Allelic Diversity of Productive, Reproductive and Fertility Traits Genes of Buffalo and Cattle

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Abstract : Identification of genes of importance regarding production traits in buffalo is impaired by a paucity of genomic resources. Choice to fill this gap is to exploit data available for cow. The cross-species application of comparative genomics tools is potential gear to investigate the buffalo genome. However, this is dependent on nucleotide sequences similarity. In this study gene diversity between buffalo and cattle was determined by using 86 gene orthologues. There was about 3% difference in all genes in term of nucleotide diversity; and 0.267 ± 0.134 in amino acids indicating the possibility for successfully using cross-species strategies for genomic studies. There were significantly higher non synonymous substitutions both in cattle and buffalo however, there was similar difference in term of dN - dS (4.414 vs 4.745) in buffalo and cattle respectively. Higher rate of non-synonymous substitutions at similar level in buffalo and cattle indicated a similar positive selection pressure. Results for relative rate test were assessed with the chi-squared test. There was no significance difference on unique mutations for non synonymous sites indicating ongoing mutagenic process that generates substitutional mutation at approximately the same rate at silent sites. Moreover, despite of common ancestry, our results indicate a different divergent time among genes of cattle and buffalo. This is the first demonstration that variable rates of molecular evolution may be present within the family Bovidae. **Keywords :** buffalo, cattle, gene diversity, molecular evolution

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