

LIST OF FIGURES

Figure No.	Title	Page No.
Figure 1	Climate change and risk for water availability at different parts of the world	4
Figure 2	Primary microRNA transcripts are transcribed from miRNA genes by RNA polymerase II and these transcripts can adapt hairpin-like structures that are recognized and processed by the RNase III enzyme DCL1 (DICER-LIKE1) with the assistance of several RNA binding proteins such as CBP20/80 (Cap Binding Protein CBP20/80), HYL1 (HYPONASTIC LEAVES 1), SE (SERRATE), DDL (DAWDLE), TGH (TOUGH) and CPL-1 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 1). DDL interacts with DCL1 and stabilizes primary miRNA transcript. TGH is a component of DCL1-HYL1-SE complex and facilitates primary miRNA recruitment to HYL1. CPL1dephosphorylates HYL1 for optimal activity. The miRNA/miRNA*duplex is stabilized by HEN1 (HUA ENHANCER1, a methyltransferase) which adds methyl group to the 2' OH group at the 3' end. The mature miRNA is transported to cytoplasm by HST (HASTY, exportin), where only miRNA strand gets loaded into RISC complex containing ARGONAUTE-1 protein. The RISC complex is guided by the miRNA to target mRNA causing target mRNA cleavage or translational repression.	22
Figure 3	Location of (a) control and (b) experimental site, and (c) the two selected Convolvulaceae species.	31

Figure 4	NanoDrop™ 1000 Spectrophotometer (Thermo Scientific) and the ‘Nucleic Acid’ application module in the software.	47
Figure 5	Soil water content measured at the two field sites (at different depths). Data are \pm SD (n=10).	54
Figure 6	Quadrat sampling for measuring species richness, density, height, stem diameter and leaf/leaflet area	54
Figure 7	SOD isoforms of <i>I. campanulata</i> (Ic) and <i>J. pentantha</i> (Jp) growing under control (C) and <i>in situ</i> water deficit conditions (D) as analysed by (a) activity staining of native PAGE. Relative intensity of (b) MnSOD, (c) FeSOD and (d) CuZnSOD isoforms in <i>I. campanulata</i> and <i>J. pentantha</i> exposed to water deficit than compared to control. (e) Immunoblot showing level of CuZnSOD in <i>I. campanulata</i> and <i>J. pentantha</i> growing under water deficit. Actin was used as loading control.	64
Figure 8	Expression level of conserved miRNAs in <i>I. campanulata</i> (Ic) and <i>J. pentantha</i> (Jp) leaves growing under <i>in situ</i> control (C) and water deficit (D) conditions as analyzed through Northern blotting. U6 (small nuclear RNA) was used as loading control and relative intensities of all miRNAs (to that of control) was quantified by normalizing their intensity values in accordance to that of U6.	67-70
Figure 9	Soil water content analyzed in control and drought-stressed pots. Data are mean \pm SD (n=10)	72
Figure 10	SOD isoforms of <i>I. campanulata</i> (Ic) and <i>J. pentantha</i> (Jp) growing under <i>ex situ</i> control (C) and water deficit conditions (D) as analyzed by (a) activity staining of native PAGE. Relative intensity of (b) MnSOD, (c)	76

FeSOD and (d) CuZnSOD isoforms in *I. campanulata* and *J. pentantha* exposed to water deficit than compared to control. (e) Immunoblot showing level of CuZnSOD in *I. campanulata* and *J. pentantha* growing under control and water deficit conditions. Actin was used as loading control.

- Figure 11** **a.** Size distribution of total unique sequences identified from *I. campanulata* control (blue) and drought stressed (red) libraries which are expressed as percentage of unique sequences/reads. **83-85**
- b.** Size Distribution of repeat sequences identified from *I. campanulata* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- c.** Size distribution of non-coding small RNA (ncRNA) sequences identified from *I. campanulata* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- d.** Size distribution of pre-miRNA sequences identified from *I. campanulata* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- e.** Size distribution of mature miRNA sequences identified from *I. campanulata* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.

- Figure 12** **a.** Size distribution of total unique sequences identified from *J. pentantha* control (blue) and drought stressed (red) libraries which are expressed as percentage of unique sequences/reads. **85-87**

- b. Size Distribution of repeat sequences identified from *J. pentantha* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- c. Size distribution of non-coding small RNA (ncRNA) sequences identified from *J. pentantha* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- d. Size distribution of pre-miRNA sequences identified from *J. pentantha* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.
- e. Size distribution of mature miRNA sequences identified from *J. pentantha* control (blue) and drought (red) stressed libraries which are expressed as percentage of unique sequences/reads.

Figure 13	Comparing the miRNAs identified in <i>I. campanulata</i> , <i>J. pentantha</i> and few other species.	90
Figure 14	Position weight matrices of (a) <i>I. campanulata</i> and (b) <i>J. pentantha</i> mature miRNAs.	90
Figure 15	Comparing the expression of miRNAs identified in control and drought stressed libraries of (a) <i>I. campanulata</i> (b) <i>J. pentantha</i> .	95
Figure 16	Expression level of conserved miRNAs in <i>I. campanulata</i> (Ic) and <i>J. pentantha</i> (Jp) leaves growing under Control (C) and Drought (D) conditions in greenhouse as analysed through Northern blotting. U6 (small nuclear RNA) was used as loading control and relative accumulation of all miRNAs (to that of Control) was quantified by normalizing their intensity values in accordance to that of U6.	99-102