




Genetic diversity analysis of pea (*Pisum sativum* L.) landraces by utilizing simple sequence repeat markers

Uzma Arif · Summaira Ali · Badr Alharthi ·
Muhammad Farhan Khan Pasha · Hafiz Muhammad Ahmad  ·
Muhammad Jamil Ahmed · Ayaz Ahmed Arif

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Abstract The objective of current study was to differentiate among 46 pea genotypes collected from different areas of Azad Jammu and Kashmir and NARC Islamabad, Pakistan. We initially experienced 20 simple sequence repeat markers among those ten primers were selected based on high level of polymorphism. The average number of the bands score per primer were 29.75% whereas, average number of monomorphic and polymorphic bands were 16.25 and 12.85%, respectively. The genetic diversity among these genotypes ranged from 0.18 to 0.98. Maximum genetic diversity were noted in genotypes i.e., M-39, L29, L32, L1, L5, L8, L11, L24, L19, L17, L25, L23, L37 and M-83, while using cluster analysis based on dice coefficients as the unweighted pair group method with arithmetic mean (UPGMA). Furthermore, principal component (PC) analysis also showed similar results of UPGMA. The eight principal components

(PC) accounted for 74.2% of the variation (21.74, 15.72, 8.76, 7.73, 6.19, 5.19, 4.50 and 4.37 for PC₁, PC₂, PC₃, PC₄, PC₅, PC₆, PC₇ and PC₈, respectively). The results of the present study will be useful in understanding the pea's genetic makeup and in the selection of suitable landraces for a future pea crop improvement program.

Keywords Genetic variation · Molecular markers · *Pisum sativum* · Principal component analysis · Crop improvement

Introduction

Pulses are significant crops influencing numbers of factors in farming, environment, animals and humans. Pea (*Pisum sativum* L.) a leguminous crop, has a

U. Arif (✉) · M. J. Ahmed · A. A. Arif
Department of Horticulture, University of the Poonch,
Rawalakot, Pakistan
e-mail: uzmaarif47@gmail.com

M. J. Ahmed
e-mail: pashamfk007@gmail.com

A. A. Arif
e-mail: ayaz.arif87@yahoo.com

S. Ali
National Agriculture Research Centre, Horticulture
Research Institute, Islamabad, Pakistan
e-mail: sumi78664@gmail.com

B. Alharthi
Department of Biology, University College of AlKhurmah,
Taif University, Taif, Saudi Arabia
e-mail: b.harthi@tu.edu.sa

M. F. K. Pasha
POD, Ministry of National Food Security and Research,
Islamabad, Pakistan
e-mail: Farhan_khan9972@yahoo.com

H. M. Ahmad (✉)
Department of Bioinformatics and Biotechnology,
Government College University, Faisalabad, Pakistan
e-mail: hafizahmad90@yahoo.com