**Table S1**

Composition of the compost used as carrier

|  |  |
| --- | --- |
| Parameter | Value |
| Ca (mg/kg) | 19.95 |
| Cd (mg/kg) | 0.48 |
| Cr (mg/kg) | 21.81 |
| Cu (mg/kg) | 0.23 |
| Fe (mg/kg) | 21.65 |
| Hg (mg/kg) | 0.11 |
| K (mg/kg) | 12.13 |
| Mg (mg/kg) | 18.34 |
| Mn (mg/kg) | 42.08 |
| N Kjeldahl (%) | 1.80 |
| Na (mg/kg) | 15.26 |
| Ni (mg/kg) | 10.32 |
| P (mg/kg) | 14.95 |
| Pb (mg/kg) | 6.08 |
| Zn (mg/kg) | 28.29 |
| Oxidizable organic carbon (%) | 21.49 |
| Organic Matter (%) | 48.01 |
| pH (soil:water) | 6.91 |
| C/N Ratio | 15.49 |
| Electrical Conductivity (ds/m) | 2.07 |

**Table S2**

Climatic and edaphic conditions corresponding to the field experiments during 2017 and 2018. The climatic data were recorded at the León - Virgen del Camino provincial meteo station.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Date | Temperatures (°C)\* | | | | | Monthly rainfall (mm) |
| 2017 | Hmax (ºC) | Havg (ºC) | Tavg (ºC) | Lavg (ºC) | Lmin (ºC) |
| May | 24.1 | 21.1 | 14.8 | 8.5 | -2.0 | 69.3 |
| June | 35.4 | 27.0 | 20.0 | 12.9 | 7.0 | 23.0 |
| July | 33.6 | 28.4 | 20.3 | 12.2 | 6.6 | 2.1 |
| August | 34.7 | 27.8 | 20.1 | 12.3 | 5.5 | 9.2 |
| September | 29.9 | 23.5 | 16.0 | 8.5 | 3.3 | 3.3 |
| October | 30.5 | 22.7 | 15.1 | 7.6 | 2.5 | 14.6 |
| 2018 |  |  |  |  |  |  |
| May | 24.1 | 19.0 | 12.7 | 6.5 | -1.5 | 72.7 |
| June | 32.9 | 23.6 | 17.5 | 11.4 | 6.3 | 111.3 |
| July | 29.8 | 25.8 | 19.2 | 12.5 | 9.5 | 57.9 |
| August | 35.3 | 29.3 | 20.7 | 12.1 | 6.6 | 2 |
| September | 31.2 | 27.1 | 19.6 | 12.0 | 5.8 | 14.1 |
| October | 27.1 | 18.1 | 11.8 | 5.5 | -0.4 | 27.1 |

|  |  |  |  |
| --- | --- | --- | --- |
| Year | | 2017 | 2018 |
| Location | | León EIAF | Oteruelo |
| Latitude | | 42°34'59.3"N | 42°34'56"N |
| Longitude | | 5°35'32.0"W | 5°36'40"W |
| Texture (%) | Sand | 24 | 22 |
| Silt | 42 | 34 |
| Clay | 34 | 44 |
| pH 1:2 | (soil:water) | 6.94 | 7.15 |
| Electric conducitiviy | (dS/m) | 0.16 | 0.14 |
| Organic matter (%) | | 3.56 | 2.34 |
| Total | nitrogen\*\* (%) | 0.22 | 0.14 |
| Ratio C/N | | 9.22 | 9.96 |
| Lime | (%) | negligible | negligible |
| P -Olsen | (mg kg-1) | 17.28 | 21.13 |
| K | (cmol(+) kg-1) | 0.23 | 0.30 |
| Ca | (cmol(+) kg-1) | 17.47 | 15.85 |
| Mg | (cmol(+) kg-1) | 2.46 | 3.18 |
| Na | (cmol(+) kg-1) | 0.09 | 0.17 |
| Nodulating rhizobia count (MPN\*\*\* | Rhizobia g soil-1 | 5.8 x 103 | 1 x 104 |

\* Hmax: maximum high temperature) (ºC); Havg: average high temperature (ºC); Tavg: average mean temperature (ºC); Lavg: average low temperature (ºC); Lmin: minimum low temperature (ºC); R: monthly precipitation (mm)

\*\*Total N: organic + nitric + ammonia nitrogen.

