



## The taxonomy of rhizobia: an overview

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### Abstract

The taxonomy of rhizobia, bacteria capable of nodulating leguminous plants, has changed considerably over the last 20 years, with the original genus *Rhizobium*, a member of the alpha-Proteobacteria, now divided into several genera. The study of new geographically dispersed host plants, has been a source of many new species and is expected to yield many more. Here we provide an overview of the history of the rhizobia, but focus on the *Rhizobium*–*Allorhizobium*–*Agrobacterium* relationship. Finally, we review recent reports of nodulation and nitrogen fixation with legume hosts by bacteria that are outside the traditional rhizobial phylogenetic lineages. They include species of *Methylobacterium* and *Devosia* in the alpha-Proteobacteria and of *Burkholderia* and *Ralstonia* in the beta-Proteobacteria.

### Introduction

The term “rhizobia”, in the strictest sense, refers to members of the genus *Rhizobium*. Over the years, however, the term has come to be used for all the bacteria that are capable of nodulation and nitrogen fixation in association with legumes and that belong to a genus that was at one time part of the genus *Rhizobium* or closely related to it.

The family *Rhizobiaceae* in the 1984 edition of Bergey’s Manual of Systematic Bacteriology, is composed of the rhizobia (at that time just including *Rhizobium* and *Bradyrhizobium*), *Agrobacterium* and *Phyllobacterium* (Jordan, 1984).

### History

By the end of the 19th century, it was realized that atmospheric nitrogen was being assimilated through the root-nodules of legume plants. In 1888, Beijerinck reported isolation of the root-

nodule bacteria and established that they were responsible for this process of nitrogen fixation. He named these bacteria *Bacillus radicumicola* (Beijerinck, 1888). Later, Frank changed the name to *Rhizobium* with originally just one species, *R. leguminosarum* (Frank, 1889).

Extensive testing of nodulation of diverse legume hosts by different bacteria in the beginning of the 20th century, led to the establishment of cross-inoculation groups, with rhizobia from one plant in a cross-inoculation group supposed to nodulate all other plants in the group (Fred et al., 1932). This concept was also used in rhizobial taxonomy, but later it was abandoned as an unreliable taxonomic marker (Graham, 1964; Wilson, 1944), in part because of aberrant cross-infection among plant groups. Beginning in the early 1960s, bacteriologists started using a large diversity of morphological, nutritional and metabolic characters (Graham, 1964; Moffet and Colwell, 1968; ‘tMannetje, 1967), as well as serology (Graham, 1963; Vincent and Humphrey, 1970) and simple DNA characteristics (De Ley and Rassel, 1965) in numerical taxonomy studies. This

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demonstrated the relatedness of *Rhizobium* and *Agrobacterium* and led to a clear distinction between the fast and slow growing rhizobia (Graham, 1964), with the latter group subsequently placed in a separate genus, *Bradyrhizobium* (Jordan, 1982).

From the 80s on, with the introduction of more genetic characteristics (DNA–DNA and DNA–rRNA hybridizations, rRNA catalogues, rDNA sequencing) more diversity was discovered among the rhizobia and their relationships with other groups of bacteria became apparent. This led to a gradual increase in the number of genera (Table 1). In parallel, there has also been a significant increase in the number of validly published species (Table 1), with 48 species of rhizobia now recognized.

Two main reasons for this increase in the number of genera and species are:

- (1) Many different legume species have now been studied. This in contrast to original efforts, which emphasized those legumes that were important food and pasture species crops, mostly from the Western world. As an example, consider Table 2, where the *Mesorhizobium* species are listed together with the host plants from which they were reported. Even now, only about 20% of the total of about 18,000 species and 57% of about 650 genera of legume plants have been studied for nodulation (Sprent, 1995). This leaves a large number of legume species to be studied and potentially many more species and genera of rhizobia to be described.

