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1-1-2006

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Chew, Yap Ching; Raza, Ashraf S.; Sarath, Gautam; and Zempleni, Janos, "Biotinylation of K8 and K12 co-occurs with acetylation and mono-methylation in human histone H4" (2006). *Publications from USDA-ARS / UNL Faculty*. 35.

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Meeting Abstract

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Biotinylation of K8 and K12 co-occurs with acetylation and mono-methylation in human histone H4

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ABSTRACT

Histones H1, H2A, H2B, H3, and H4 are proteins that are critical for folding of DNA into chromatin. Posttranslational acetylation, methylation, and biotinylation of histones participate in gene silencing, mitotic condensation of chromatin, and the cellular response to DNA damage. Various modifications of histones are known to interact ("cross-talk") in chromatin-remodeling events; interactions may be synergistic or antagonistic. Here, we sought to identify biotinylation sites in human histone H4 by using mass spectrometry (MS/MS), and we sought to determine whether biotinylation co-exists with acetylation and methylation in the same H4 molecule. Nuclear histones from human lymphoid (Jurkat) cells were digested with trypsin and analyzed by using a QStar XL mass spectrometer. Evidence was provided that K8, K12, and K16 in histone H4 are targets for biotinylation. Moreover, we observed that K8-biotinylated H4 may be mono-methylated at K5, and that K12-biotinylated H4 may be acetylated at K5 and K8 and mono-methylated at K16. This is the first study to identify biotinylation sites in histones by using mass spectrometry and to demonstrate co-occurrence of biotinylation, acetylation, and mono-methylation in the same histone molecule. This research is likely to unravel novel functions of biotinylated histones in chromatin remodeling events fundamental to human health.

(Supported by NIH grants DK 60447, DK 063945, COBRE 1P20RR17675, and by NSF EPSCoR grant EPS-0346476.)