\*\*\* Most Probable Number

**Table S3**

Raw data from δ15NAIR (‰) values obtained for the common bean plants and the reference plants (*Sinapis arvensis* L., *Chenopodirum album* L. and *Oxalis corniculata* L., one third in weight from each).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Treatment | Block | Year 2017 | | Year 2018 | |
| d15Ncommon bean | d15Nreference plants | d15Ncommon bean | d15Nreference plants |
| Negative control | 1 | 3.4 | 9.7 | 5.1 | 8.1 |
| Negative control | 2 | 4.3 | 9.7 | 4.9 | 8.1 |
| Negative control | 3 | 3.8 | 9.7 | 4.7 | 8.1 |
| N fertilizedsed non-inoculated control | 1 | 4.1 | 9.7 | 4.8 | 8.1 |
| N fertilizedsed non-inoculated control | 2 | 3.8 | 9.7 | 5.0 | 8.1 |
| N fertilizedsed non-inoculated control | 3 | 4.0 | 9.7 | 5.8 | 8.1 |
| Rlp LCS0306 (Co) | 1 | 3.4 | 9.7 | 5.1 | 8.1 |
| Rlp LCS0306 (Co) | 2 | 3.1 | 9.7 | 4.1 | 8.1 |
| Rlp LCS0306 (Co) | 3 | 3.2 | 9.7 | 4.1 | 8.1 |
| Rlp LCS0306 (CC) | 1 | 2.9 | 9.7 | 4.6 | 8.1 |
| Rlp LCS0306 (CC) | 2 | 2.6 | 9.7 | 4.0 | 8.1 |
| Rlp LCS0306 (CC) | 3 | 2.7 | 9.7 | 4.5 | 8.1 |
| Rlp LCS0306 (PB) | 1 | 2.5 | 9.7 | 4.7 | 8.1 |
| Rlp LCS0306 (PB) | 2 | 3.0 | 9.7 | 3.9 | 8.1 |
| Rlp LCS0306 (PB) | 3 | 2.6 | 9.7 | 4.1 | 8.1 |
| Rlp LCS0306 (perlite) | 1 | 2.2 | 9.7 | 4.6 | 8.1 |
| Rlp LCS0306 (perlite) | 2 | 2.5 | 9.7 | 4.4 | 8.1 |
| Rlp LCS0306 (perlite) | 3 | 2.8 | 9.7 | 3.8 | 8.1 |
| Re CFN42T (perlite) | 1 | 3.3 | 9.7 | 5.1 | 8.1 |
| Re CFN42T (perlite) | 2 | 3.6 | 9.7 | 5.0 | 8.1 |
| Re CFN42T (perlite) | 3 | 3.5 | 9.7 | 4.2 | 8.1 |
| Rp ATCC 14482T (perlite) | 1 | 2.8 | 9.7 | 4.7 | 8.1 |
| Rp ATCC 14482T (perlite) | 2 | 3.2 | 9.7 | 4.5 | 8.1 |
| Rp ATCC 14482T (perlite) | 3 | 3.3 | 9.7 | 4.1 | 8.1 |