Table 1. Rising number of species in the genera of the rhizobia

Genus	Original publication	Number of species					
		Before 1980	81–85	86–90	91–95	96–00	01–06
<i>Agrobacterium</i>	Cohn (1942)	4	4	5	5	5	5
<i>Rhizobium</i>	Frank (1889)	4	5	5	10	10	16
<i>Bradyrhizobium</i>	Jordan (1982)		1	1	3	3	7
<i>Sinorhizobium</i>	Chen et al. (1988)			2	5	8	11
<i>Azorhizobium</i>	Dreyfus et al., (1988)			1	1	1	2
<i>Mesorhizobium</i>	Jarvis et al. (1997)					7	11
<i>Allorhizobium</i>	de Lajudie et al. (1998a)					1	1
Total		8	9	13	23	34	53

Table 2. Overview of the species of *Mesorhizobium* (Jarvis et al., 1997) and the plants they were isolated from

Name	Year <sup>a</sup>	Host plants	Reference
<i>M. loti</i>	1982	<i>Lotus</i> , <i>Lupinus</i> , <i>Anthyllis</i> , <i>Leucaena</i>	Jarvis et al. (1982)
<i>M. huakuii</i>	1991	<i>Astragalus</i> (China)	Chen et al. (1991)
<i>M. ciceri</i>	1994	<i>Cicer arietinum</i> (Spain, USA, India, Russia, Turkey, Morocco, Syria)	Nour et al. (1994)
<i>M. tianshanense</i>	1995	<i>Glycyrrhiza</i> , <i>Sophora</i> , <i>Caragana</i> , <i>Halimodendron</i> , <i>Swainsonia</i> , <i>Glycine</i> (China)	Chen et al. (1995)
<i>M. mediterraneum</i>	1995	<i>Cicer arietinum</i> (Spain, Syria, India, Lebanon, Syria, Tunisia)	Nour et al. (1995)
<i>M. plurifarum</i>	1998	<i>Acacia</i> , <i>Prosopis</i> , <i>Chamaecrista</i> , <i>Leucaena</i> (Senegal, Sudan, Brazil)	de Lajudie et al. (1998b)
<i>M. amorphae</i>	1999	<i>Amorpha fruticosa</i> (China)	Wang et al. (1999)
<i>M. chacoense</i>	2001	<i>Prosopis</i> (Argentina)	Velázquez et al. (2001)
<i>M. septentrionale</i>	2004	<i>Astragalus adsurgens</i> (China)	Gao et al. (2004)
<i>M. temperatum</i>	2004	<i>Astragalus adsurgens</i> (China)	Gao et al. (2004)
<i>M. thiogangeticum</i>	2006	Rhizosphere of <i>Clitoria ternatea</i> (India)	Gosh and Roy (2006)

<sup>a</sup>Year of first description.

(2) The other reason for increasing numbers of rhizobial species is the ongoing evolution of taxonomic research. Improvements and new developments in the methods to study cell DNA and RNA have led to a more detailed characterization resulting in phylogenetic and polyphasic classifications. Currently an increasing number of total bacterial genomes are becoming available. This will undoubtedly have a further major impact on bacterial taxonomy. Most recent taxonomic studies have made use of a polyphasic approach (Graham et al., 1991; Vandamme et al., 1996), with genetic, phenotypic, chemotaxonomic, phylogenetic data combined to establish a comprehensive picture of the relationships of the bacteria, and to propose a suitable classification.

### *Sinorhizobium*

Chen et al. (1988) proposed a separate genus for the fast-growing soybean rhizobia, renaming *R. fredii* as *Sinorhizobium fredii*, and proposing a second species, *S. xinjiangense* (the original spelling *S. xinjiangensis* was later corrected [Euzéby, 1998]). This new genus was controversial at first since genetic evidence to justify its creation and to separate it from *R. fredii* was not presented at the time (Jarvis et al., 1992). Later, phylogenetic data were presented to support a third genus of rhizo-

bia, not restricted to the fast-growing soybean rhizobia (de Lajudie et al., 1994) and the genus definition was emended. *R. meliloti* was transferred to *Sinorhizobium* as *S. meliloti* and two additional species, *S. saheli* and *S. teranga* (the original spelling *S. teranga* was later corrected [Trüper and De'Clari, 1997]), were proposed for isolates from *Acacia* and *Sesbania* from Senegal. The genus *Sinorhizobium* is now widely accepted and currently has 11 valid species (Table 3). New genetic evidence in support of the separation of *S. xinjiangense* and *S. fredii* has been presented (Peng et al., 2002). However, this strongly relies on DNA–DNA hybridizations performed with DNA from the *S. fredii* type strain USDA 205<sup>T</sup> the quality of which was not validated by homologous hybridization with *S. fredii* strains.

