Internal transcribed spacer region was used to discriminate eighteen *Saccharomyces cerevisiae* strains isolated from North-Western Himalayas and to compare them with other known lineages available in the literature. The phylogenetic tree obtained after analysis, grouped these strains into two clusters, first comprising of Malaysian, North American, Sake, West African and Wine/European strains and second comprising of all the Indian strains along with certain other strains from different countries. In both the clusters, region based grouping was observed to some extent. For functional diversity, exposition of baking and brewing abilities of these strains were studied. Four strains viz. Sc06, Sc11, Sc19 and Sc20 were found promising for baking and three strains viz. Sc04, Sc05 and Sc24 were found promising for brewing, thereby indicating the existence of functional diversity. Out of 18 *S. cerevisiae* strains, only one strain Sc02 was found positive for killer toxin production. At genetic level, phylogenetic tree obtained from mining of *ADH1* gene of ten randomly selected yeast strains, showed a very little variation in the gene sequence irrespective of their alcohol production ability, and most of them clustered together according to their geographical origin. However, mining of *ATF1* gene showed a lot more variation in the gene sequences without depicting any region based clustering behavior. Thus *ATF1* gene seems to be an appropriate tool to reveal differences among these indigenous *S. cerevisiae* strains. Organoleptic studies of six native yeast strains suggested Sc21 as the potential candidate for soft cider whereas, Sc01 for hard cider. A wide variation was observed in bio-emulsifier production; the maximum emulsification activity was recorded in Sc10 (64.82%) yeast strain.