (VCP) in AG-8. Mycol. Res 1997;100:61-68.
35. Martin SB, Campbell CL, Lucas LT. Horizontal distribution and characterization of *Rhizoctonia* spp. in tall fescue turf. Phytopathol 1983;73:1064-1068.
36. Martin SB, Lucas LT. Characterization and pathogenicity of *Rhizoctonia* spp. and binucleate *Rhizoctonia*-like fungi from turfgrasses in North Carolina. Phytopathol 1984;74:170-175.
37. Mazzola M. Identification and pathogenicity of *Rhizoctonia* spp. isolated from apple roots and orchard soils. Phytopathol 1997;87:582-587.
38. McCoy RJ, Kraft JM. Resistance in *Pisum sativum* to epicotyl rot caused by *Rhizoctonia solani*. Plant Dis 1984;68:491-93.
39. Meyer L, Wehner FC, Nel LH, Carling DE. Characterization of the crater disease strain of *Rhizoctonia solani*. Phytopathol 1998;88:366-371.
40. Naito S. Rhizoctonia diseases: Taxonomy and population biology. Proceeding of the International Seminar on Biological Control of Soilborne Plant Diseases, Japan-Argentina Joint Study, Buenos Aires, Argentina 2004,18-31p.
41. Naito S, Kanematsu S. Characterization and pathogenicity of a new anastomosis subgroup AG-2-3 of *Rhizoctonia solani* Kühn isolated from leaves of soybean. Ann. Phytopath. Soc. Japan 1994;60(6):681-690.
42. Naito S, Mohamad D, Nasution A, Purwanti H. Soilborne diseases and ecology of pathogens on soybean roots in Indonesia. JARQ 1993;26:247-253.
43. Neate SM, Warcup JH. Anastomosis grouping of some isolates of *Thanatephorus cucumeris* from agricultural soils in South Australia. Trans. Br. Mycol. Soc 1985;85:615-20
44. Nicoletti R, Lahoz E, Kanematsu S, Naito S, Contillo R. Characterization of *Rhizoctonia solani* isolates from tobacco fields related to anastomosis groups 2–1 and BI (AG 2–1 and AG BI). J. Phytopathol 1999;147(2):71-77.

45. Ogoshi A. Studies on the anastomosis groups of *Rhizoctonia solani* Kuhn and on their perfect stages. Bull. Natl. Inst. Agric. Ser. 1975;30:1-63.
46. Ogoshi A. Grouping of *Rhizoctonia solani* Kuhn and their perfect stages. Rev. Plant Prot. Res 1975a;8:93-103
47. Ogoshi A. Studies on the taxonomy of the genus *Rhizoctonia*. Ann. Phytopathol. Soc. Jpn 1984;50:307-9
48. Ogoshi A. Ecology and pathogenicity of anastomosis and Intraspecific groups of *Rhizoctonia solani* Kuhn. Ann. Rev. Phytopathol 1987;25:125-43.
49. Ogoshi A, Oniki M, Sakai R, Ui T. Anastomosis grouping among isolates of binucleate Rhizoctonia. Trans. Mycol. Soc. Jpn 1979;20:33-39
50. Oniki M, Kobayahsi K, Araki T, Ogoshi A. A new disease of turfgrass caused by binucleate *Rhizoctonia*, AG-Q. Ann. Phytopath. Soc. Japan 1986;52:850-853.
51. Oniki M, Ogoshi A, Araki T, Sakai R, Tanaka S. The perfect state of *Rhizoctonia oryzae* and *R. zeae* and the anastomosis groups of *Waitea circinata*. Trans. Mycol. Soc. Jpn 1985;26:189-98
52. Parmeter JR, Whitney HS. Taxonomy and nomenclature of the imperfect state 1970,7-19p.
53. Parmeter JR, Sherwood RT, Platt WD. Anastomosis grouping among isolates of *Thanatephorus cucumeris*. Phytopathol 1969;59:1270-78
54. Pope EJ, Carter DA. Phylogenetic placement and host specificity of mycorrhizal isolates belonging to AG-6 and AG-12 in the *Rhizoctonia solani* species complex. Mycologia 2001;93(4):712-719.
55. Priyatmojo A, Escopalao VE, Tangonan NG, Pascual CB, Suga H, Kageyama K *et al*. Characterization of a new subgroup of *Rhizoctonia solani* anastomosis group 1 (AG-1 ID), causal agent of a necrotic leaf spot on coffee. Phytopathol 2001;91:1054-1061.
