

Integrative genome-wide association studies (GWAS) to understand complex genetic architecture of quantitative traits in chickpea

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Development of high-yielding stress-tolerant chickpea cultivars is essential to enhance its yield potential and productivity amidst climate change scenario. Unfortunately, superior lines/recombinants producing higher pod and seed yield under stress are not available in world chickpea collection. Therefore, genetic dissection of complex stress tolerance and yield-contributing quantitative traits is the prime objective in current chickpea genomics and breeding research. Our study employed diverse GWAS-assisted integrated genomic strategies involving classical genetic inheritance analysis, QTL mapping, differential transcript profiling, molecular haplotyping and haplotype-based gene domestication/evolution study for rapid quantitative dissection of complex yield and stress tolerance traits in chickpea. To accomplish this, multi-location/years replicated yield traits-related field phenotyping and high-throughput marker genotyping information generated from numerous natural germplasm accessions (association panel) and multiple intra- and inter-specific mapping populations of chickpea were deployed in the aforesaid

combinatorial genomic approaches. These analyses delineated 12 novel alleles and six haplotypes from 10 transcription factor genes and 16 major QTLs/eQTLs governing yield and stress tolerance traits that were mapped on 10 ultra-high density chickpea genetic linkage maps. The superior natural alleles/haplotypes of two major genes (QTLs) regulating seed weight and pod/seed number identified from cultivated and wild *Cicer* gene pools are being introduced into multiple high-yielding Indian varieties of chickpea for its marker-assisted genetic improvement. The potential molecular signatures delineated using integrated genomics-assisted breeding strategies have functional significance to understand the molecular genetic mechanism and natural allelic diversity-led domestication pattern underlying these complex quantitative traits at a genome-wide scale, leading to fast-paced translational genomics for chickpea genetic enhancement. These essential outcomes will be useful for devising the most efficient strategies to produce high-yielding climate-resilient chickpea cultivars for sustaining global food security.

Understanding the genetics of biomass formation in barley assessed by non-invasive phenotyping

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Barley is the fourth most important cereal crop worldwide and Germany is the third largest barley-producing country. Despite the outstanding environmental adaptability of barley, which outcompetes any other cereal crop, future yield improvement is hampered by biotic and abiotic stresses. In Germany, barley yields showed a strong fluctuation during the last 15 years, reflecting the impact of climate change. One factor is the increased frequency of drought events, especially in spring during the vegetative growth phase. Understanding the genetics of biomass formation under well-watered and seasonal drought conditions can provide a basis for stabilizing and increasing grain yield. In our studies, a pot based imaging system was used to evaluate daily biomass assessed in a diverse reference collection of barley developed from the IPK genebank. The experimental setup comprised a drought period of 18 days with watering regime corresponding to 20% field capacity (well-watered: 90%)

and a 14-day long recovery period. Drought treatment started in the tillering phase and experiments ended around tipping time. We obtained high heritability for biomass under both conditions over the whole observation period, which made this trait amenable for genome-wide association scans (GWAS). GWAS were performed for each day independently within the well-watered and within the drought stress treatments. Different genetic loci were identified for early and later vegetative biomass. Similarly, specific loci were identified for biomass under well-watered and stress conditions. Results point at candidate genes involved in plant growth hormone regulation and phenology. Although plants were quickly recovering upon the end of drought, the results demonstrate a strong effect of drought on grain yield. In addition, we observed a positive correlation of vegetative biomass to grain yield, which might blaze a trail to further increase yield potential.