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The Genetic diversity of Bangladeshi Buffaloes

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ABSTRACT: The most buffaloes in Bangladesh are indigenous in origin. There are 5 populations of buffaloes in Bangladesh. Karyotypic experiment indicated that Bangladesh East population had 48 chromosomes while other populations had 50 chromosomes. Blood protein polymorphism study revealed the existence of polymorphism for 7 loci: albumin, transferrin, hemoglobin- α , hemoglobin- β , carbonic anhydrase, alkaline phosphatase and peptidase-B. *Alb^X*, gene for typical swamp buffalo, was detected in populations of BDE and BDS. Another gene of swamp buffalo viz., *Tf^A* was found only in the population of BDE. mtDNA study further confirmed the occurrence of haplotypes for swamp buffaloes in BDE. Swamp buffaloes are distributed in the northeastern part of Bangladesh. River buffaloes are distributed other parts of Bangladesh.

Key words: Bangladeshi buffaloes, Polymorphism, Types.

INTRODUCTION - The domestic water buffaloes play important role in providing milk, meat and draught power in Bangladesh. The water buffalo population has been increasing in Bangladesh for the last 30 years. Most of the Bangladeshi water buffaloes are native and non-descriptive types. Introgression of Nili-Ravi breed from Pakistan occurred in some areas in the 1960's; nevertheless, almost all the water buffaloes are still native. There is no recognized breed, but a number of geographically distinct populations are found. Faruque ((2001) classified them into five populations on the basis of their geographical distribution and morphological differences. Those populations were: (1) Native buffaloes in eastern and southern part (BDE), (2) Native buffaloes in western part (BDW), (3) Native buffaloes in central part (BDC), (4) Crossbred buffaloes (Native buffaloes X Nili- Ravi breed) in southern part (BDS) and (5) Nili Ravi breed (PKS). Buffaloes are imported from India everyday for slaughtering. These buffaloes have been termed as IND. Genetic investigation for these populations has been conducted since 1984. This paper addresses the work done so far by different investigators on genetic diversity of these 6 buffalo populations and to describe their breeds / types.

RESULTS AND CONCLUSIONS - Karyotypes of BDC and BDE were studied by Amano *et al.* (1987). They reported that the most of BDC and BDE possessed 50 chromosomes indicating that those buffaloes were river types. However buffaloes of northeastern part in

BDE population possessed 48 chromosomes indicating the existence of swamp buffaloes in that region (Figure 1).

Figure 1. Karyotypes of Bangladeshi female swamp Buffalo.

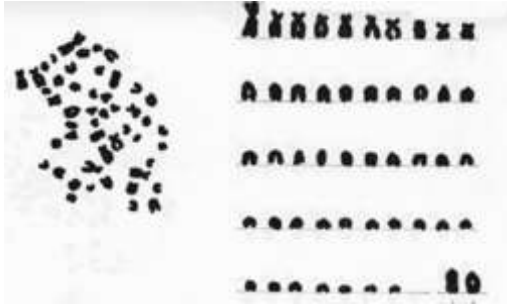
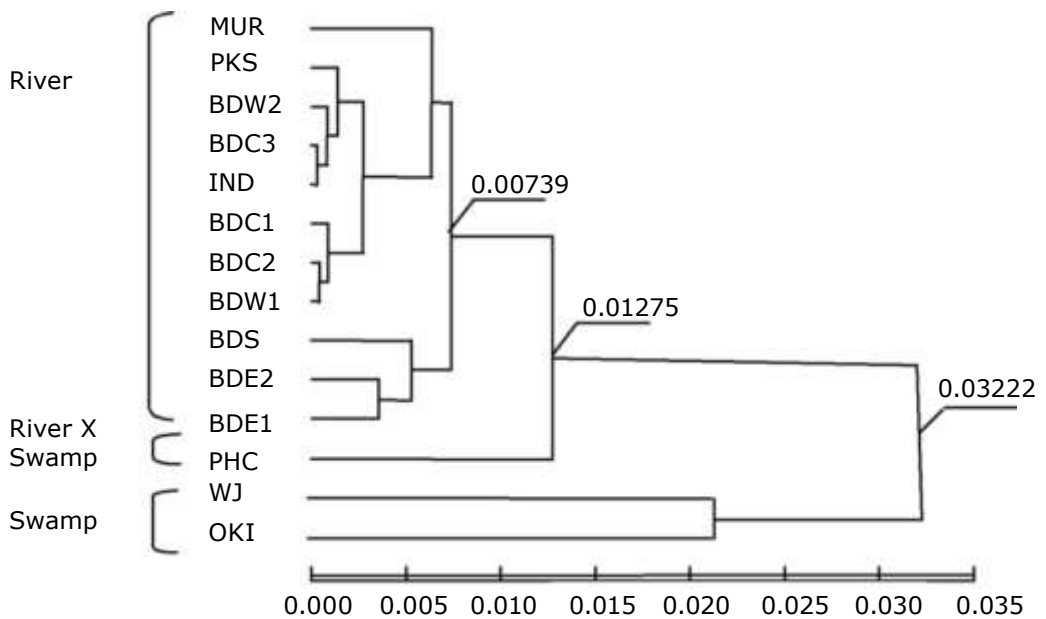


Figure 2. Dendrogram drawn from Nei's genetic distance estimated by gene frequencies of blood protein types of 14 water buffalo populations.

