Genetic Diversity in the Chinese Pangolin (*Manis pentadactyla*) Inferred from Protein Electrophoresis

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We examined protein polymorphism of Chinese pangolins (*Manis pentadactyla*) from Yunnan Province of China, including two forms of three brown and nine dusky Chinese pangolins. Sixty-two genetic loci were screened; 12 loci were found to be polymorphic. The percentage of polymorphic loci (P) is 0.194, the mean individual heterozygosity (H) is 0.078, and the mean number of alleles (A) is 1.258. Furthermore, we calculated the genetic distance (D) between the two forms and found a low level of genetic divergence (D = 0.0206) between them, which indicates an almost-indistinguishable divergence at the level of proteins.

KEY WORDS: *Manis pentadactyla*; protein electrophoresis; genetic diversity.

INTRODUCTION

There are three Asian species in the genus *Manis*, the Indian pangolin (*M. Crassicaudata*), Malayan pangolin (*M. Javanica*), and Chinese pangolin (*M. pentadactyla*) (Corbet and Hill, 1986). Chinese pangolins are widely distributed in Formosa, in southern China from Yunnan eastward to Fujian, in the north to Kiungsu, including Hainan; in Burma, westward to Sikkim and Nepal; and in Indo-China (Ellerman and Morrison-Scott, 1951). Morphologically, two forms can be recognized according to the shape and color of the scales. These have local names, dusky and brown Chinese pangolins. There exists extensive chromosome polymorphism in Chinese pangolins (Chen et
su, liu, wang, and shi al., 1991). Additionally, studies on mtDNA RFLP in Chinese pangolins suggested that there is considerable divergence, and brown and dusky Chinese pangolins may be quite different forms or, at least, belong to different maternal groups (zhang and shi, 1991).

In this study, we used starch gel electrophoresis to analyze protein polymorphism in Chinese pangolins derived from yunnan province of china, to get information about their present state of genetic diversity and the relationships between the two forms.

MATERIALS AND METHODS

A total of 12 individuals was sampled, 3 brown and 9 dusky Chinese pangolins, all came from the yunnan province of china. Several kinds of tissues were used for analysis, including liver, kidney, and blood. Liver and kidney were treated by homogenization and centrifugation, while blood was separated into plasma and hemolysate by centrifugation. The sampling methods followed pasteur et al. (1990).

Horizontal starch gel electrophoresis was used in our experiments to separate soluble proteins. The starch gel is 12% in concentration, and eight buffer systems were prepared for different proteins: (I) Tris–citrate (pH 7.0), (II) Tris–borate–EDTA (pH 8.0), (III) borate–NaOH (pH 7.8), (IV) HCOOH–NaOH (pH 3.8), (V) Borate–LiOH (pH 8.0), (VI) Tris–citrate–LiOH–borate (pH 8.0), (VII) Tris–borate–EDTA (pH 8.6), and (VIII) Tris–citrate (pH 8.0). Histochemical staining methods followed previous reports (pasteur et al., 1990; ferrand, 1990; shaw et al., 1970; harris and hopkinson, 1976).

Products of 62 genetic loci were examined. They are aconitase-1,2 (ACO-1,2), acid phosphatase (ACP), adenosine deaminase (ADA), alcohol dehydrogenase-1,2 (ADH-1,2), adenylate kinase (AK), albumin (ALB), aldolase (ALD), phosphatase (ALP), amylase (AMY), carbonate dehydrogenase (CAR), catalase (CAT), creatine kinase (CK), ceruloplasmin (CP), diaphorase (DIA), esterase-1,2,3 (ES1,2,3), fumarase (FUM), glyceraldehyde phosphate dehydrogenase (GAPD), glucose-6-phosphate dehydrogenase (G6PD), NAD-glucose dehydrogenase (GLC), glutamate dehydrogenase (GLD), glyoxalase-I (Go-I), glutamate oxaloacetate transaminase-1,2 (GOT-1,2), β-hydroxybutyrate dehydrogenase (HBDH), hemoglobin-α,β (HB-α,β), hexokinase (HK), haptoglobin (HAP), isocitrate dehydrogenase (IDH), leucine aminopeptidase (LAP), lactate dehydrogenase-A,B (LDH-A,B), malate dehydrogenase-1,2 (MDH), mannose phosphate isomerase (MPI), purine nucleoside phosphorylase (NP), peptidase-A,B (PEP-A,B), peroxidase (PER), pyruvate kinase (PK), phosphoglucomutase-1,2 (PGM-1,2), 6-phosphogluconate dehydrogenase (6PGD), phosphohexose isomer-