Canada is currently in the midst of a dire opioid crisis. According to a National report released September of 2018 by the Special Advisory Committee on the Epidemic of Opioid Overdoses, there have been over 8000 opioid-related deaths in Canada between January 2016 and March 2018, with 1473 of these deaths occurring in BC in 2017 alone. It has been proposed that epigenetic modifications can underlie substance use disorder predisposition, dependence, tolerance, and relapse. Mu-opioid receptor 1 (OPRM1) functions in pain and mood responses, as well as in reward-seeking and addictive behaviours. Hypermethylation at the -18, +18 and +126 CpG sites within the OPRM1 gene promoter has been observed in rodents and humans with opioid use disorder. Despite this evidence, there has been no previous investigation of whether chronic opioid use is sufficient to induce hypermethylation within the OPRM1 promoter region. This experiment proposes to bridge this gap in the knowledge by inducing heroin use disorder in rats using an intravenous self-administration protocol. Once addiction has been established, brain tissue DNA extracted from heroin dependent and drug-naive rats will be subjected to bisulfite sequencing to assess the OPRM1 DNA methylation profile. I hypothesize that heroin use disorder in rats is sufficient to induce DNA hypermethylation at the -18, +84, and +126 CpG sites within the OPRM1 promoter. The results of the proposed experiment will advance understanding within the field on the effects of DNA methylation on addiction, and potentially provide further insight into the complexities and mechanisms underlying opioid use disorders.