**Table S4**

Mean squares corresponding to the combined ANOVA of the dependent variables related to nodulation, nitrogen fixation, yield, yield components and harvest index, collected in the field trial trial. Two different ANOVA were carried out, the first analysing the effect of the **inoculation** with different rhizobia strains (*R. leguminosarum* bv. phaseoli LCS0306, *R. phaseoli* ATCC 14482T and *R. etli* CFN 42T) plus two uninoculated controls, one of them fertilised with mineral nitrogen. The second ANOVA analyses the effect of the **formulation** of the *R. leguminosarum* bv. phaseoli LCS0306 strain, using perlite as control (see text for more details). Significance levels: \*\*\* p≤0.001; \*\* 0.001<p≤0.01; \*0.01<p≤0.05; ns not significant.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Treatments  analysed | Source of variation | DF | Number of nodules per plant | Dry nodule biomass (g per plant) | Dry aerial biomass (kg/ha) | Aerial biomass N content (%) | Ndfa (%) | N fixed (kg/ha) | Soil N uptake (kg/ha) | Grain yield  (air dried)1 (kg/ha) | Pods per plant | Seeds per pod | 100-seeds weight  (dry) (g) | Harvest index |
| **Inoculation** treatment (rhizobia strain plus controls) | Analysis of the repetition (R) | 2 | 42.146 ns | 0.014 ns | 172902.437 ns | 0.092 ns | 5.896 ns | 58.557 ns | 95.106 ns | 69220.23 ns | 1.446 ns | 0.039 ns | 7.833 ns | 1.192 ns |
| Analysis of the treatment | | | | | | | | | | | | | |
| Treatment (T) | 4 | 63.211ns | 0.421\*\*\* | 3808183.48\*\*\* | 0.046 ns | 92.116\*\* | 1034.93\*\*\* | 615.937\*\*\* | 1560018 \*\*\* | 17.086 \*\*\* | 0.324 \*\*\* | 11.147 ns | 54.522 \* |
| T x Year | 5 | 8.021 ns | 0.007 ns | 100139.655 ns | 0.053 ns | 3.283 ns | 99.616 ns | 35.231 ns | 593239.9\*\*\* | 4.379\*\* | 0.355\*\* | 65.791\*\*\* | 123.941\*\*\* |
| T x R | 8 | 75.765 ns | 0.026 ns | 63948.271 ns | 0.064 ns | 7.348 ns | 55.184 ns | 45.77 ns | 4668.15 ns | 0.402 ns | 0.01 ns | 3.442 ns | 5.781 ns |
| **Formulation** for the LCS0306 strain (Formulation with Perlite was the control) | Analysis of the repetition (R) | 2 | 8.667 ns | 0.001 ns | 118374 ns | 0.053 ns | 15.167 ns | 32.596 ns | 90.791 ns | 87751.5 ns | 0.353 ns | 0.062 ns | 4.314 ns | 5.399 ns |
| Analysis of the treatment | | | | | | | | | | | | | |
| Treatment (T) | 3 | 55.667 ns | 0.031 ns | 429316.819 ns | 0.054 ns | 23.667 ns | 350.339 \* | 297.946 \* | 292425.042 \*\* | 1.373 \*\* | 0.061 ns | 4.095 \*\* | 12.332 ns |
| T x Year | 3 | 8.944 ns | 0.007 ns | 162426.264 ns | 0.035 ns | 2.5 ns | 44.112 ns | 8.092 ns | 13856.931 ns | 0.076 ns | 0.089 ns | 5.338 \*\* | 6.563 ns |
| T x R | 6 | 129.667 \* | 0.044 ns | 116453.444 ns | 0.024 ns | 3.167 ns | 42.927 ns | 23.648 ns | 33450.167 ns | 0.284 ns | 0.028 ns | 2.144 \* | 23.569 ns |

1 Corresponds to the commercial beans (11.57 % dry matter)

**Table S5**

Rlp LCS0306 genome statistics.

|  |  |
| --- | --- |
| Genome ID | Rlp LCS0306 |
| Total length (bp) | 7,395,396 |
| GC (%) | 60.72 |
| N50 | 340,266 |
| N75 | 161,667 |
| L50 | 7 |
| L75 | 14 |
| # N's | 0.00 |
| # N's per 100 kbp | 0.00 |
| # contigs (>= 0 bp) | 135 |
| # contigs (>= 1000 bp) | 58 |
| Total length (>= 0 bp) | 7,395,396 |
| Total length (>= 1000 bp) | 7,360,538 |
| # contigs | 71 |
| Largest contig | 929,560 |
| Genes (total) | 7,172 |
| CDSs (total) | 7,115 |
| Genes (coding) | 6,906 |
| Genes (RNA) | 57 |
| rRNAs | 2, 1, 4 (5S, 16S, 23S) |
| tRNAs | 46 |
| ncRNAs | 4 |
| Pseudo Genes (total) | 209 |

**Table S6**

LCS0306 search for Cluster of Orthologous Groups (COG). The values reflect the number of protein families, coverage and abundance in LCS0306 genome as a result of the comparison of LCS0306 functional annotation to protein sequences encoded in complete genomes from the COG protein database (WebMGA server).

