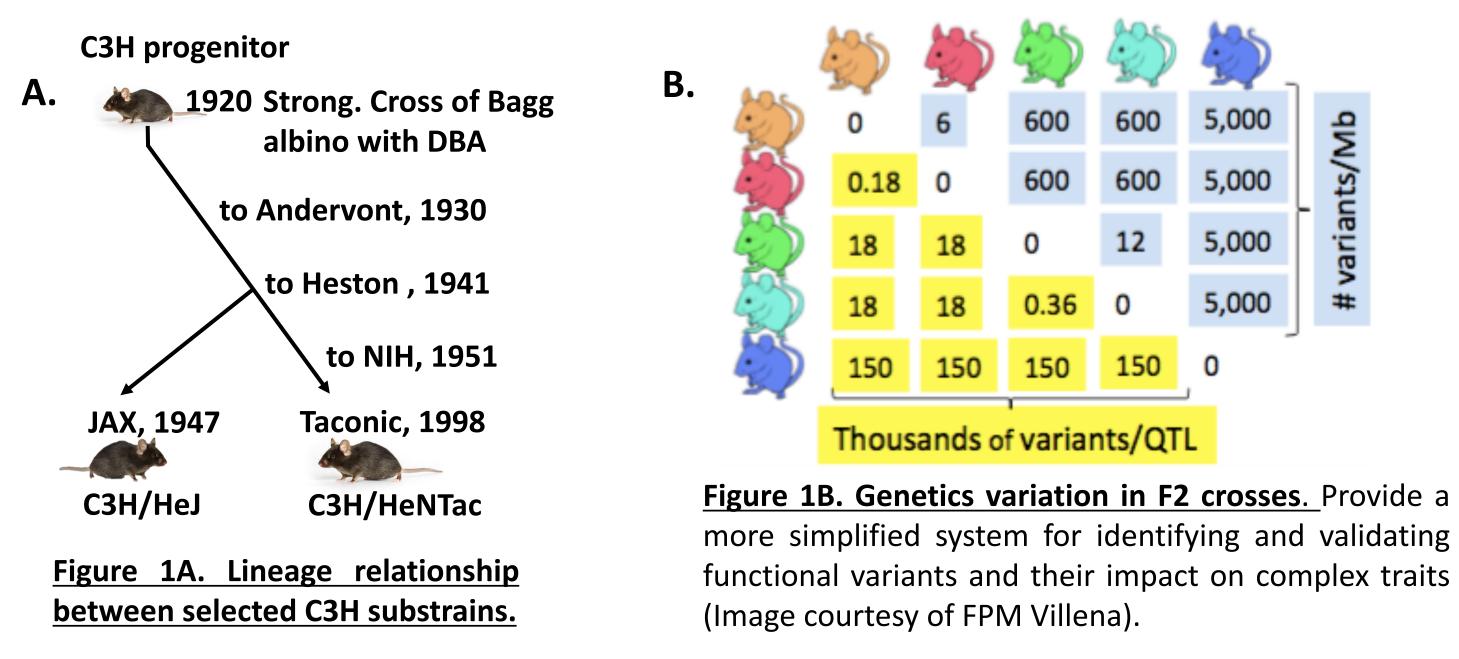
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INTRODUCTION

Cocaine use disorder (CUD) is highly prevalent and poses significant personal, economic and societal burdens. Despite the high prevalence, there are no FDA-approved treatments due to significant gaps in our knowledge about the etiology of CUD. The risk for developing a CUD is influenced by genetic background, the environment and complex gene by environment interactions.

