Chapter 5

SUMMARY

Phylogenetic analysis of *CCD* genes shows duplication has occurred that leads to emergence of new sub-class gene *CCD7/CCD8*.

Functional divergences analysis revealed critical amino acid residues, leading to subgroup-specific functional evolution after their phylogenetic diversification.

No duplication has occurred only slight diverge in *NCED* sub-families and critical amino acid residues, leading to tissue specific functional divergence.

Codon bias in *CCD* and *NCED* genes shows that nucleotide composition mutational bias is the common major factor that shaping the codon usage in *CCD* and *NCED* genes.

Hierarchical cluster tree based RSCU value revealed the better relationship with closeness in function.

The CAI and RCB values indicate that all *CCD* subclass genes across the species might have low expression profile.

Molecular modeling and dynamic simulation shows the structure function relationship confirmed that duplication in *CCD4* affects structural conformation that leads to functional variation.

Database (Plant CCD Database) is created that contains the gene annotation information of *CCO* genes to the scientific community.