

Table 5. Percentage of probable orthologs between pairs of genomes of the order Rhizobiales

Genomes	Retl	Smel	Atuc	Atuw	Mlot	Bmel	Bsui	Babo	Bhen	Bqui	Bjap	Rpal
<i>R_etli</i>		58.40%	54.00%	53.80%	54.40%	34.70%	34.20%	33.30%	16.50%	15.40%	43.80%	34.90%
<i>S_meliloti</i>	56.80%		50.90%	50.50%	52.50%	34.40%	33.80%	32.90%	16.40%	15.30%	42.60%	34.50%
<i>A_tumefaciens_C58_Cereon</i>	61.50%	59.60%		92.80%	54.00%	39.60%	39.10%	37.90%	19.10%	17.80%	46.00%	38.90%
<i>A_tumefaciens_C58_UWash</i>	60.10%	58.10%	91.10%		52.70%	38.70%	38.30%	37.00%	18.70%	17.40%	44.90%	37.90%
<i>M_loti</i>	48.70%	48.30%	42.40%	42.20%		31.90%	31.10%	30.20%	14.80%	13.70%	42.50%	33.00%
<i>B_melitensis</i>	65.60%	66.70%	65.60%	65.50%	67.30%		88.40%	85.90%	32.10%	30.10%	58.90%	53.20%
<i>B_suis_1330</i>	61.00%	61.90%	61.20%	61.00%	61.90%	83.40%		86.40%	30.10%	28.20%	54.80%	49.80%
<i>B_abortus_9-941</i>	65.10%	66.20%	65.10%	64.80%	66.20%	89.00%	94.80%		32.80%	30.60%	58.30%	53.40%
<i>B_henselae_Houston-1</i>	67.90%	69.60%	69.10%	68.90%	68.10%	70.10%	69.70%	69.10%		74.40%	63.90%	62.40%
<i>B_quintana_Toulouse</i>	82.00%	83.50%	82.90%	82.70%	81.60%	84.50%	84.10%	82.90%	95.90%		77.40%	76.30%
<i>B_japonicum</i>	31.70%	31.80%	29.30%	29.20%	34.50%	22.60%	22.30%	21.60%	11.30%	10.60%		38.80%
<i>R_palustris_CGA009</i>	43.50%	44.20%	42.60%	42.30%	46.10%	35.20%	34.90%	34.10%	18.90%	17.90%	66.70%	

Percentages were calculated in relation to the total protein-coding genes for each species row-wise. The total number of genes per genome are as follows: *R_etli* (Retl), 6,034; *S_meliloti* (Smel), 6,205; *A_tumefaciens_C58_Cereon* (Atuc), 5,299; *A_tumefaciens_C58_UWash*, (Atuw), 5,402; *M_loti* (Mlot), 6,752; *B_melitensis* (Bmel), 3,197; *B_suis_1330* (Bsui), 3,338; *B_abortus_9-941* (Babo), 3,085; *B_henselae_Houston-1* (Bhen), 1,465; *B_quintana_Toulouse* (Bqui), 1,137; *B_japonicum* (Bjap), 8,317; *R_palustris_CGA009* (Rpal), 4,836. Probable orthologs were identified as bidirectional best hits (BDBHs) as described in *Methods*.