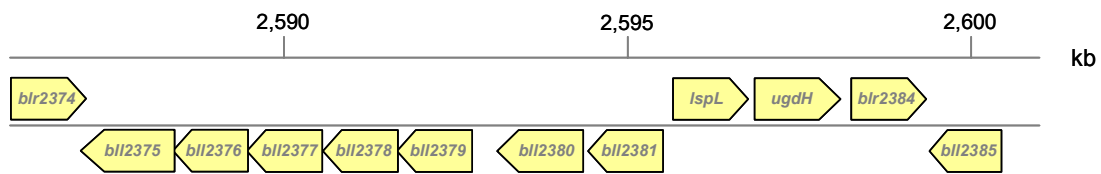
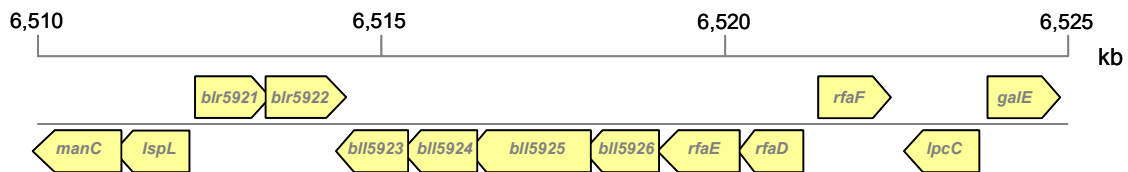


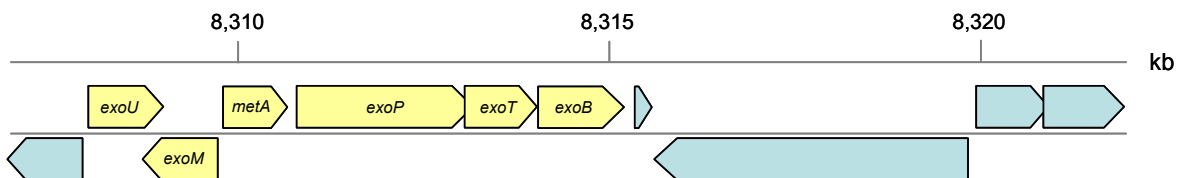
**Analysis of gene clusters.** We analyzed the complete genomic sequence of *B. japonicum* USDA 110 (Kaneko *et al.*, 2002) to find the genomic contexts of the genes under study. As schematically represented in Fig. S1, the tandem *lspL-ugdH* (*blr2382-blr2383*) and the gene *exoB* (*blr7578*) are surrounded by genes probably involved in EPS synthesis, while the *lspL* paralog *bll5920* as well as *galE* (*blr5931*) are in a cluster of genes probably involved in LPS synthesis. The cluster illustrated in Fig. S1C was described by Becker *et al.* (1998).



**Figure S1A.** *B. japonicum* USDA 110 gene cluster that might be related with EPS synthesis and assemblage.



**Figure S1B.** *B. japonicum* USDA 110 gene cluster that might be related with LPS synthesis.



**Figure S1C.** *B. japonicum* USDA 110 gene cluster related with EPS synthesis and assemblage (yellow boxes). Becker *et al.*, 1998.

**Figure S1.** Scheme of *B. japonicum* gene clusters related with the synthesis of EPS and LPS, containing the genes referred to in the paper. Available information about the gene products is resumed in the following list:

