Research Article

N-TERMINAL SEQUENCE ANALYSIS OF FEW AMINO ACIDS OF RUBISCO PROTEIN IN Casuarina equisetifolia CLONES

Dr.N.Malathi
Department of Zoology, Fatima College, Madurai-625018, Tamil Nadu India

DOI: http://dx.doi.org/10.24327/ijrsrc.2020.1106.5384

INTRODUCTION

Interest is generally centered on the extent to which different populations within the species have differentiated over the time since the ancestral population. The process of genetic sampling, e.g. drift, between successive generations will result in intra specific differentiation and this differentiation is conveniently quantified with the F-statistics (Holmes and Farell, 1993) or the analogous measures (El-Lakany, 1983 and Wright, 1978). These quantities measure the degree of relatedness of various pairs of genes. Many researchers have studied the genetic variability in intra and inter populations of natural forests for the purpose of gene applications in forest genetics and tree breeding research, including genetic diversity, population structure, phylogeny, mating systems and tree classification (Campbell and Sorrenson, 1984).

Casuarina is one of the most important genera of multipurpose tree and found to be the most suitable for large scale plantations in Indian conditions. The use of Casuarina in agroforestry systems has expanded over the last decade, though research has not kept pace. The main use of Casuarina is used for windbreaks for orchards and crop fields, where the trees provided fuel wood and sometimes fodder in addition to the nitrogen fixation, the symbiosis with Frankia (Midgley et al., 1983). The effective management practices developed for agroforestry coupled with quality planting stock, production makes it the most appropriate species which is ecologically, environmentally compatible, socially acceptable and capable of income and employment generation (Subramanian et al., 1992). There is need for more research and understanding the growth pattern and variation between the clones of same species of plantation forestry and for gene pool conservation, which will provide model for sustainable development.

A large proportion of proteins showed a different response to drought according to the genotype in both species. Proteins up- or down- regulated by abiotic stress were identified by micro-sequencing (Manson at al., 1994). Micro-sequencing of 3 proteins induced by ABA in rice roots was observed (Thompson et al., 2012). Indirect consequences of metabolic changes provoked by a mutation were also found in a nicotinamine-deficient mutant of tomato (Frankell and Bennet, 1970).

In this paper we ascribe some critical changes in the polypeptide profile in the SDS-PAGE technique. The specific quantitative changes in the Rubisco (Ribulose-1,5-bisphosphate carboxylase/oxygenase) (E.C. 4.1.1.39) or called Fraction I protein, which constitutes nearly 60-70% of total soluble plant protein, localized exclusively within the chloroplast, directed us to perform protein sequencing at the N-terminal end (Sambrook and Maniatis, 1989).

*Corresponding author: Dr.N.Malathi
Department of Zoology, Fatima College, Madurai-625018,,Tamil Nadu India

Key Words:
Casuarina clones, N-terminal amino acid sequencing, genetic variation

ABSTRACT
This paper mainly focus on the genetic variation within Casuarina equisetifolia population, of the same species, which is basic requirement for sustainable development of forest ecosystem. The aim of our study is to estimate genetic variation in Casuarinas for developing strategy of its gene pool conservation, by selecting a superior clone. We report the genetic diversity indices and the genetic variability within and among populations through peptide profile and amino acid sequencing.

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ACKNOWLEDGEMENTS

We gratefully acknowledge Dr. Anil K. Lala, National facility for Photolabeling and Peptide Sequencing in Biomolecular Systems, IIT, Mumbai for the sequencing analysis. The Indian Council of Forestry Research and Education, Dehradun under the World Bank Project for funds. Malathi thank for CSIR for SRF award.

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