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| #Class | No families | Coverage | Abundance | Description |
| J | 245 | 0.0082 | 0.1242 | Translation, ribosomal structure and biogenesis |
| A | 25 | 0 | 0 | RNA processing and modification |
| K | 231 | 0.0087 | 0.0567 | Transcription |
| L | 238 | 0.0126 | 0.2313 | Replication, recombination and repair |
| B | 19 | 0 | 0 | Chromatin structure and dynamics |
| D | 72 | 0 | 0 | Cell cycle control, cell division, chromosome partitioning |
| Y | 2 | 0 | 0 | Nuclear structure |
| V | 46 | 0 | 0 | Defense mechanisms |
| T | 152 | 0 | 0 | Signal transduction mechanisms |
| M | 188 | 0 | 0 | Cell wall/membrane/envelope biogenesis |
| N | 96 | 0 | 0 | Cell motility |
| Z | 12 | 0 | 0 | Cytoskeleton |
| W | 1 | 0 | 0 | Extracellular structures |
| U | 158 | 0 | 0 | Intracellular trafficking, secretion, and vesicular transport |
| O | 203 | 0.0049 | 0.0298 | Posttranslational modification, protein turnover, chaperones |
| C | 258 | 0.0155 | 0.2372 | Energy production and conversion |
| G | 230 | 0.0087 | 0.0966 | Carbohydrate transport and metabolism |
| E | 270 | 0.0074 | 0.0420 | Amino acid transport and metabolism |
| F | 95 | 0.0105 | 0.0341 | Nucleotide transport and metabolism |
| H | 179 | 0 | 0 | Coenzyme transport and metabolism |
| I | 94 | 0 | 0 | Lipid transport and metabolism |
| P | 212 | 0.0047 | 0.0210 | Inorganic ion transport and metabolism |
| Q | 88 | 0 | 0 | Secondary metabolites biosynthesis, transport and catabolism |
| R | 702 | 0.0028 | 0.1419 | General function prediction only |
| S | 1347 | 0.0007 | 0.0210 | Function unknown |
|  |  |  |  |  |
| TOTAL | 5163 | 0.0848 | 1.0358 |  |

**Table S7**

Use of carbon and nitrogen sources by reference *Rhizobium* strains and the autochthnous strain *R. leguminsarum* bv. phaseoli LCS0306. Characterisation and selection of rhizobia nodulanting common bean (*Phaseolus vulgaris* L.) in the P.G.I. “*Alubia de la Bañeza-León*”. Unpublished data from Mulas, D. 2010. PhD. Dissertation. University of León. Spain. 191 pp.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Carbon sources** | *R. phaseoli* ATCC 14482T | *R. leguminosarum* USDA 2370T | *R etli* CFN42T | *R. leguminsarum* bv. phaseoli LCS0306 |
| D-rafinosa | + | + | + | + |
| Galactose | + | + | + | + |
| Maltose | + | + | + | + |
| D-celobiose | + | + | + | + |
| Melibiose | + | + | + | + |
| D-sucrose | + | + | + | + |
| D-salicine | - | - | - | + |
| D-trehalose | + | + | + | + |
| L-ramnose | + | + | + | + |
| L-sorbose | + | + | + | + |
| D-manose | + | + | + | + |
| Fructose | + | + | + | + |
| Xilose | + | + | + | + |
| Melecitose | - | + | + | + |
| Xilitol | + | + | + | + |
| D-sorbitol | + | + | + | + |
| Meso-eritritol | + | + | - | + |
| Inositol | + | + | + | + |
| Manitol | - | + | + | + |
| Na Piruvate | + | + | + | + |
| Na Glucuronate | - | - | - | - |
| Na Propionate | + | - | - | + |
| Na Gluconate | - | - | - | - |
| Na Citrate | - | + | + | + |
|  |  |  |  |  |
| **Nitrogen sources** |  |  |  |  |
| L-serina | - | - | + | + |
| DL-valina | - | - | + | + |
| L-alanina | - | + | + | + |
| L-prolina | + | + | + | + |
| Betaína | + | + | + | + |
| L-arginina | - | - | - | - |
| L-lisina | - | - | - | - |
| L-histidina | + | - | + | + |
| Sarcosina | + | + | + | + |
| Aspartato Mg | + | + | + | + |
| Glutamato Na | + | - | + | + |

**Table S8**

Distribution of genes linked to competitiveness in Rlp LCS0306 genome compared to reference *Rhizobium* strains. Homologue genes are indicated in the corresponding column.

