ABSTRACT

Curcuma Zedoaria, commonly known as white turmeric, a perennial herb recognized for its health benefits including anti-cancerous properties. It has been widely used as a phytotherapeutic agent, with its rhizomes containing a various bioactive phytocompounds traditionally used as a medicine. The rizhome of white turmeric is aromatic, bitter taste and its fragrance reminisces mango. It is known for its anti-inflammatory, anti-cancer and anti-fungal properties. Molecular taxonomy plays a major role in identifying the phylogenetic relationships among curcuma species. It provides the genetic insights of Curcuma species, to understand their genetic variations and aids in development of molecular markers associated with genetic diversity and molecular markers. It involves various molecular techniques including mapping through genetic markers. It compares the whole genome data among the species and provides more accurate evolutionary information about the species. The current study focuses on the investigation of Molecular taxonomy of Curcuma Zedoaria in comparison with other species, identification of disease resistance markers linked to the disease resistance. Computational analysis of rhizome of white turmeric and identification of bioactive compounds associated with the pathways of disease resistance. Further, the study includes the development of disease resistance turmeric cultivars, their gene expression studies, and their associated biochemical pathways.