**Genome-Wide Identification of KEA Transporter Family in *Arabidopsis halleri***

**Part 1: Sequence Retrieval and Phylogenetic Analysis**

1. Retrieve the full-length DNA sequences of KEA transporter genes from the genome database. predict protein subcellular localization and physiochemical properties.

2. Perform a phylogenetic analysis using a neighbor-joining method to group the KEA genes into classes based on their similarity.

3. Identify the conserved motifs and transcription factors that bind to these motifs in the promoter regions of KEA genes.

**Part 2: Conserved Motifs and Transcription Factors**

1. Identify common cis- elements from a cluster of KEA gene promoter sequences.

2. Determine the relative position and spatial distribution of these motifs on the promoter regions.

3. Identify the transcription factors that bind to these motifs and their respective binding sites.

**Part 3: Functional Characterization**

1. Analyze the functional characteristics of the identified KEA genes (Gene Structure), including their exon number, number of ORFs, and gene length.

2. Determine the expression patterns of KEA genes under different abiotic stress conditions.

3. Identify the potential regulatory elements in the promoter regions of KEA genes that may contribute to their expression.

**Part 4: Discussion and Conclusion**

1. Discuss the implications of the identified KEA genes in Arabidopsis and their potential roles in ion homeostasis and nutrient uptake.

2. Highlight the potential applications of the identified KEA genes in crop improvement and stress tolerance.