It has recently become evident from 16S rDNA comparisons that *Ensifer adhaerens* is also phylogenetically a member of the *Sinorhizobium* lineage (Balkwill, 2005). This organism is a soil bacterium that can adhere to and lyse other soil bacteria, and that was initially described mostly on the basis of phenotypic data (Casida Jr, 1982). Our own polyphasic studies have shown that a small group of four diverse rhizobial isolates and two soil isolates cannot be distinguished clearly from *Ensifer adhaerens* on the basis of DNA–DNA hybridizations and phenotypic features and we should therefore include these rhizobia in *Ensifer*. Phylogenetically, *Ensifer* and *Sinorhizobium*

Table 3. Species of *Sinorhizobium*

Name	Year <sup>a</sup>	Host plants	Reference
<i>S. meliloti</i>	1926	<i>Melilotus</i> , <i>Medicago</i> , <i>Trigonella</i>	Dangeard (1926)
<i>S. fredii</i>	1984	<i>Glycine</i> , <i>Vigna</i> , <i>Cajanus</i>	Scholla and Elkan (1984)
<i>S. xinjiangense</i>	1988	<i>Glycine</i>	Chen et al. (1988)
<i>S. saheli</i>	1994	<i>Sesbania</i> , <i>Acacia</i> (Senegal)	de Lajudie et al. (1994)
<i>S. teranga</i>	1994	<i>Sesbania</i> (Senegal)	de Lajudie et al. (1994)
<i>S. medicae</i>	1996	<i>Medicago</i> (Syria, France)	Rome et al. (1996)
<i>S. arboris</i>	1999	<i>Acacia</i> , <i>Prosopis</i> (Sudan, Kenya)	Nick et al. (1999)
<i>S. kostiense</i>	1999	<i>Acacia</i> , <i>Prosopis</i> (Sudan)	Nick et al. (1999)
<i>S. kummerowiae</i>	2002	<i>Kummerowia stipulacea</i>	Wei et al. (2002)
<i>S. morelense</i>	2002	<i>Leucaena leucocephala</i> (Mexico)	Wang et al. (2002)
“ <i>S. adhaerens</i> ” <sup>b</sup>	2003	<i>Medicago sativa</i> (Spain), <i>Leucaena leucocephala</i> (Brazil), <i>Pithecellobium dulce</i> (Brazil)	Willems et al. (2003)
<i>S. americanum</i>	2003	<i>Acacia</i> spp. (Mexico)	Toledo et al. (2003)

<sup>a</sup>Year of first description.

<sup>b</sup>*Ensifer adhaerens* was proposed to belong *Sinorhizobium*, however the name “*Sinorhizobium adhaerens*” remains not valid pending a judicial opinion (Willems et al., 2003).

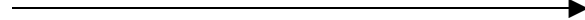
form a single group in the 16S rDNA dendrogram of the alpha-Proteobacteria and may therefore be regarded as a single genus. This has important nomenclatural consequences because the older name *Ensifer* would have precedence. There are several reasons why a change from *Sinorhizobium* to *Ensifer* may not be the best solution, and allowing an exception to Rule 38 may be more appropriate. We have therefore proposed the creation of the species *Sinorhizobium adhaerens* comb. nov. and submitted a request for Opinion on the conservation of *Sinorhizobium adhaerens* over *Ensifer adhaerens* (Willems et al., 2003). This proposal was regarded unjustified by Young (2003) who proposed that all *Sinorhizobium* species should be transferred to *Ensifer* instead. While the request for opinion is pending the combination “*Sinorhizobium adhaerens*” is not valid and *Ensifer adhaerens* remains the correct name.

