

00-11 Absence of CpG observed/expected ratio depletion in *Haemonchus contortus* evidences a non-methylated genome

Simone Cristina Méo Niciura*, Patricia Tholon

Embrapa Pecuária Sudeste, São Carlos, SP, Brazil. *simone.niciura@embrapa.br

Haemonchus contortus is a blood-sucking helminth, which parasites the abomasum of small ruminant and leads to production losses, anemia, and death. DNA methylation is an epigenetic event that regulates gene expression, cell and tissue differentiation and also cell cycle transition in parasites. Due to the absence of DNA methylation in the genome of *Caenorhabditis elegans*, it was assumed that this epigenetic mark was absent in all nematode species. However, studies confirmed DNA methylation in *Trichinella spiralis* and nine other nematodes. Thus, the objective of this study was to *in silico* investigate whether DNA methylation is present in the *H. contortus* genome. DNA methylation occurs in cytosine in the CpG context, and methylated cytosines are prone to deamination to thymine. Then, in methylated genomes there is a depletion in the ratio between observed and expected CpG (CpGo/e) content in methylated regions of DNA over time compared to unmethylated regions, leading to a bimodal CpGo/ e distribution. To assess this, a total of 23,100 expressed sequenced tags (EST) of *H. contortus* were retrieved from NCBI-dbEST public database and filtered by size (≥ 500 bp), resulting in 10,940 EST subjected to CpGo/e analysis with CpG Island Promoter Detection (<http://doua.prabi.fr/software/cpgprod>). Normality and Kolmogorov-Smirnov tests performed in SAS (SAS Inst., Inc., Cary, NC) fitted the data in a normal curve with mean 0.91 (± 0.18), which indicates a unimodal CpGo/ e distribution. This absence of CpGo/e depletion in *H. contortus* suggests that its genome lacks DNA methylation.

Keywords: Epigenetics, DNA methylation, gastrointestinal nematode, barber's pole worm.

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