

A polymorphism in the *OPRM1* 3' untranslated region is associated with methadone efficacy in treating opioid dependence

Richard C. Crist^{1*}, Glenn A. Doyle^{1*}, Elliot C. Nelson², Louisa Degenhardt³, Nicholas G. Martin⁴, Grant W. Montgomery⁴, Andrew J. Saxon⁵, Walter Ling⁶, Wade H. Berrettini¹

¹ Center for Neurobiology and Behavior, Department of Psychiatry, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania, United States

² Department of Psychiatry, Washington University School of Medicine, St. Louis, Missouri, United States

³ National Drug and Alcohol Research Centre, UNSW Australia, Sydney, Australia

⁴ QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia

⁵ Veteran's Affairs Puget Sound Health Care System, Seattle, Washington, United States

⁶ University of California, Los Angeles, Integrated Substance Abuse Programs, Los Angeles, California, United States

*These authors contributed equally to this work.

Abstract:

The mu-opioid receptor (MOR) is the primary target of methadone and buprenorphine. The primary neuronal transcript of the *OPRM1* gene, MOR-1, contains a large 3' untranslated region with five common haplotypes in European-Americans. We analyzed the effects of these haplotypes on the percentage of opioid positive urine tests in European-Americans (n = 582) during a 24-week, randomized, open-label trial of methadone or buprenorphine/naloxone (Suboxone) for the treatment of opioid dependence. A single haplotype, tagged by rs10485058, was significantly associated with patient urinalysis data in the methadone treatment group. Methadone patients with

the A/A genotype at rs10485058 were less likely to have opioid-positive urine drug screens than those in the combined A/G and G/G genotypes group (Relative Risk = 0.68, 95% confidence intervals = 0.64-0.73, $p = 0.0013$). Genotype at rs10485058 also predicted self-reported relapse rates in an independent population of Australian patients of European descent ($n = 1215$) who were receiving opioid substitution therapy ($p = 0.003$). *In silico* analysis predicted that miR-95-3p would interact with the G, but not the A allele of rs10485058. Luciferase assays indicated miR-95-3p decreased reporter activity of constructs containing the G, but not the A allele of rs10485058, suggesting a potential mechanism for the observed pharmacogenetic effect. These findings suggest that selection of a medication for opioid dependence based on rs10485058 genotype might improve outcomes in this ethnic group.