#### *Mesorhizobium*

The genus *Mesorhizobium* was proposed for five rhizobial species (*R. loti*, *R. huakuii*, *R. ciceri*, *R. mediterraneum* and *R. tianshanense*) that are phylogenetically related and distinct from the large phylogenetic grouping that includes *Rhizobium*, *Agrobacterium* and *Sinorhizobium* (Jarvis et al., 1997). They are characterized by a growth rate intermediate between the fast- and slow-growing rhizobia. On the basis of 16S rDNA sequence data, *Mesorhizobium* is phylogenetically separated from the fast-growing rhizobia by the genera *Bartonella*, *Defluviobacter*, *Aquamicrobium*, *Phyllobacterium*, *Aminobacter* and *Pseudaminobacter* (Figure 1).

#### *Bradyrhizobium*

*Bradyrhizobium* was created for the slow-growing species *Rhizobium japonicum* (Jordan, 1982). Originally the soybean-nodulating *B. japonicum* was the only species described, although it was recognized that slow-growing strains occur on various legume genera (Elkan and Bunn, 1992). To date, five additional species have been validly named in this genus, two of them nodulating *Glycine* (*B. elkanii* [Kuykendall et al., 1992] and *B. liaoningense* [Xu et al., 1995]), *B. yuanmingense* nodulating *Lespedeza* (Yao et al., 2002),

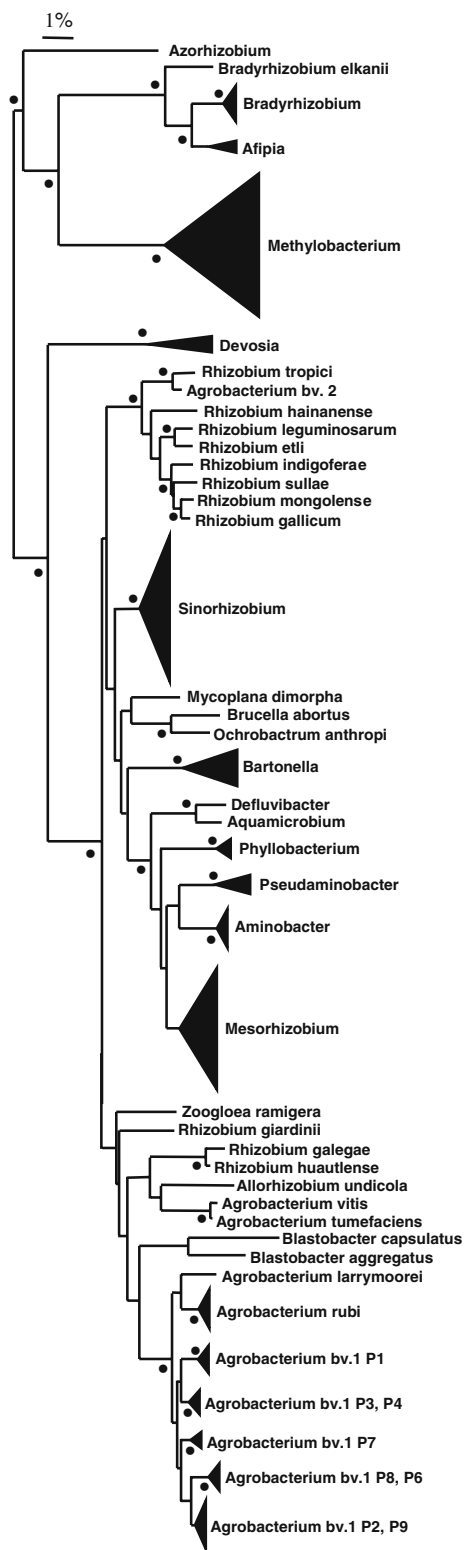


*Figure 1.* 16S rDNA phylogeny of rhizobia and relatives in the alpha-Proteobacteria. The tree was calculated with the neighbor joining method, using Kimura-2 corrections. A bootstrap analysis was performed on 500 replicates and the groupings that were recovered in 95 or more percent of trees are marked in the dendrogram by a black dot at the branching point. Numbers P1–P9 refer to the *Agrobacterium* DNA groups of Popoff et al. (1984).

