Higher plants survive in a constantly fluctuating environment, which has driven the evolution of highly flexible metabolism, growth and development necessary for their sessile lifestyle. Many plants have adapted to altered environments better than the rest while few species have not been able to do so. This variation among the plants has led to distribution of species in selective environmental niches. Plants are frequently exposed to a plethora of abiotic stress such as low temperature, salt, drought, flooding, heat, oxidative stress and heavy metal toxicity. Various anthropogenic activities have accentuated the existing stress factors. Heavy metals and salinity have begun to accumulate in the soil and water tables and may soon reach toxic levels. All these stress factors prevent plants from realising their full genetic potential and limit crop productivity. Due to paucity of information about the performance of Field bean under these adverse conditions, the present study was initiated to understand the biochemical and physiological aspect of the plant’s adaptation to abiotic stress.

Stressing the plant with salt, heavy metals and drought resulted in gross alterations in morphological, biochemical and physiological parameters. While growth retardation was noticed in all stressed seedlings; the biochemical parameters such as antioxidants, antioxidant enzymes, and other stress-specific factors, exhibited considerable differences between the leaf and root tissues; wherein roots exhibiting an overall lowered antioxidant response. All types of stress displayed a time- and concentration-dependent variation, in response parameters; in addition, metal stressed plants demonstrated metal-dependent variation. The enzymes CAT, POX, INV and AP to a greater extent responded in a similar manner to these stresses, while GR and AMY decreased only in metal and salt stressed seedlings respectively. This further strengthened the belief that the plant responded to these different stresses in diverse manners. The isozyme patterns of POX, GR and AMY during these stresses also substantiated the above fact. Major antioxidants, proline ASC, GSH, TP and TSS showed significant elevation. Other stress markers such as Chl, MDA, signaling molecules like H$_2$O$_2$ and other parameters indicated the overlapping patterns of responses to different stress. Application of exogenous proline (5 mM) exhibited an ameliorating effect on salinity stress by enhancing the antioxidative response of Field bean while exogenous CaCl$_2$ only supported the superficial growth capability of the plant, causing the plant to succumb upon prolonged stress even in its presence. Thus, proline treatment may provide an environmentally friendly, easy to apply, and inexpensive way of preconditioning seedlings. Further research is
necessary to test the long term effectiveness of proline preconditioning of Field bean in the field.

Field bean primarily cultivated under arid and semi-arid areas is frequently exposed to abiotic stresses such as drought, heat and salinity. In response to these stress factors various genes are upregulated, which can mitigate the effect of stress and lead to adjustment of the cellular environment and plant tolerance. Plants have the ability to acquire thermotolerance rather rapidly so as to survive lethal temperatures. Field bean was exposed to a conditioning pretreatment, involving exposure to sub-lethal temperature of 30 °C for 2 h; and 100 mM NaCl for 24 h prior to heat stress at 45 °C, followed by recovery. Only the former method of pretreatment was found beneficial allowing plants to cope with the heat stress. Though cost intensive, this method is important and a potential vital strategy for enabling plant survival under high temperatures.

Drought stress induced changes in gene expression can serve as a powerful tool in understanding the mechanism of tolerance to dehydration and battery of genes responsible for adaptation. An initiation to comprehend the basic mechanisms underlying the functioning of stress genes was made by DDRT-PCR. Drought stress being a multigenic trait resulted in the alteration of a number of genes as visualized by the transcripts (Up-, down-regualted and newly expressed) obtained. Two such ESTs were cloned and the cloned fragment showed homology to stress-induced genes. Sequence alignment by bioinformatic methods enabled us to predict the function of these gene products in maintenance of water content in the leaf. As the response of the plant to drought stress involves multiple genes, and the predicted function of the ESTs are from partial sequences, the behaviour of the plant under drought cannot be solely attributed to putative functions of these genes. Although biochemical parameters to a considerable extent correlate with demonstrated drought tolerance of Dolichos lablab, a comprehensive profiling of genes responding under drought stress is necessary to substantiate the biochemical and physiological responses.