Maize, one of the most important crop, was domesticated approximately 10,000 yers ago in the Balsas River basin of southwestern Mexico. Despite its tropical origins, nowadays it is cultivated almost all around the world, including temperate climate regions of North America and Europe. Although maize was subject to “bottleneck” effect during domestication, which lead to decrease in genetic diversity, it retained large portion of it from its wild ancestor – *teosinte*. Genetic and phenotypic diversity allowed maize adaptation to regions beyond occurrence its wild ancestor.

Maize adaptation to higher latitude required adjustment to environmental conditions much different then those in central Mexico. One of the most important factor limiting maize growth in temperate conditions is cold stress. Initial adaptation relied on selection genotypes with short vegetation life cycle which allowed late sowing and avoiding seedling contact with low temperature appearing in early spring. Subjecting maize seedling temperature below 13°C might have very negative consequence, since many inbred lines cannot developed fully functional photosynthetic apparatus and died after fully exhausted the seed reserves. Nerveless, many modern inbred lines show undisturbed growth in cold stress condition. Genetic mechanism underlying this adaptation remains unknown.

The goal of this proposal will be identification gnomic region and gene underlying this region responsible for modern maize inbred lines adaptation to cold spring conditions. To achieve this goal, in first step of the study phenotypic diversity at morph-physiological level in response to cold in diverse panel of 200 inbred lines will characterize. This panel contains three groups of lines: tropical, old inbred material, released before 2000 year and modern inbred lines released after 2000 year. Such selection of material to study allowed tracking effect of selection on maize adaptation to cold. In parallel to phenotypic study material for RNA-seqencing will be collected from entire panel to identified differently expressed genes across different groups and growth conditions.

Next, association study will be conducted between morph-physiological traits, gene expression level in each growth conditions as well as polymophysim in genomes of study lines. In parallel, population genetic analysis will be performed to detect regions of genome subjected to strong selection. In last step, overlaps between region selected in each above analysis will be identified. Genes underlying this region will be subject to further study with classical molecular biology methods in order to better understand mechanism underlying maize adaptation to cold spring condition.

Recent study indicated that ancient people from Southwestern North America needed about 2000 years to adapt maize to temperate climate of highlands of this region. With current human population growth and predicted climate change, faster and sustainable production of highly adapted varieties is required. This can be achieve with precision breeding with genome-edited crops, but this approach require precise knowledge about targeted gene. Therefore, this project not only greatly expand current knowledge about process of maize adaptation to northern hemisphere but also provide valuable candidate genes, which can be potentially used to produce new, highly adapted inbred to cold spring condition using genome-editing.