2. Aims and Objectives

2.1 Overall aim

To study the nucleotide variations in the reverse transcriptase and protease regions of the *pol* and *env* genes of HIV-1 that determine drug resistance and investigate the influence on co-receptor usage for clade C.

2.2 Specific objectives

1) To sequence the HIV-1 *pol* gene from plasma and assess the frequency of mutations in the reverse transcriptase and protease gene sequence of drug naïve infected population and in those showing treatment failure.

2) To compare differences in interpretation of the different HIV-1 genotypic drug resistance algorithms on the effects of mutation in the RT and Pr of HIV-1 on susceptibility towards drugs used in the ART regimen.

3) To study 3D model constructs of HIV-1 RT based on amino acid sequences derived from treatment naïve and treatment failure individuals and postulate mechanism of mutations.

4) To study 3D model constructs of HIV-1 protease based on amino acid sequences derived from treatment naïve and treatment failure individuals and postulate mechanism of mutations.

5) To sequence the *env* region (V3) of HIV-1 for prediction of co-receptor usage and predict susceptibility to co-receptor antagonist.