The Living Fossil (Horseshoe crab)

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Editors,
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Revision on the molecular phylogeny of horseshoe crabs – Part 1

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Abstract

Present study was aimed to reinvestigate the existing molecular phylogeny of cryptic horseshoe crabs using universal barcode gene (cytochrome oxidase subunit 1). Phylogenetic trees were constructed using Distance matrix method: NJ and UPGMA. Genetic distance (GD) data analysis revealed the distant genetic relatedness of American horseshoe crab (Limulus polyphemus) with Asian conspecifics. More interestingly, the monophyletic origin of Tachypleus gigas and Tachypleus tridentatus was noted in constructed phylogram which other molecular markers failed to address.

Key words: molecular phylogeny, genetic conservation, horseshoe crabs, COI gene.

Introduction

The little morphological differentiation among horseshoe crab lineages has resulted in substantial controversy concerning the phylogenetic relationship among the extant species of horseshoe crabs, especially among the three species in the Indo-Pacific region. Earlier studies suggest that the three species constitute a phylogenetically irresolvable trichotomy (Xia, 2000). For elucidating their phylogenetic relationships, two proteins, coagulogen and hemocyanin, have been investigated (Shishikura et al., 1982; Srimal et al., 1985). Miyazaki et al. (1989) first investigated tropomyosin which is one of the major structural proteins involved in many types of cells, to elucidate prevailing phylogenetic relationships among horseshoe crabs and his result suggested that L. polyphemus is phylogenetically differentiated far from the three Asian species.