*B. betae* from the roots of *Beta vulgaris* afflicted with tumor-like deformations (Rivas et al., 2004), *B. canariense* from genistoid legumes from the Canary Islands (Vinuesa et al., 2005). In addition to the species subdivision, a number of serogroups have been described among slow-growing soybean symbionts (Date and Decker, 1965). Many other slow-growing rhizobia have been isolated from other legume hosts and are commonly referred to as *Bradyrhizobium* sp., followed by the name of the legume host. A special feature of the *Bradyrhizobium*–legume symbiosis is that some bradyrhizobia can form stem nodules on some plant species, produce bacteriochlorophyll and perform photosynthesis (Alazard, 1985; Evans et al., 1990; Molouba et al., 1999). Some photosynthetic bradyrhizobia have also been reported as endophytes of African wild rice (Chaintreuil et al., 2000).

A major factor complicating the evaluation of the taxonomic status and interrelationships of bradyrhizobia is the high similarity of 16S rDNA gene sequences. Many strains have 16S rDNA sequence divergences of 0.1–2.0%. Only sequences for *B. elkanii* and related strains differ by up to 4% from those of other bradyrhizobia (Willems et al., 2001a). A further complicating factor is the very slow growth of these organisms, often precluding the use of the standard phenotypic test procedures (e.g. Biolog, API systems). As a consequence many bradyrhizobia have been characterized more thoroughly by genotypic methods. Our own work using AFLP, DNA–DNA hybridizations and 16S–23S internal transcribed spacer (ITS) analyses has resulted in the delineation of at least 11 *Bradyrhizobium* genospecies, including the named species (Willems et al., 2001c).

From 16S rDNA phylogeny, the genera *Afipia*, *Rhodopseudomonas* and *Nitrobacter* also appear closely related to the bradyrhizobia, with *B. elkanii* occupying a more peripheral phylogenetic position (Willems et al., 2001a). This is in contrast to ITS



sequence data that show that *B. elkanii* is more closely related to the bradyrhizobia than are the three non-rhizobial genera. Based on ITS sequence data, the photosynthetic bradyrhizobia isolated from stem-nodules of *Aeschynomene*, form a distinct group closely related to *Blastobacter denitrificans* (Willems et al., 2001b; van Berkum and Eardly, 2002). As a result of a comprehensive study of both groups, van Berkum et al. (2006) recently proposed to transfer *Blastobacter denitrificans* to *Bradyrhizobium* and unite the species with the isolates from *Aeschynomene indica* as the species *Bradyrhizobium denitrificans*.

### The Rhizobium–Allorhizobium–Agrobacterium issue

Figure 1 provides an overview of the phylogeny of the rhizobia and relatives in the alpha-Proteobacteria based on 16S rDNA sequence data. *Bradyrhizobium* and *Azorhizobium* are quite separate. *Sinorhizobium* and *Mesorhizobium* also form separate clusters, but it is clear that *Agrobacterium*, *Allorhizobium* and *Rhizobium* are rather more closely related. The recent proposal (Young et al., 2001) to abandon the genera *Agrobacterium* and *Allorhizobium* and incorporate them in *Rhizobium* has not met with universal approval (Farrand et al., 2003).

The genus *Allorhizobium* contains a single species, *Al. undicola*, for isolates from nodules of *Neptunia natans* from Senegal (de Lajudie et al., 1998a). Phylogenetically (Figure 1), it takes a separate position in the large *Agrobacterium*–*Rhizobium* 16S rDNA cluster, with *A. vitis* (96.3% 16S rDNA sequence similarity), *R. galegae* (95.1%) and *R. huautlense* (95.3%) as its nearest neighbors. In view of its remoteness from the *Rhizobium* type species, *R. leguminosarum*, and the confused taxonomic situation in *Agrobacterium* (see below) and because the *Neptunia* isolates can be distinguished phenotypically and genotypically from related taxa, it was considered most appropriate that they be placed in a separate genus (de Lajudie et al., 1998a). This genus may need emendation or revision in a future scheme to correct the classification and

nomenclature of *Agrobacterium* and *Rhizobium* species, in particular *A. vitis*, *R. galegae* and *R. huautlense*.