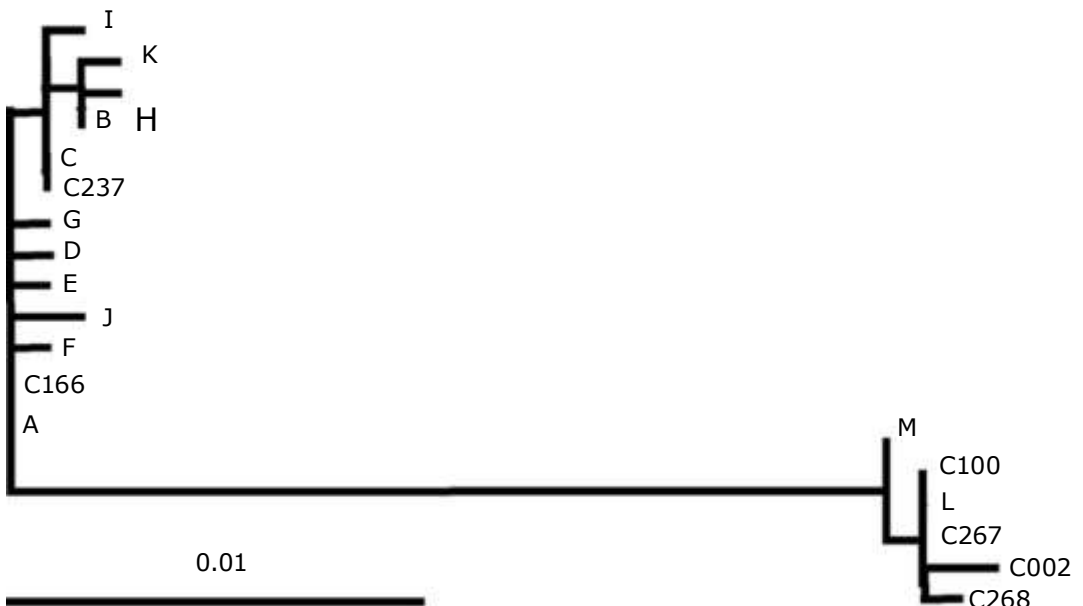


Legends: MUR: Sri Lanka Murrah, PKS: Pakistan, BDW2: Bangladesh West 2, BDC3: Bangladesh Central 3; IND: India, BDC1: Bangladesh Central 1, BDC2: Bangladesh Central 2, BDW1: Bangladesh West 1, BDS: Bangladesh South, BDE2: Bangladesh East 2, BDE1: Bangladesh East 1, PHC: Philippines crossbred, WJ: West Java, OKI: Japan Okinawa

Blood protein polymorphism of BDW 1, BDC 1 and BDC 2, BDS and BDE 1 of was studied by Amano *et al* (1987); of PKS, BDW 2, BDC 3, BDS and BDE 2 by Faruque (2004); and of BDS and BDE 2 by Alim (2005). Starch gel electrophoresis, polyacrylamide gel electrophoresis and iso-electric focusing techniques were used for that purpose. These studies reveal the existence of polymorphism for 7 loci: albumin (Alb), transferrin (Tf), hemoglobin- α (Hb- α), hemoglobin- β (Hb- β), carbonic anhydrase (CA), alkaline phosphatase (Alp) and peptidase-B (Pep-B). *Alb^X*, gene for typical swamp buffalo, was detected in populations of BDE and BDS. Another gene of swamp buffalo viz., *Tf^A* was found only in the population of BDE. Faruque (2004) compared his data (BDE2, BDW2, BDC3, BDS, PKS and IND) to those (MUR, BDC1, BDC2, BDE1, PHC, WJ and OKI) of Amano *et al.* (1998) as shown in Figure 2. In the dendrogram, all the populations of Bangladeshi buffaloes clustered in river buffalo group.

For study of mtDNA polymorphism, sequencing of *cytochrome b* gene were conducted by Kikkawa *et al* (1995) and Faruque (2004). Faruque (2004) found 13 (A to M) haplotypes for the 6 populations. He constructed the phylogenetic trees using 13 haplotypes of Bangladeshi buffaloes, 2 (C237, C166) of Murrah and 4 (C001, C002, C267, C268) of swamp buffaloes (Figure 3). Out of 13 haplotypes, 11 haplotypes (A to K from BDW, BDC, BDS, BDE, PKS and IND) clustered with the haplotypes of Murrah buffaloes, whereas haplotypes L and M obtained from buffaloes of northeastern part of BDE clustered with the haplotypes of swamp buffaloes. mtDNA sequence study, therefore, confirmed the existence of swamp buffaloes in the northeastern part of Bangladesh.

Figure 3. Neighbor joining trees drawn from 19 haplotypes of Bangladeshi buffaloes, swamp buffaloes and Murrah breed.



All the genetic investigations reveal the existence of swamp buffaloes in the Northeastern part of the country. The buffaloes in other parts of the country are river types. The findings of these results will assist in formulating the conservation and genetic improvement program of Bangladeshi buffaloes. These will also contribute to the phylogenetics of Asian buffaloes.

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