



Inheritance of cytosine methylation patterns in purebred versus hybrid chicken lines

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ABSTRACT. We used methylation-sensitive amplified polymorphism to examine DNA methylation levels and CCGG patterns in parents and offsprings of 3 groups of adult chickens, purebred White Leghorn (AA), White Plymouth Rock (EE), and crossbred individuals (EA) using 10 primer combinations. We found that about 66% of the cytosines at CCGG sites were not methylated. Fully methylated sites were less frequent than hemi-methylated sites in the chicken genome; these frequencies were different from those of plants. We observed that the probability that the offspring would inherit the methylation pattern for any given site from the parents was 88%; consequently, unexpected methylation patterns in offspring occurred at a rate of about 12%. The methylation degree in offspring was lower than in parents, and there were more sites with altered methylation patterns in EA crossbreds compared with AA and EE purebreds. Seven differentially methylated fragments between parental lines and their offspring were isolated, sequenced, and characterized, 4 of which were located in the coding

regions. We conclude that most of the methylation status is transferred from parents to offspring in chickens, and that there are differences in the inheritance of methylation status in purebred versus crossbred offspring. We also concluded that methylation-sensitive amplified polymorphism is highly efficient for large-scale detection of cytosine methylation in the chicken genome.

Key words: Chicken, Methylation pattern, MSAP, Blood genome