The genus *Rhizobium* currently has 15 species, from various hosts (Table 4 – not including *Sinorhizobium* and *Agrobacterium*). *Agrobacterium*, a genus proposed in 1942 (Conn, 1942) that comprises bacteria responsible for various kinds of hypertrophies in plants, has six valid species. The oldest species were – for practical purposes – described mainly on the basis of phytopathological properties. For example, *A. tumefaciens* groups those strains that cause tumors on plants; *A. radiobacter* unites strains that are not pathogenic and *A. rhizogenes* comprises strains that cause hairy root growth (Conn, 1942). Of the other species, *A. rubi* is pathogenic on *Rubus* (Starr and Weiss, 1943), *A. vitis* on grapevine (Ophel and Kerr, 1990) and *A. larrymoorei* on *Ficus* (Bouzar and Jones, 2001).

Using a polyphasic approach, various authors have recognized three large groups or biovars among strains assigned to *A. tumefaciens*, *A. rhizogenes* and *A. radiobacter* in the official (phytopathology-based) classification (summarized in Kersters and De Ley, 1984). The taxonomic situation is complicated by the fact that these biovars do not correspond to the existing

species, with biovar 1 containing strains of *A. tumefaciens*, *A. rhizogenes* and *A. radiobacter*. Among these strains are the type strains of *A. tumefaciens* and *A. radiobacter*. Biovar 2 also contains strains of all three species, including the type strain of *A. rhizogenes*, whereas biovar 3 contains *A. tumefaciens* and *A. vitis* strains. Furthermore, *Agrobacterium* biovar 1 has been shown to contain several genospecies by DNA–DNA hybridizations (De Ley, 1974; Popoff et al., 1984), some of which contain clinical isolates that do not have virulence genes but were originally named *Agrobacterium* because of biochemical features (Lautrop, 1967; Riley and Weaver, 1977). A further complicating factor is that the genus *Agrobacterium* was declared conserved by the Judicial Commission, with *A. tumefaciens* as the type species (Judicial Commission, 1970). However, as Young et al. (2006) recently pointed out, the species name *A. tumefaciens* is not a conserved name as some authors may previously have believed.

The phytopathology-based taxonomy and the polyphasic classification (Kersters and De Ley, 1984) of the genus *Agrobacterium* is shown in Table 5. No species names were proposed for the biovars described by Kersters and De Ley (1984) because the rules of the Bacteriological Code

Table 4. Species of *Rhizobium*

Name	Year <sup>a</sup>	Host plant(s)	Reference
<i>R. leguminosarum</i>	1879	<i>Pisum, Lathyrus, Vicia, Lens, Phaseolus, Trifolium</i>	Frank (1879)
<i>R. lupinii</i> <sup>b</sup>	1886	<i>Lupinus, Ornithopus</i>	Schroeter (1886)
<i>R. galegae</i>	1989	<i>Galega</i>	Lindström (1989)
<i>R. tropici</i>	1991	<i>Phaseolus vulgaris, Leucaena</i>	Martínez-Romero et al. (1991)
<i>R. etli</i>	1993	<i>Phaseolus vulgaris</i>	Segovia et al. (1993)
<i>R. gallicum</i>	1997	<i>Phaseolus vulgaris</i>	Amarger et al. (1997)
<i>R. giardinii</i>	1997	<i>Phaseolus vulgaris</i>	Amarger et al. (1997)
<i>R. hainanense</i>	1997	<i>Desmodium, Stylosanthes, Centrosema, Tephrosia, Acacia, Zornia, Macroptilium</i>	Chen et al. (1997)
<i>R. mongolense</i>	1998	<i>Medicago ruthenica</i>	van Berkum et al. (1998)
<i>R. huautlense</i>	1998	<i>Sesbania herbacea</i>	Wang et al., (1998)
<i>R. yanglingense</i>	2001	<i>Coronilla, Gueldenstaedtia, Amphicarpaea</i>	Tan et al. (2001)
<i>R. sullae</i>	2002	<i>Hedysarum coronarium</i>	Squartini et al. (2002)
<i>R. indigoferae</i>	2002	<i>Indigofera</i>	Wei et al. (2002)
<i>R. loessense</i>	2003	<i>Astragalus</i>	Wei et al. (2003)
<i>R. daejeonense</i>	2005	<i>Medicago</i>	Quan et al. (2005)

<sup>a</sup>Year of first description.

