Linker Histone H1.b is Polymorphic in Grey Partridge (*Perdix perdix*)

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This study was aimed at characterizing allelic variations of erythrocyte histone H1.b by comparing the electrophoretic patterns of histone H1.b from individuals of grey partridge (*Perdix perdix*) population. As two alloforms, H1.b1 and H1.b2, were discerned in the screening gels, the histone H1.b was regarded to be a polymorphic protein encoded by a gene with two codominant alleles, b^1 and b^2, at a locus. The tested population was found to be at Hardy-Weinberg equilibrium ($\sigma^2 = 0.834$, $p = 0.361$), with only a minor heterozygote deficiency (fixation index $F = 0.136$). Since the histone H1.b alloforms were identified in a two-dimensional gel containing sodium dodecyl sulfate, with no significant differences in their migration pattern in an one-dimensional acetic acid polyacrylamide gel, we assumed that the H1.b alloforms possessed a similar net charge and differed in their apparent molecular weights. A comparison of *N*-bromosuccinimide-cleaved and Ŭ-chymotrypsin-digested products of histone H1.b alloforms revealed slight differences in the velocity of C-terminal peptides and a similarity in migration of their N-terminal peptides in one-dimensional sodium dodecyl sulfate-polyacrylamide gel. Therefore, it seemed that the histone H1.b alloforms might differ in this amino acid sequence in a protein segment between *N*-bromosuccinimide cleavage site and the very C-terminus.

Key words: Avian Erythrocyte, Histone H1.b, Alloforms, Chemical Cleavage and Limited Proteolysis