ERRATUM

Erratum to: The high diversity of *Lotus corniculatus* endosymbionts in soils of northwest Spain

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This paper was unfortunately published with error. The geographical origin of strain MAF 303099 was Japan, not New Zealand as was written in the text and in Figures 2, 3 and 4. The corrected paragraphs as well as the updated figures are shown below.

“The strain CSLC22N representing RAPD pattern type V clustered with the type strain of *M. erdmanii* USDA 3471^T (cluster III). This cluster also included strains isolated in Sweden (Ampomah and Huss-Danell 2011), Norway (Gossmann et al. 2012), Uruguay (Sotelo et al. 2011) and two strains nodulating *L. corniculatus*, R7A and MAFF 303099, isolated in **New Zealand and Japan, respectively**, and whose genome has been sequenced (Kelly et al. 2014; Kaneko et al. 2000). The strains isolated in Sweden are also misnamed as *M. loti* because the strain USDA 3471^T was considered to be the type strain of this species before its reclassification as *M. erdmanii* (Martínez-Hidalgo et al. 2015).”

“The strain N3 isolated in Uruguay (Sotelo et al. 2011) formed an independent lineage related to the cluster II, which

also includes several type strains of *Mesorhizobium* species nodulating legumes other than *Lotus*. The cluster III contains the strain CSLC22N isolated in this study and several strains isolated from *L. corniculatus* nodules in Sweden (Ampomah and Huss-Danell 2011), the strain N33 in Uruguay (Sotelo et al. 2011) and the strains MAFF303099 and R7A isolated **in Japan and New Zealand, respectively** (Kaneko et al. 2000; Kelly et al. 2014). Moreover, this cluster includes the type strain *M. erdmanii* USDA 3471^T isolated from *L. corniculatus* nodules.”

“The analysis of the *atpD* gene showed that our strains are divided into four clusters with some differences in their distribution with respect to that found after *recA* gene analysis (Figure 4). The strains from 16S rRNA gene cluster I, have different *atpD* gene sequences being particularly divergent in the *atpD* gene of the strain CSLC14N. This strain formed an independent lineage related to the type strain of *M. caraganae* CCB AU 11299^T with 92.5 % similarity. The remaining strains were phylogenetically related to the type strains of two species nodulating *L. corniculatus*, *M. jarvisii* ATCC 33669^T and *M. erdmanii* USDA 3471^T. The phylogenetic lineage formed by the strain CSLC14N belongs to a cluster that also included two strains, S1302 and S789 isolated from *L. corniculatus* nodules in Uruguay (Sotelo et al. 2011). The strains CSLC01N, CSLC36N and CSLC28N were equidistant between *M. jarvisii* ATCC 33669^T and *M. erdmanii* USDA 3471^T (similarity higher than 98.5 % in all cases) (Table 1). This makes difficult the identification of these strains as *M. jarvisii*, as suggested the *recA* gene analysis. The strain CSLC42N was also related to the type strain of *M. jarvisii* ATCC 33669^T with 98.3 % similarity, but in this case *M. erdmanii* USDA 3471^T was less closely related, with 96.7 % similarity (Table 1). This *atpD* gene cluster, also contains the strain CSLC22N from 16S rRNA gene cluster III, which present 97.8 % similarity with respect to its closest

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relative *M. jarvisii* ATCC 33669^T (Table 1). The *L. corniculatus* nodulating strains R7A and MAFF303099 isolated in **New Zealand and Japan, respectively** (Kaneke et al. 2000; Kelly et al. 2014) and the strain N105 isolated in

Uruguay (Sotelo et al. 2011) also belong to this cluster. However, the strains R88b and CJ3sym, isolated from *L. corniculatus* nodules in New Zealand, formed two different lineages that are phylogenetically divergent.”