| Gene function | Gene name | Locus\_tag | Contig | *R. leguminosarum* UMP791 | *R. phaseoli* ATCC14482T | *R.etli*  CFN42T |
| --- | --- | --- | --- | --- | --- | --- |
| ABC transporters | *aapJQMP*  *teuBAC1C2*  *nocR,*  *nocQCT* | FML87\_20425-  FML87\_20440  FML87\_29775 -  FML87\_29760  FML87\_29495  FML87\_29500-  FML87\_29510 | Node 9  Node 19\*  Node 19\* | RLV\_4523- RLV\_4520 |  | RHE\_PD00128-RHE\_PD00131  RHE\_PD00181  RHE\_PD00180-  RHE\_PD00178 |
| Motility | *motA*  *motB*  *flg* and *fli* genes | FML87\_25710  FML87\_25610  FML87\_25750-  FML87\_25545 | Node 13  Node 13 | RLV\_3097  RLV\_3117  RLV\_3089- RLV\_3131 |  |  |
| Chemotaxis | *cheAWRBYD* (Che1 cluster) | FML87\_25785-  FML87\_25760 | Node 13 | RLV\_3082- RLV\_3087 |  |  |
| EPS biosynthesis and transport | *pssSRMLKJIFCDE*  *pssTONP*  *prsED* | FML87\_17650-  FML87\_17705  FML87\_17755-  FML87\_17740  FML87\_17715-  FML87\_17720 | Node 7  Node 7  Node 7 | RLV\_5915-  RLV\_5925  RLV\_5932- RLV\_5935  RLV\_5927  RLV\_5928 |  |  |
| Peptidoglycan biosynthesis | *ftsI murEF mraY murD ftsW murGBC,* | FML87\_12315-  FML87\_12275 | Node 4 | RLV\_5562- RLV\_5560 | EFD56\_29325- EFD56\_29285 |  |
| RSI bacterial invasion switch | *pckA chvIG*  *hprK manX npr* | FML87\_28000-  FML87\_27975 | Node 16 | RLV\_7039- RLV\_7044 |  |  |
| PHB | *phbC1* | FML87\_20625 | Node 9 | RLV\_4485 |  |  |
| Type III secretion system (T3SS) | *rhcJ, rhcLNQRSTU, hrpW, rhcVD, rhC1O* | FML87\_34175-  FML87\_34265 | Node 33 |  |  | RHE\_PD00051-  RHE\_PD00067 |
| Type IV secretion system - pilus (T4SS) | *virB1-virB11* | FML87\_29685 –  FML87\_29510 | Node 19 | RLV\_0329-  RLV\_0340 |  |  |
| Type IV secretion system – *tra* conjugal system (T4SS) | *traCDG*  *traA-traFBHMR* | FML87\_29555 - FML87\_29565  FML87\_29550 - FML87\_29525 | Node19\* |  |  | RHE\_PD00167- RHE\_PD00175 |
| Type VI secretion system (T6SS) | *tssABC Hcp tssEFGI*  *tssKLM* | FML87\_29395 - FML87\_29430  FML87\_29375 - FML87\_29360 | Node 19 |  | EFD56\_30825- EFD56\_30795 |  |
| Quorum sensing (bacteriocin production) | *cinRIS* | FML87\_12665-  FML87\_12675 | Node 4 | RLV\_5631-  RLV\_5632 |  |  |

\*Note that Node\_19 aligns with the symbiotic plasmid of *R.etli* CFN42 T (p42d)

**Table S9**

Distribution of genes contributing to symbiosis in Rlp LCS0306 genome compared to reference *Rhizobium* strains. Homologue genes are indicated in the corresponding column.

| Gene function | Gene name | Locus\_tag | Contig | *R. leguminosarum* UMP791 | *R. phaseoli*  ATCC14482T | *R.etli*  CFN42T |
| --- | --- | --- | --- | --- | --- | --- |
| Nitrogenase | *rpoN-nifUSW*  *nifAB fdxN nifZT*  *nifDKEX fdxB* | FML87\_33610 –  FML87\_33625  FML87\_33650 -  FML87\_33670  FML87\_34560 –  FML87\_34585 | Node 30  Node 30  Node 36 |  | EFD56\_29645- EFD56\_29620  EFD56\_29595-EFD56\_29575 | RHE\_PD00218- RHE\_PD00222  RHE\_PD00228- RHE\_PD00231  RHE\_PD00307-RHE\_PD00302 |
| Nitrogen fixation | *fixNOQPGHIS* (FIX1 region)  *fixABCX* (FIX2 region) | FML87\_34615-  FML87\_34655  FML87\_33630 –  FML87\_33645 | Node 36  Node 30 | RLV\_1827-RLV\_1834 |  | RHE\_PD00296- RHE\_PD00289  RHE\_PD00224- RHE\_PD00227 |
| Nodulation | *nodA*  *nodBCSUIJ*  *nodD1*  *nodD2*  *nodD3* | FML87\_35315  FML87\_34775-  FML87\_34745  FML87\_34730  FML87\_34950  FML87\_34945 | Node 47  Node 37  Node 37  Node 39  Node 39 |  |  | RHE\_PD00310  RHE\_PD00282- RHE\_PD00277  RHE\_PD00275  RHE\_PD00316  RHE\_PD00318 |
| Regulation | *fnrN1*  *fnrN2*  *rosR* | FML87\_28695  FML87\_33600  FML87\_24335 | Node 17  Node 30  Node 12 | RLV\_5077  RLV\_1980  RLV\_3788 |  | RHE\_CH02479  RHE\_PD00216  RHE\_CH01249 |