

To phenotype chickpea wild accessions and cultivars for drought tolerance, as a first year research of a Global Crop Diversity Trust project, two experiments were conducted in series at both Dicle University in Turkey and at ICRISAT in India.

Transpiration rate and fraction of transpirable soil water (FTSW) measurements were analyzed at Dicle University from February 2016 until late May 2016. Full assessment of FTSW was not yet complete when this was poster prepared. 26 wild chickpea accessions multiplied at Harran University and 4 commercial cultivars were evaluated in accordance with project aims. Leaf transpiration rates under naturally changing vapor pressure deficits (VPD) were determined by weighing pots at one hour intervals, from morning (09:00 am) to late afternoon (04:00 pm) under greenhouse conditions. Temperature and relative humidity were recorded using a data logger to determine atmospheric VPD. Among genotypes "Gökçe (check)", "Derei-072" and "CudiB-022C" had the lowest transpiration rates suggesting their higher relative drought tolerance. By contrast, "Deste-080" and "Sirnak-060" had the highest recorded transpiration rates.

Similar experiments were conducted with 10 genotypes by Fatma Basdemir during a brief internship in the laboratory of Vincent Vadez at ICRISAT. Transpiration rates gradually increased under rising VPD conditions in all tested genotypes. Relatively tolerant genotypes possessed the lowest transpiration rates at low VPD and continued this trend throughout increasing VPD.

Key words: Transpiration rate, wild chickpea, drought tolerance

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### **Status of genomic assisted resistance breeding for the development of *Fusarium wilt (Fusarium oxysporum fsp.ciceris)* resistant Chickpea (*Cicer arietinum L.*) genotypes in Ethiopia**

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#### **Abstract**

Although the yield potential of present day chickpea cultivars exceeds 5.0t/ha, in Ethiopia the average national yield is below 2t/ha. The wide gap between average yield and potential yield is mainly due to different biotic and abiotic stresses at various crop growth and development stages, leading to low productivity. Recent advances in next generation sequencing and genotyping technologies have enabled generation of significant genomic resources that can support the development of biotic and abiotic stresses tolerant genotypes in chickpea. Fusarium wilt caused by soil borne fungus, *Fusarium oxysporum f.sp. ciceris* (FOC), is the most devastating disease of chickpea in Ethiopia which needs very efficient and robust genomic tools to generate resistant chickpea genotypes. However, only little works have been done on chickpea Fusarium wilt, and limited information is available to generate resistant genotypes in Ethiopia. Tackling such challenge has got the top priority in Ethiopian chickpea improvement program. From 217 farmers fields, samples of diseased plants, seeds and soils were collected and isolated. A total of 209 *Fusarium oxysporum* isolates were identified based on their morphological characteristics such as abundance of micro and macro conidia, short and unbranched monophialides, white to creamy white colony color on PDA medium. These isolates will be genotyped using a genotyping by sequencing method (RAD-GBS), and the SNP data will be used to calculate standard population genetic and diversity metrics to describe the diversity of FOC in Ethiopia. Besides, based on the pathogenicity test and efficient phenotyping of reverse introgressed lines (reVILs) and advanced backcross introgression lines (ABIs) segregating populations, FOC resistance genes in chickpea will be mapped. Subsequently, marker assisted backcrossing will be used for the introgression of Fusarium Wilt resistant gene into adapted Ethiopian chickpea cultivars.

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### **Effect of inoculation of chickpea and lentil with stress tolerant rhizobia of Morocco.**

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#### **Abstract**

Chickpea and lentil are important pulse crops grown mainly in arid and semi-arid regions where numerous environmental factors including drought, salinity, extreme temperatures and soil pH may dramatically affect nodulation, nitrogen fixation and biomass production. Thus the yield remains very low despite an increasing demand for food. To enhance the productivity and limit the use of chemical fertilizers, it is necessary to support the use of biofertilizers based on

stress-tolerant microorganisms for an economic and ecologically-sustainable agriculture.