<sup>b</sup>The relationships of *R. lupinii* (Kuykendall et al., 2005) are unclear because of doubts on the purity of the type strain, but the species was included on the approved lists.

Table 5. Official and polyphasic classification of *Agrobacterium*

Official classification <sup>a</sup> (phytopathology)	Polyphasic classification <sup>b</sup> (Kerstens and De Ley, 1984)
<i>A. tumefaciens</i> (tumors)	Biovar 1: tumorigenic ( <i>A. tumefaciens</i> ), rhizogenic ( <i>A. rhizogenes</i> ) and avirulent ( <i>A. radiobacter</i> ) strains, includes type strains of <i>A. tumefaciens</i> and <i>A. radiobacter</i>
<i>A. radiobacter</i> (no symptoms)	Biovar 2: tumorigenic ( <i>A. tumefaciens</i> ), rhizogenic ( <i>A. rhizogenes</i> ) and avirulent ( <i>A. radiobacter</i> ) strains, includes type strain of <i>A. rhizogenes</i>
<i>A. rhizogenes</i> (hairy roots)	Biovar 3: tumorigenic on <i>Vitis</i> ( <i>A. tumefaciens</i> and <i>A. vitis</i> )
<i>A. rubi</i> ( <i>Rubiaceae</i> )	<i>A. rubi</i>
<i>A. vitis</i> ( <i>Vitis</i> )	
<i>A. larrymoorei</i> ( <i>Ficus</i> )	

<sup>a</sup>The official classification includes the species that are in the Approved List of Bacterial Names (Skerman et al., 1980) or were subsequently published in International Journal of Systematic Bacteriology (now International Journal of Systematic and Evolutionary Microbiology). All *Agrobacterium* species are transferred to *Rhizobium* in the proposal of Young et al. (2001).

<sup>b</sup>The polyphasic classification is a consensus classification based on different methods as presented in Bergey's Manual of Systematic Bacteriology (Kerstens and De Ley, 1984).

would have required biovar 1 to be named *A. tumefaciens* and biovar 2 *A. rhizogenes*. These names would then apply to strains with and without the phytopathological properties their name implies. This was regarded as unacceptable at the time and thus the official species classification and the polyphasic biovar system have been used in parallel for many years. This situation is clearly unsatisfactory and in 1993 Sawada et al. (1993) proposed that biovar 1 be named *A. radiobacter* and biovar 2 *A. rhizogenes*. This was thought to go against Opinion 33 of the Judicial Commission (Bouzar, 1994) and was not widely adopted.

From the 16S rDNA phylogeny (Figure 1), it is clear that *Rhizobium* and *Agrobacterium* are highly related and their species are interwoven. In particular, biovar 2 groups with the majority of *Rhizobium* species. Biovar 1 consists of several smaller groups representing different genospecies. *A. rubi* and *A. larrymoorei* are closely related to these biovar 1 genospecies. *A. vitis* is close to *Allorhizobium*. *Rhizobium giardinii* is the most peripheral of the whole group. Young et al. (2001) proposed the transfer all these taxa to *Rhizobium*. They proposed to unite *A. radiobacter* and *A. tumefaciens* in *R. radiobacter*, which thus represents biovar 1, while *A. rhizogenes* becomes *R. rhizogenes* and represents biovar 2. *A. rubi* and *A. vitis* are transferred to *Rhizobium* as distinct species and also *A. larrymoorei* is transferred as *R. larrymoorei* (Young, 2004). This proposal solves the species matching the biovars and the placement of *A. rhizogenes* in *Rhizobium*

is clearly justified, but it is not widely accepted (Farrand et al., 2003) and several problems remain to be addressed:

- (1) Many strains of *Agrobacterium* species have in the past been named on the basis of phytopathological effects they cause on plants and are listed in culture collection catalogues as such, often without their biovar status being known. It is not clear which *Rhizobium* species these should be classified as. For example, an *A. tumefaciens* strain may belong to biovar 1, 2 or 3 and depending on this should be classified as *R. radiobacter*, *R. rhizogenes* or *R. vitis*, respectively.
- (2) The biovar 1 genospecies are ignored in the new scheme.
- (3) The incomplete phenotypic differentiation of these genospecies.
- (4) The proposed enlarged genus *Rhizobium* would be a large, widely defined and phylogenetically deep genus (Figure 1).
- (5) The species *Blastobacter capsulatus*, *Blastobacter aggregatus* and *Zooglea ramigera*, that group with the *Agrobacterium*–*Rhizobium* phylogenetic cluster (Figure 1) and therefore would group in the proposed large genus *Rhizobium*, should be taken into account.

