AIMS AND OBJECTIVES

India comprises one of the largest populations globally, known for its enormous diversity, which provides an excellent opportunity to study socio-culture and genetic variability. Large family sizes and high levels of endogamy in Indian population provide a unique resource for dissecting complex disease etiology and pathogenesis. T2D being one of the complex disease, whose prevalence in India is increasing at alarming rate is attributed to the genetic predisposition known as Asian Indian phenotype (Joshi, 2003), green and white revolution which lead to the better prosperity, improved socio economic status, better economy, nutritional shift from traditional food to junk foods, improved diets and finally rural to urban migrations associated with sedentary life style over a short span of time (Reddy and Yusuf, 1998; Chan et al., 2009) in Indian populations. These changes involving shift from diet pattern, decreased physical activity and increased levels of mental stress (Mohan, et al., 1986, Ramchandran et al., 2003). Punjab, not being far from this socio-economic and nutritional transition has faced changes in the dietary and lifestyle pattern, which has inflicted upon its population risk of metabolic disorders like T2D. The severity of such risks increases manifolds when combined with the genetic factors.

The present study was designed to add to the pool of information on genetic association of some of the unexplored population groups, mainly endogamous groups of Punjab with the differential risk of developing T2D, the complex disease in which many genes as well as confounding factors play an important role.

Keeping the above in view, the proposed study is focused to:

- Explore the frequency of polymorphisms in KCNJ11 (rs5219), TCF7L2 (rs7903146) and MT-ND3 (rs2853826) genes in cases and controls from the studied population groups.
Aims and Objectives

- Analyse the association of various risk factors such as BMI, dietary pattern and physical activity with development of T2D.
- Apply statistical tools to find whether the above mentioned polymorphisms along with risk factors impart any susceptibility towards T2D in studied endogamous groups of Punjab.
- Explore SNP–SNP interaction if any, to understand the broader aspect of T2D development.