

1. INTRODUCTION

World crop production is limited largely by environmental stresses. Dudal (1976) estimated that only 10% of the world's arable land may be categorized as free of stress. However, statistics on the extent and impact of environmental stresses on crop production varies with the source.

Many of the high yielding varieties that contributed to production increases over the past few decades were deliberately developed to maximize yield under favourable environmental conditions. However, where it is not feasible to modify the environment to suit the plant, scientists are now being challenged to modify the plant to suit adverse environments while maintaining reasonable and reliable yields. In subsistence agriculture, which characterizes many third world countries, consistent performance under varying conditions is more important than high yield under favourable environments (Tal, 1985).

Salinity in arid and semi-arid regions of the world constitutes a major detrimental factor for crop production (Epstein, 1978). There are 344 million hectares of saline soils on the earth's land surface (Massoud, 1974) and, of these, 230 million hectares are not strongly saline and have crop production possibilities. The bulk of these soils are in arid and semi-arid lands where actual and potential salinity problems are most severe. An estimated area equivalent to 33% of irrigated land is affected by salinity, primarily caused by inadequate drainage (Carter, 1975). Prospects for the future are even

more ominous. According to some estimates, 40,000 hectares of irrigated land on the Indian sub-continent are becoming useless for crop production each year on account of secondary salinization (Raheja, 1966). In many of the agricultural ecosystems, more salt is delivered to the soil each year from irrigation than is removed by drainage. The inevitable consequence is a gradual build up of salts in the soil (Pillsbury, 1972).

Previously, this problem was tackled by means of one of two possible strategies. Saline soils have been reclaimed, drainage systems have been installed to remove excess salts, soil amendments have been used and high quality water has been conveyed long distances for irrigation and leaching. In short, the approach has been to modify the environment to make it suitable for the growth of conventional, that is salt sensitive, crop plants. Reclamation and drainage projects are extremely expensive operations, and subject to the availability of energy and high quality water. In many of the developing countries, there are neither the financial, technical nor the managerial resources available for installing and operating huge reclamation and irrigation schemes.

Application of a genetic approach to salinity is an idea whose time has come. No longer can agricultural scientists, addressing the staggering world-wide and threatening spectre of salinity, deal with it exclusively in management terms, although these endeavours have been continuing and will remain to continue. It is essential that a genetic dimension be added to the traditional approach of reclamation, drainage and use of excess irrigation water to leach salts below the root zone (Epstein, 1978). It is known that there is no biological

incompatibility between plant life and even highly saline conditions as evidenced by halophytes. The logical task would be to combine within the same plant the economic utility of a crop with the salt tolerance that plants evidently are capable of possessing.

In crop species, there is genetic diversity with regard to many agronomically useful traits. Salinity tolerance can not be an exception. The world collections of important crops are the chief repositories of this genetic wealth. Of the various crops, legumes are unique in several ways, for example, the ability to fix nitrogen, but are generally considered to be not very salt tolerant (Maas and Hoffman, 1977). These types of conclusions are often perfunctory, and the fact remains that their potential has not been explored and exploited so far. Certain legumes like Acacia and Prosopis can show extreme tolerance to salinity which can grow even with sea-water (ECe 46.3 dS/m) (Felkar et al., 1981). Variation for salinity tolerance has been reported in legumes although genetic variation within a crop species has been reported only in few cases (Ashraf et al., 1987). Legumes present additional challenges in finding tolerance to salinity as compared to cereals or other non-legumes, as one must take in to account the plant as well as its symbiosis with Rhizobium.

Pigeonpea is one of the important grain legumes cultivated in the arid and semi-arid regions where salinity problems tend to be acute. Over 90% of the world's pigeonpea production comes from India where salinity problems are becoming severe. An extensive world collection of pigeonpea germplasm and its wild relatives are being maintained at ICRISAT Center, Patancheru, Andhra Pradesh, India. These sources may have genetic diversity for salinity tolerance as they do for many

other characters. This possibility has not been very well explored so far since there is little information available on the genetic variability for salinity tolerance in pigeonpea. Since improvement of crop species took place outside their native areas or under favourable conditions, their gene pools have become limited (Rick, 1982). In addition, there is a growing feeling that physiological traits that are likely to play a role in salinity tolerance may have been lost in the cultivated crop gene pools over hundreds of years of domestication under favourable environments (Mudie, 1974; Maas and Nieman, 1978). Since wild relatives of the crop species were not passed through such selection pressure, the chances of obtaining high levels of tolerance to salinity may be good.

Although, introduction of genes from the wild salt tolerant species can be used to enrich crop species gene pools (Tal, 1985), the information on the genetic variability for salt tolerance in wild species that can be hybridized to crop plants is very limited (Epstein, 1978). In pigeonpea, slightly over 270 accessions of wild relatives of pigeonpea belonging to genera Atylosia, Rynchosia, Dunbaria, Paracalyx, Eracalyx, Eriosoma and Flemingia are available in the ICRISAT germplasm bank (Remanandan et al., 1988). Most of these wild types are compatible with the cultivated pigeonpea but there is no information about their salinity tolerance.

Genetic basis of many of the environmental stresses (salt, drought and others) are still considered as 'complex traits' (Ramage, 1980; Woolhouse, 1981). Much of the complexity stems from the lack of knowledge about the physiological mechanisms conferring tolerance and one of the important ways would be to resort to co-ordinated

physiological genetic research (Tal, 1985). Identification of specific physiological traits that play a major role in the tolerance mechanisms and establishment of their genetic basis is very crucial in the development of breeding strategies for the genetic improvement of crops to salinity tolerance. It is felt (Blum, 1988) that it is time to integrate plant physiology with plant genetic improvement towards a more comprehensive approach to breeding for environmental stress resistance in general, and salinity tolerance in particular.

Lastly, it is to be mentioned that the agricultural importance of legumes is particularly related to their ability to fix nitrogen in their root nodules. Any assessment of feasibility of growing legumes under saline conditions needs to consider the effects of salinity stress on legume-Rhizobium symbiosis. There is little information on the response of the pigeonpea-Rhizobium symbiotic system to salinity stress.

The major objectives of this research work are:

- a. to assess the exploitable genetic variation for salinity tolerance in pigeonpea and its wild relatives.
- b. to identify specific physiological traits involved in salinity tolerance and to understand the physiological and genetic basis of these traits.
- c. to study the response of the pigeonpea-Rhizobium symbiotic system to salinity stress and to ascertain the range of variability among rhizobial strains in their symbiotic ability under salinity.