**Draft genome of *Cicer reticulatum* L., the wild progenitor of chickpea provides insights into the domestication process**

**SUPPORTING INFORMATION**

**Supporting Text.**

**Text S1.** CDS and Protein sequences of 4 RGH obtained by mapping the identified RGF in the advanced draft genome of chickpea ICC4958, onto the *C. reticulatum* genome.

**Text S2.** Sequence alignment of domestication-associated candidate gene orthologues in cultivated and wild chickpea. Pepetide and CDS sequences were aligned using ClustalW. Functional annotations are mentioned at the top of the box. Cr represents *C. reticulatum*, Ca represents C. arietinum ICC4958 (*desi*). GenBank accession numbers (XP) are used to denote genes/peptides of chickpea CDC Frontier (*kabuli*).

**Supporting Tables S1-S20**

**Table S1.** Sequencing data generated for *Cicer reticulatum* PI489777

**Table S2.** ALLPATH-LG assembly output

**Table S3.** Anchoring of scaffolds to linkage groups

**Table S4.** Statistics of *C. reticulatum* assembly

**Table S5.** Statistics of *C. reticulatum* reads mapped back on assembly

**Table S6.** Statistics of reference-based *C. reticulatum* assembly

**Table S7:** Polymorphic simple sequence repeats (SSR) between the wild and two domesticated chickpea draft assemblies and their flanking sequences (submitted as an excel file)

**Table S8.** Statistics of protein-coding gene annotation in *C. reticulatum* assembly

**Table S9.** Functional annotation of *C. reticulatum* protein-coding genes

**Table S10.** Sequence similarity of *C. reticulatum* genes to those of *C. arietinum* ICC4958 (Desi) and CDC Frontier (Kabuli)

**Table S11.**  *C. reticulatum* statistics of euchromatic and pericentromeric region determination.

**Table S12.** Colinear genes (A) and blocks (B) between *C. reticulatum* and *Medicago truncatula* pseudomolecules.

**Table S13.** Sequence diversity between *C. reticulatum* and *C. arietinum* ICC4958

and CDC Frontier.

**Table S14.** List of genes (Ka/Ks>1) common to desi and kabuli chickpeas positively selected during domestication (submitted as an excel file).

**Table S15.** List of genes showing positive selection in one cultivated but showing purifying selection in another cultivated chickpea with respect to *C. reticulatum* (submitted as an excel file).

**Table S16.** List of resistance gene homologues predicted in *C. reticulatum* genome assemblies (submitted as an excel file).

**Table S17.** Colinear RGHs between *M. truncatula* and *C. reticulatum* genome assemblies (submitted as an excel file).

**Table S18.** Mapping of wild and cultivated *Cicer* species on *C. reticulatum* genome assembly. Numbers of accessions used are mentioned in bracket.

**Table S19.** Flanking sequences of identified SNPs for cultivated mapped on reticulatum for generating markers for large-scale genotyping (submitted as an excel file).

**Table S20.** Statistics of SNPs obtained by mapping sequence reads of wild and cultivated Cicer species on *C. reticulatum* genome assembly.

**Supporting Figures S1-S9**

**Figure S1.** Fragment distribution of *C. reticulatum*genome assembly.Number of fragments covering different percentile of the assembly plotted against different length percentile.

**Figure S2.** Venn diagram showing clustering of gene families (A) and genes (B) shared among Chickpea cultivars ICC4958 (Desi) and CDC Frontier (Kabuli) and wild chickpea *C. reticulatum*.

**Figure S3**. Multidimentional topography of linkage groups of *Cicer reticulatum.* Delineation of pericentromeric regions of LG1-8 was marked based on comparison of physical distance (X-axis) with gene density (left Y-axis, black dotted line), repeat density (right Y-axis, grey dotted line) and average genetic distance (Y-axis, black line). Vertical bars indicate position of transition from euchromatic region to pericentromeric region.

**Figure S4**. Comparison of *C. reticulatum and* *C. arietinum* ICC4958 chickpea genome assemblies. A dot-plot matrix comparing the chickpea (ICC 4958) and the *C. reticulatum* draft assemblies of eight pseudomolecules corresponding to each linkage groups. Pairwise comparison of all the pseudomolecules two draft genome assemblies were performed using synteny blocks and anchor filtering algorithms of tool SyMap v4.0.

**Figure S5.** Pairwise collinearity analysis of orthologous genes present in the linkage groups of *desi* (Ca1-8) and *C. reticulatum* (Cr1-8) draft assemblies. Analysis was performed using default parameters of tool MCScanX.

**Figure S6.** Pairwise collinearity analysis of resistance gene homologues present in the linkage groups of *M. truncatula* (Mt1-8) and *C. reticulatum* (Cr1-8) assemblies. Analysis was performed using default parameters of tool MCScanX and viewed using Circose.

**Figure S7a.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG1. Sequence reads were mapped on LG1 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7b.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG2. Sequence reads were mapped on LG2 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7c.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG3. Sequence reads were mapped on LG3 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7d.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG5. Sequence reads were mapped on LG5 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7e.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG6. Sequence reads were mapped on LG6 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7f.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG7. Sequence reads were mapped on LG7 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S7g.** Traces of gene pool transfer, as analysed by common SNP pattern, from wild Cicer species to domesticated chickpea LG8. Sequence reads were mapped on LG8 of *C. reticulatum*. Gene density was drawn on the top and the *Cicer* species analyzed were described at the left. Physical distance scale of the LG in Mb was mentioned at the bottom.

**Figure S8.** Amplification of the polymorphic sequence present at the 5’UAS of the VRN1 orthologues in different accessions of the domesticated (*desi* and *kabuli* types) and wild (*C. reticulatum*) chickpeas. Accessions numbers are mentioned above.

**Figure S9.** Amplification of the polymorphic sequence present at the 5’UAS of the VRN2 orthologues in different accessions of the domesticated (*desi* and *kabuli* types) and wild (*C. reticulatum*) chickpeas. Accession numbers are mentioned above.