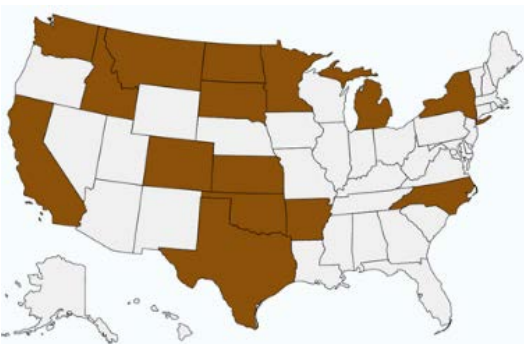


## Improving wheat yield: Combining known genes and traits

Identifying genes associated with wheat yield components is an essential first step to understand their mode of action, how they interact with each other and the environment, and combining them efficiently to accelerate the rates of genetic gain. Previous research in the USDA NIFA Collaborative Agricultural Project (CAP) identified several wheat chromosomal regions having a beneficial effect on yield. However, the underlying genes responsible remained unknown. Now, a large USDA NIFA supported Wheat Coordinated Agricultural Project (WheatCAP) and IWYP Research Project led by Jorge Dubcovsky at the University of California, with 35 participants from 19 institutions in 15 US states and CIMMYT in Mexico, “**Validation, Characterization and Deployment of QTL For Grain Yield Components In Wheat**”, uses cutting edge genomic tools to rapidly identify, validate and deploy genes, currently from



- 6 QTL for Grain Yield
- 5 QTL for Spikelet Number per Spike
- 8 QTL for Kernel Size/Weight
- 2 QTL for Reproductive Tiller Number

21 genomic regions, into elite germplasm. These mainly “sink-based” genes are currently being combined in wheat lines with genes for “source-based” traits such as high biomass to explore boosting grain yield. The first yield trials at CIMMYT from 2020 combining positive alleles for grain size, grain number in high biomass lines have showed significant positive effects on grain yield. Identifying and characterizing gene networks controlling source and sink traits, in combination with modern breeding approaches, should accelerate the development of more productive varieties in farmers’ fields.

## What Solutions have been Identified?

- Several new genes for the sink traits were identified affecting grain size (e.g. *GW2*, *GW7* and *GS3*) and grain number (*WAPO1*, *CKX2*, *FUL2*, *ELF3*, *FT2* and *LFY*).
- The most promising sink genes are being combined into elite wheat varieties and a set of high biomass (source) wheat lines for subsequent yield testing.

## What has been Transferred to the Wheat Improvement Pipelines?

- The *GW-A2* mutation for larger grains and the *TmElf3* allele for increased grain number were introduced into the elite variety Kingbird and three IWYP high-biomass lines. Large trials in 2020 at CIMMYT revealed significant (2.4%) increases in yield across all the wheat lines containing *TmElf3*. The *gw-A2* mutation was not associated with an increase in grain yield in all lines but did induce increases in grain size and protein. In similar trials using durum wheat, the *gw-A2* mutation also induced increases in grain protein but also increased levels of iron and zinc in the grain.

