Spinocerebellar ataxias (SCAs) are a genetically and clinically heterogeneous group of rare neurodegenerative disorders characterized by abnormal gait, tremors, slurring of speech, walking difficulty, nystagmus and many more with dysfunction of cerebellum and its afferent and efferent connections. A large variety of genetic mutations are associated with SCAs including dynamic tandem nucleotide repeat (TNR) expansion, point mutation, insertation and deletion. The prevalence of SCAs has been estimated to be 4.8–13.8 per 100,000 individuals, but it varies with ethnical background and geographical regions (Ruano *et al.* 2014).

Genetic confirmation of SCA patients depends on the type and inheritance of disorder. Autosomal dominant SCAs are more often due to repeat expansion which validate by fluorescent labelled primer based pcr reaction or triplet primed (TP) pcr followed by fragment analysis method, whereas autosomal recessive inheritance due to repeat expansion (FRDA) or point mutation which confirm using TP pcr followed by fragment analysis or sanger sequencing method. NGS technologies especially exome sequencing usually used to solve genetically negative samples.