When considering the 16S rDNA phylogeny of part of the alpha-Proteobacteria (Figure 1), it is obvious that the new genus *Rhizobium* is rather large and represents a phylogenetically more divers (deeper) group than the other genera in its phylogenetic vicinity. However, to present an

alternative proposal, additional data are essential. The current proposal was based mostly on 16S rDNA data. It is clear that data from other genes can provide useful insights to unravel relationships in these groups. With the new complete genome sequence data that are now becoming available, it may soon become possible to make a more comprehensive comparison and arrive at a suitable classification. Meanwhile, microbiologists should be aware that all validly published names can be used: it is the scientific community that decides on the value of any new proposal by either using it or, alternatively, by using a previously validly published classification.

### Other nitrogen-fixing legume symbionts

Recently, a number of isolates have been reported from legume nodules, capable of nitrogen fixation but phylogenetically located outside the traditional groups of rhizobia in the alpha-Proteobacteria. New lines that contain nitrogen-fixing legume symbionts include *Methylobacterium*, *Devosia*, *Ochrobactrum* and *Phyllobacterium* in the alpha-Proteobacteria and *Burkholderia*, *Ralstonia* and *Cupriavidus* in the beta-Proteobacteria.

In *Burkholderia*, a genus that contains over 20 species of plant pathogens, soil and plant-associated bacteria and clinical isolates, the following symbiotic, nitrogen fixing strains have been identified: (1) two strains from *Mimosa* were found to belong to *B. caribensis*, a species that was first described for soil isolates from Martinique; (2) one strain from *Alysicarpus* was found to belong to *B. cepacia* genomovar VI (now *B. dolosa* [Vermis et al., 2004], a group previously only found in cystic fibrosis patients; (3) one strain from *Machaerium* was identified as a new species for which the name *B. phymatum* has been proposed and (4) one strain from *Aspalathus* was identified as a second new species for which the name *B. tuberum* was proposed (Moulin et al., 2001; Vandamme et al., 2003).

In *Ralstonia*, like *Burkholderia* a genus of plant pathogenic or plant associated, soil and clinical organisms, *Ralstonia taiwanensis* was proposed for strains from *Mimosa* species in Taiwan (Chen et al., 2001).

In the alpha-Proteobacteria, *Devosia neptuniae* was proposed for strains from *Neptunia natans*

from India (Rivas et al., 2003) and *Methylobacterium nodulans* for strains from *Crotalaria* (Jourand et al., 2004; Sy et al., 2001). *Ochrobactrum lupinus* was described for nodule isolates from *Lupinus* sp. (Trujillo et al., 2005) and *Phyllobacterium lupinii* for isolates nodulating *Trifolium* and *Lupinus* (Valverde et al., 2005).

All these new nodulating bacteria are phylogenetically (16S rDNA) distinct from the rhizobia, but do carry nod genes similar to those of rhizobia. These genes encode for Nod factors, signal molecules in the bacterium–legume communication that accompanies nodulation. It is in fact from studies of nod gene diversity that some discoveries of new nodulating strains outside the rhizobia have originated. The nod genes were most probably obtained by these new nitrogen-fixing legume symbionts through lateral-gene transfer (Moulin et al., 2001; Sy et al., 2001). Most of the new nodulating bacteria belong to genera that have at least some plant-associated species and that are therefore likely to have the molecular strategies to overcome plant defenses. Recent reports confirm that it is quite likely that more such bacteria, capable of effective nodulation will be discovered outside the traditional rhizobia (Barret and Parker, 2006; Rasolomampianina et al., 2005; Zakhia et al., 2006).

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