CONCLUSION

Computational approach was explored to identify three dimensional structure analysis of TaAGPase. EST based SNPs were mined and validated in diverse set of wheat genotypes available at Indian Institute of Wheat and Barley Research, (IIWBR) Karnal. The following points were concluded.

1. AGPase encode conserved signature motif (GGGtGTqLfpLTstrAtPAV), the percentage of serine residue was higher than tyrosine in particular amongst other residues. In the small subunit of AGPase, large number of un-ordered regions was more as compare to large subunit of AGPase.

2. Phylogenetic analysis revealed separate clusters of LS and SS of AGPase of various plants. It was also noticed that large subunit of barley and wheat clustered in group II and small subunit of barley and rice in cluster I.

3. First time documented molecular dynamic studies in wheat AGPase to resolve the heterotetrameric structure of AGPase. In this study critical amino acid i.e. CYS 335, ASP 333 of LS and VAL 350, ASP 352 of SS were identified to be crucial as they were having bond length less than 2.5 Å. These residues interact with each other during the native heterotetrameric structure formation.

4. Two SNPs named SNP 829 and SNP 937 were developed by mining ESTs sequences of AGPase. These newly identified SNP distinguishes high and low yield genotype. Single marker analysis explained 57.55% and 19.41% phenotypic variation for grain yield. This is the first report of AGPase derived SNP marker associated with grain yield in wheat which can be used by the breeders for improving starch quality in wheat.
5. First time knowledge base database of AGPase was developed comprising of sequence and structure related information. This database will assist plant breeder and researcher to select the most appropriate genotype for their wheat breeding program. A web-based workbench has been developed to provide quick access to information related to wheat varieties. The users will be able to analyze, compare and retrieve desired information from remote places through a simple interface on web.

**Future prospectives**

Findings of present study generated information to enhance the knowledge about structure and function of different subunits of AGPase genes in wheat.

> Recently wheat genome sequence has been decoded, hence it will provide opportunities to develop more number of next generation marker like SNPs. The predicted SNPs can be validated on the large set of diverse wheat genotype.

> Critical amino acids derived from interaction study responsible for functionality of the enzyme needs to be validated using experimental method.