gene annotation	Putative protein in <i>B. japonicum</i> USDA 110	Similar protein in certain rhizobia (in parenthesis % identity)	Phenotype of mutant	References
blr2374	probable glycosyl transferase			
blI2375	unknown protein			
blI2376	probable glycosyl transferase			
blI2377	probable glycosyl transferase			
blI2378	unknown protein			
blI2379	putative polysaccharide export protein	exopolysaccharide production protein ExoF precursor of <i>R. sp.</i> pNGR234ab (28.0))	EPS with sugars alterations, colonies red and nonmucoid in agar plates with Congo Red	Stachelin <i>et al.</i> , 2006
blI2380	probable glycosyl transferase			
blI2381	probable glycosyl transferase			
blr2382	UDP-glucuronic acid epimerase	UDP-glucuronic acid epimerase of <i>S. meliloti</i> (47.3), <i>R. etli</i> CFN42 (46.2)	LPS that lacks O- antigen	Keretsz <i>et al.</i> , 1998; Keating <i>et al.</i> , 2002
blr2383	UDP-glucose 6-dehydrogenase	UDP-glucose 6-dehydrogenase protein of <i>S. meliloti</i> (70.4) and <i>R. etli</i> CFN42 (68.5)	KPS and LPS alterations	Keretsz <i>et al.</i> , 1998
blr2384	hypothetical protein			
blI2385	hypothetical protein			
<i>manC</i> (blI5919)	mannose-1-phosphate guanylyltransferase (GDP)	NoeI of <i>M. loti</i> MAFF303099 (41.6) and <i>R. sp.</i> NGR234ab (47.5)	truncated LPS core in <i>R. tropici</i> CIAT 899	Ormeño Orrillo <i>et al.</i> , 2008
<i>lspL</i> (blI5920)	UDP-glucuronic acid epimerase	UDP-glucuronic acid epimerase of <i>S. meliloti</i> (49.3) and <i>R. etli</i> CFN42 (54.8)	LPS that lacks O- antigen in <i>S. meliloti</i>	Keretsz <i>et al.</i> , 1998; Keating <i>et al.</i> , 2002
blr 5921	Hypothetical protein	glycosyltransferase of <i>M. loti</i> MAFF303099 (33.9)	not studied	
blr 5922	probable glycosyl transferase		not studied	
blI 5923	putative UDP-glucose 4-epimerase	putative UDP-glucose 4-epimerase protein of <i>R. etli</i> CFN42 (45.2)	not studied	
blI 5924	probable glycosyl transferase	putative glycosyltransferase protein of <i>R. etli</i> CFN42 (38.8)	not studied	
blI 5925	putative capsular polysaccharide biosynthesis protein	lipopolysaccharide biosynthesis protein of <i>M. loti</i> MAFF303099 (35.7)	LPS that lacks O- antigen	D'Antuono <i>et al.</i> , 2005
blI 5926	unknown protein	putative O-antigen ligase <i>rfaL</i> like of <i>Bradyrhizobium</i> sp ORS278 (63.1)	not studied	
<i>rfaE</i> (blI 5927)	probable ADP-heptose synthase	bifunctional protein RfaE of <i>A. caulinodans</i> ORS571 (50.0)	LPS that lacks O- antigen in <i>A. caulinodans</i>	Suzuki <i>et al.</i> , 2007
<i>rfaD</i> (blI 5928)	probable ADP-L-glycero-D-manno-heptose-6-epimerase	ADP-L-glycero-D-mannoheptose-6-epimerase of <i>M. loti</i> MAFF303099 (43.4)	hypersensitive to hydrophobic antibiotic in <i>B. japonicum</i> 61A101C (heterologous complementation in <i>E. coli rfaD</i> )	Noh <i>et al.</i> , 2002
<i>rfaF</i> (blr 5929)	probable ADP-heptose-LPS heptosyltransferase	ADP-heptose-LPS heptosyltransferase II of <i>Bradyrhizobium</i> sp ORS278 (80.0)	hypersensitive to hydrophobic antibiotic in <i>B. japonicum</i> 61A101C (heterologous complementation in <i>S. thymurium rfaF</i> )	So <i>et al.</i> , 2000
<i>lpcC</i> (blI 5930)	lipopolysaccharide core biosynthesis mannosyltransferase	putative lipopolysaccharide core biosynthesis mannosyltransferase protein of <i>R. leguminosarum</i> bv <i>viciae</i> 3841 (50.7) and <i>S. meliloti</i> (40.9)	lack most core and all O-antigen in LPS of <i>R. leguminosarum</i> Altered core polysaccharide in LPS of <i>S. meliloti</i>	Kadmas <i>et al.</i> , 1998 Lagares <i>et al.</i> , 2001 Hozbor <i>et al.</i> , 2004
<i>galE</i> (blr 5931)	UDP-galactose 4-epimerase	UDP-glucose 4-epimerase protein of <i>S. meliloti</i> 1021 (58.1)	lack O-antigen in LPS of <i>B. japonicum</i> 61A101C	Chang <i>et al.</i> , 2008

**Genetic manipulations.** The construction of *B. japonicum* mutants is depicted in the following Figures S2 (*lspL-ugdH*) and S3 (*exoB*). In these figures, details are provided about how the diverse constructions were checked. All other experimental information is described in the Experimental Procedures section of the paper.

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