The aim of this study is to characterize populations of rhizobia nodulating lentil and chickpea in order to select the most tolerant and effective ones for use as inocula by farmers. To achieve this objective 207 and 206 isolates were purified from chickpea and lentil nodules respectively. Isolates were characterized using rep-PCR which showed the presence of 23 groups among lentil rhizobia and 40 groups for chickpea rhizobia. Examination for their tolerance to environmental stresses (pH, salinity, water stress, and extreme temperatures) revealed large phenotypic variability for these conditions. Two highly efficient and tolerant strains were selected for each crop for a field inoculation test. The experiment was carried out at two sites in Morocco, Merchouch (clay-silty) and Ain Sbit (clay-sandy) in a Randomized Complete Block Design (RCBD) design, with four treatments: Control (no inoculation and no N application), S1 (inoculation with strain 1) and S2 (inoculation with strain 2) and N fertilization (N 120kg/ha), each with four replications.

Results showed that inoculation with the selected strains significantly increased nodules number for chickpea and lentil especially in Merchouch trial. Effect of inoculation on shoot dry weight and nitrogen content at both sites was statistically similar to the effect of nitrogen application. Grain and straw yield were significantly enhanced compared to the control indicating that the used strains were more competitive and effective than native ones except for chickpea in Ain Sbit where the yield was enhanced but not significantly.

Used strains were efficient in both sites with different degree of significance. This suggests that nodulation, nitrogen fixation and grain yield of chickpea and lentil can be improved by inoculation using competitive stress tolerant rhizobia as an inexpensive way to increase the productivity of these crops in arid and semi-arid areas for sustainable agriculture.

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### **Sequencing chickpea genomes: genotyping and high-quality reference genomes for association studies and breeding.**

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Abstract:

Natural populations of species closely related to cultivated chickpea (*Cicer arietinum*) were identified and collected systematically using ecological principles from their native range in southeastern Turkey. Collection was focused primarily on *C. reticulatum* (wild progenitor of the cultigen) and *C. echinospermum*, a sister species, and with limited co-incident collection of the more distantly related species *C. bijugum* and *C. pinnatifidum*.

Over 1,000 wild individuals sampled in 2013 were genotyped using Restriction-enzyme Associated DNA Genotyping By Sequencing (RAD-GBS). Based on this sequencing, allele-frequency based population assignment was conducted for all genotypes leading to the choice of the focal genotypes as donor parents for introgression population development.

Both the currently available reference genomes for cultivated chickpea are draft assemblies containing several ambiguous regions, and whole genome assemblies of wild relatives are currently unavailable. To address these limitations, focal genotypes for high-resolution reference genomes for each of the three species were selected based on: i) their use in introgression population development; ii) genetic relationships to genotypes from other sites of the same species; and iii) likelihood of long-term stability of the collection site for potential future in-situ studies. Genotypes CDCFrontier (*C. ari*), Besev\_079 (*C. ret*) and S2Drd\_065 (*C. ech*) represent the three species. For each genotype, sequence data from ~60x short-read Illumina and ~30x long-read PacBio are being integrated with BioNano optical mapping data. Assemblies will be assessed via high-density linkage mapping (RAD-GBS) of early generation progenies derived from wild x wild and wild x cultivated crosses.

In addition, 26 wild accessions that represent ecological and molecular variation within the species and serving as potential introgression donors and recipient cultivars were sequenced to ~30x coverage via Illumina short read sequencing, data that allow for analysis of genome-wide signatures of selection and for trait-gene associations. To identify rare alleles among populations and to calculate linkage disequilibrium, and association studies with native site ecological parameters, ~200 genotypes from the same populations were sequenced to medium depth (~10x) via Illumina short-read sequencing.

Together these genome data represent a novel resource for chickpea biology, to improve the accuracy and precision of association mapping, trait-marker discovery and introgression breeding.

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### **Towards the characterization of adaptive genetic differentiation in wild chickpea**

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