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Dialogue between epigenetic mechanisms and microbiome in the progress of drug addicts' rehabilitation

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Background: Previous studies in animal models of drug craving delineated broad longitudinal changes in DNA methylation profiles in the brain and T-cells. Several studies in both nonhuman primates and primates suggest that differences in gut microbiota are associated with changes in mood.

Rational/Significance Substances of abuse are major stressors. Environmental and dietary stress alters the gut microbiome, affecting factors that regulate the population levels of microorganisms along the GI tract. A number of key energy metabolites serve as essential cofactors for many epigenetic enzymes that regulate DNA methylation, posttranslational histone modifications, and nucleosome position, therefore may affect addiction.

Hypothesis Significant contributors in the epigenomic machinery are formed during energy metabolism signifying that any disorder in these processes can lead toward wide variety of diseases associated with epigenetic modifications. Treatment with food supplements may affect the addicts' gut microbiome and attenuate drug relapse in parallel with DNA methylation trajectories.

Results and Discussion In a preliminary study, we first demonstrate that DNA methylation profiles, exist in T-cells of substance-use addicts, may differentiate them from normal controls. Moreover, these profiles overlap with methylation pattern we previously described in the accumbens in a rat model of cocaine craving. Treatment with a food supplement, DHEA, attenuated drug relapse in parallel with reversal of specific genes' methylation and correlated with the PANSS. DHEA also caused a significant shift of the addicts' gut microbiome towards the normal community. A concert between the gut and brain mechanisms may contribute to the pathology drug craving and rehabilitation.