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DNA Homologies among Members of the Genus *Azorhizobium* and Other Stem- and Root-Nodulating Bacteria Isolated from the Tropical Legume *Sesbania rostrata*

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[redacted]

TABLE 1. Origin of strains tested

Strain(s)[a]	Location	Isolated from:
Strains from North Senegal		
A. caulinodans ORS 571[T]		Stem nodules

the pH was 4.25, the flow rate was 1.0 ml/min, and absorption was measured at 260 nm.

DNA-DNA hybridization and thermal stability of duplexes. DNA-DNA hybridization tests were carried out at 70°C (the optimal temperature for DNA reassociation) with tritium-

TABLE 2. Levels of DNA hybridization among strains

Source of unlabeled DNA	G+C content (mol %)	% Reassociation at 70°C with labeled DNA from:					
		Strain ORS 571^T	Strain SD02	Strain SG28	Strain RT12	Strain RT14	Strain TAL 674
Typical *Azorhizobium* strains							
Genomic species 1							
ORS 571^T	67	100[a]	47	49	2	5	
SV01	66	91					
SV06	66	98					
SV07	67	103		53			
SV08	66	96					
SV20	66	96					
SV25	68	84	53	55			
SV26		96			3		
SV31	68	87					
SV33		87 (1.3)[b]					
SV34		95	58				
BD01	66	98					
BD05	67	92					
RT01	66	88					
RT06	67	94					
RT10		104	51	46			
RT15	66	84					
RT18	67	92	51				
FY01	66	93					
FY10	68	81					
FY18	67	96					
FY29	67	89	48	50			
PR01	66	97	55	44			
SG01	66	97					
SG07	67	82					
SG10	67	94					
SG24	67	91					
SG26	66	85					
SG27	67	101	49	54			
SG31		106	53				
DP04	67	92					
DP13	67	92					
DP18	66	98	57	53			
DP19	67	105					
DP20		85	57				
DP22	67	98	55				
DP23	67	81					
KL03	66	94					
KL06	67	82 (1.5)	51 (17.8)				
KL11	68	99	53		2	7	4
KL14	66	90					
KL16	66	101					
KL17	67	92	59	58			
SD01	67	104					
SD03	67	83 (1.7)	55 (15.2)		2		
SK02	66	99					
IRG10	67	92					
IRG40		89	50				
IRG44	68	102					
IRG23	67	100					
Genomic species 2							
SD02	67	53 (8.8)	100	87			
SD04	67	44 (7.9)	86		5		
SG28	66	47 (7.2)	92	100			
SG05	67	44 (9.1)	79 (2.2)	90	5		
SG06	66	46 (9.7)	94		7		
SG09	66	51 (6.7)	76 (1.6)	92			
SG19	66	51 (6.6)	83 (3.0)				
SG22	67	48 (7.0)	89	86			
SG25	67	50 (6.4)	90				
Other strains							
Genomic species 3							
RT12	63	0	2	1	100		
Genomic species 4							
RT14	60	4	0	1	3	100	7

Continued on following page

TABLE 2—*Continued*

Source of unlabeled DNA	G+C content (mol %)	% Reassociation at 70°C with labeled DNA from:					
		Strain ORS 571^T	Strain SD02	Strain SG28	Strain RT12	Strain RT14	Strain TAL 674
Genomic species 5							
TAL 674	59	4	3	2	11		100
Unclassified							
RT09	61	4	0	1	5	10	7
RT11	61	2	−1	2	5	10	10
DP21	61	0	6	1	6	8	10
KL13	61	−2	4	6	−2	9	15

[a] Level of relatedness at 70°C.
[b] The numbers in parentheses are ΔT_m values (in degrees Celsius).

than 86% related to strain SG28 (Table 2). These strains were only 44 to 53% related to strain ORS 571^T (ΔT_m, 6.4 to 9.7°C).

The remaining seven strains (strains RT12, RT14, TAL 674, RT09, RT11, DP21, and KL13) had lower G+C contents (59 to 63 mol%) and exhibited very low levels of DNA binding with strain ORS 571^T (less than 4%) or strains SD02 [redacted]

expressed nitrogenase activity both in vitro and in symbiosis with the host plant.

According to Grimont (11), strains that exhibit less than 60% reassociation and more than 7°C divergence do not belong to the same genomic species. Thus, the results obtained with the nine strains belonging to genomic species 2 showed that these organisms are sufficiently different from [redacted]

TABLE 3. Levels of DNA hybridization between strain ORS 571^{T} and typical *Azorhizobium* strains belonging to genomic species 1

Source of unlabeled DNA	% Reassociation at 70°C with labeled DNA from strain ORS 571^{T}	Source of unlabeled DNA	% Reassociation at 70°C with labeled DNA from strain ORS 571^{T}
SV02	97	SG03	96
[illegible]	[illegible]	[illegible]	[illegible]

TABLE 4. Nitrogenase activities of strains under free-living conditions and in symbiosis with *Sesbania rostrata*

Strain	Acetylene reduction test performed in culture[a]	Symbiotic conditions	
		Stem and root nodulation[b]	Acetylene reduction activity (μmol of C_2H_4/plant/h)

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