

Wheat amylase/trypsin bi-functional inhibitors (ATIs) are protein stimulators of innate immune response, with a recently established role in promoting both gastrointestinal and extra-gastrointestinal inflammatory syndromes. These proteins have been reported to trigger downstream intestinal inflammation upon activation of TLR4, a member of the Toll-like family of proteins that activates signalling pathways and induces the expression of immune and pro-inflammatory genes. These findings have broad implications not only for celiac disease but also for other intestinal inflammatory disorders of the gastrointestinal tract. The project aims to investigate ATI in a panel of wheat accessions. In particular, an evolutionary approach will be adopted to study differences at gene sequences coding for ATI and to investigate the different level of such proteins in a panel of genotypes that were sampled on the basis of an evolutionary transect that spans the entire diversity of tetraploid wheat.

We aim to compare the different level of ATI present in seeds of different genotypes, taking carefully into account and to account environmental effect, GXE (genotype x environment interactions). Seeds will be used to produce flours from which to extract and quantify ATI proteins. This will allow the identification of accessions with high and low level of such proteins, which will be used for in vitro and in vitro stimulations experiments.

We will apply population genetics approaches to analyze the genetic diversity of these proteins in the different evolutionary groups and to look at changes at genomic level due to domestication.