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Gut Microbiome Analysis in Morphine Exposure and Naltrexone-Induced Withdrawal

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Introduction and Objectives:

Relatively little is understood about the underlying physiological changes that occur in the withdrawal state of opiate users. Research on the effects of alcohol withdrawal on the Gut-brain axis (GBA) has revealed shifts in relative numbers of specific bacterial species that correlate with increased central nervous system (CNS) inflammation via neurological crosstalk. The purpose of this research was to determine if similar shifts in the relative abundance of bacterial populations occur in the opiate withdrawal state.

Methods:

Fourteen rats were randomized into four groups. Control and experimental rats were administered 75 mg morphine pellets or placebo (sugar) pellets subdermally. Within these two groups, the rats were given either naltrexone (simulates withdrawal) or nothing. Rats given naltrexone injections were sacrificed on day five and control rats on day 6. The rats were dissected, and stool from the cecum was extracted using the Qiagen DNA extraction mini kit. Finally, qPCR was run to examine changes in bacterial colonies in the control, opiate, and withdrawal groups.

Results:

The results showed a general shift in genus predominance from *Firmicutes* (control) to *Bacteroides* (withdrawal). This shift was only seen in rats in the withdrawal state and not in those only exposed to morphine or in the control conditions.

Discussion:

These bacterial shifts were similar to those seen in the numerous alcohol withdrawal studies that this research was modeled after. This may suggest similar underlying pathogenesis of gut dysbiosis from opiate withdrawal leading to CNS inflammation via vagal nerve signaling in the GBA.

Credit: This research is based on the primary research of Sean O'Sullivan who I assisted in a small portion of his extensive research on the Gut-Brain axis in opiate withdrawal.