56. Ravanlou A, Banihashemi Z. Isolation of some anastomosis groups of *Rhizoctonia* associated with wheat root and crown in Fars province. Iranian J. Plant Pathol 2002;38(3-4):67-69.
57. Rollins PA, Keinath AP, Farnham MW. Effect of inoculum type and anastomosis group of *Rhizoctonia solani* causing wirestem of cabbage seedlings in a controlled environment. Can. J. Plant Pathol 1999;21(2):119-124.
58. Rovira AD, Ogoshi A, McDonald HJ. Characterization of isolates of *Rhizoctonia solani* from cereal roots in South Australia and New South Wales. Phytopathol 1986;76:1245-48.
59. Salazar O, Schneider JHM, Julian MC, Keijer J, Rubio V. Phylogenetic subgrouping of *Rhizoctonia solani* AG 2 isolates based on ribosomal ITS sequences. Mycologia 1999;91:459-467.
60. Salazar O, Julian MC, Hyakumachi M, Rubio V. Phylogenetic grouping of cultural types of *Rhizoctonia solani* AG 2-2 based on ribosomal ITS sequences. Mycologia 2000;92:505-509.
61. Satoh Y, Kanehira T, Shinohara M. Occurrence of seedling damping-off of Jew's mallow, *Corchorus olitorius* caused by *Rhizoctonia solani* AG-2-1. Nippon Kingakukai Kaiho, (Japanese with English abstract) 1997;38(2):87-91.
62. Sneh B, Burpee L, Ogoshi A. Identification of *Rhizoctonia* species. The APS, St. Paul, Minesota 1991.
63. Sumner DR. First report of *Rhizoctonia solani* AG-2-4 on carrot in Georgia. Plant Dis 1985;69:25-27.
64. Sumner DR, Phatak SC, Carling DE. Characterization and pathogenicity of a new anastomosis subgroup AG-2-3 of *Rhizoctonia solani* Kuün isolated from leaves of soybean. Plant Dis 2003;87(10):1264.
65. Takahashi K, Matsuura Y. Studies on the plant diseases caused by *Rhizoctonia solani* Kuhn. On the taxonomic studies of *Rhizoctonia solani* Kuhn. Sci. Rep. Fac. Agric. Ibaraki Univ 1954;2:9-18.
66. Talbot PHB. Studies of 'Pellicularia' and associated genera of Hymenomycetes. Persoonia 1965;3:371-406
67. Tu CC, Cheng YH, Kimbrough JW. A new species of *Thanatephorus* from jute in Taiwan. Mycologia 1977;69:400-13
68. Vilgalys R, Gonzalez D. Ribosomal DNA restriction fragment length polymorphism in *Rhizoctonia solani*. Phytopathol 1990;80:151-158.
69. Warcup JH, Talbot PHB. Perfect states of some *Rhizoctonias*. Trans. Br. Mycol. Soc 1966;49:427-35
70. Yang GH, Chen HR, Naito S, Wu JY, He XH, Duan CF. Occurrence of foliar rot of pak choy and Chinese mustard caused by *Rhizoctonia solani* AG-1 IB in China. J. Gen. Plant Pathol 2005b;71:377-379.
71. Yokoyama K, Ogoshi A. Studies on hyphal anastomosis of *Rhizoctonia solani*. IV. Observation of imperfect fusion. Ann. Phytopathol. Soc. Jpn 1984;50:398
72. Yokoyama K, Hyakumachi M, Ogoshi A. Studies on hyphal anastomosis of *Rhizoctonia solani* III. Hyphal anastomosis in non-self anastomosis isolates. Mem. Fac. Agric. Hokkaido Univ 1985;14:41 6-21
73. Yokoyama K, Ogoshi A, Ui T. Studies on hyphal anastomosis of *Rhizoctonia solani.* I. Observation of perfect fusion with light microscopy. Trans. Mycol. Soc. Jpn 1983;24:329-40
74. Yokoyama K, Ogoshi A, Ui T. Studies on hyphal anastomosis of *Rhizoctonia solani*. The ultrastructural changes of fungal cells during the perfect fusion. Trans. Mycol. Soc, Jpn 1985a;26:199-207.
75. Zhang M, Dernoeden PH. Facilitating anastomosis grouping of *Rhizoctonia solani* isolates from cool season turfgrasses. Hort Science 1995;30:1260-1262.