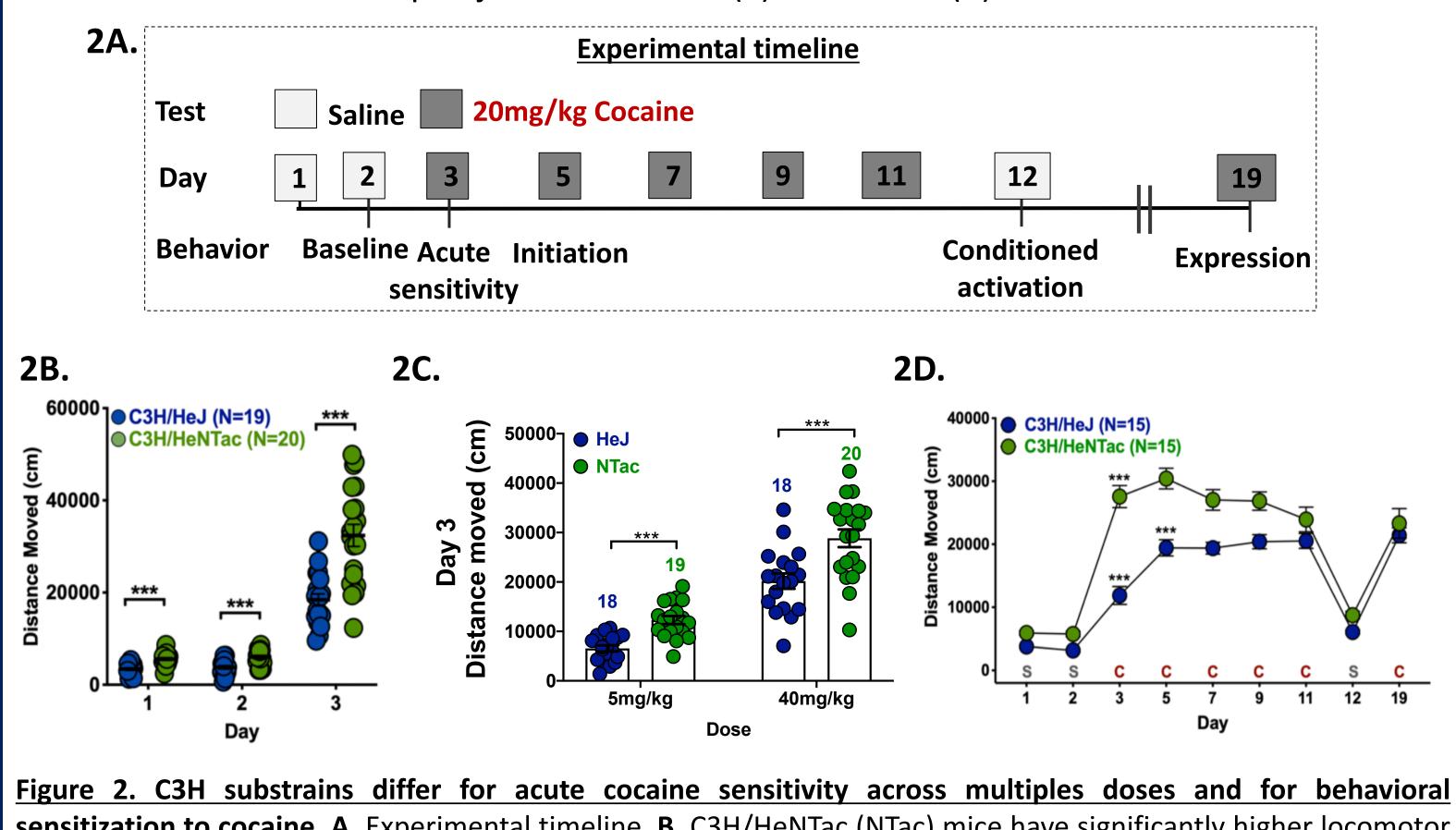
Mice have been used successfully as an experimental system to identify genetic loci implicated in addiction-related behaviors. Previous studies have used crosses between genetically and phenotypically divergent inbred mouse strains resulting in the identification of genomic regions that span tens of megabases and contain hundreds to thousands of potentially causal SNPSs, hindering identification of the specific causal polymorphism. To overcome this issue, we are using a reduced complexity cross (RCC) between two closely related inbred mouse substrains.



Polymorphisms segregate between these subpopulations at regions of the genome for which the parental strain has not yet become fixed, or from genetic drift, resulting in sets of strains that are genetically very closely related. Inbred substrains harbor enough genetic polymorphisms to allow for genetic mapping but have a limited number of functional polymorphisms in mapped regions, thereby accelerating gene discovery. We identified a striking difference in cocaine-induced locomotor activation in HeJ and NTac substrains. An RCC detected one suggestive locus implying that non-genetic factors may also be contributing to the behavioral differences observed in the two substrains. Further investigation identified significant differences in the composition of the gut microbiota between these C3H substrains. This project aims to determine whether differences in the gut microbiota of these two substrains drive behavioral differences in sensitivity to the locomotor stimulating effects of cocaine. Establishing the role of the gut microbiome in the behavioral effects of cocaine provides a potential avenue for novel treatments.

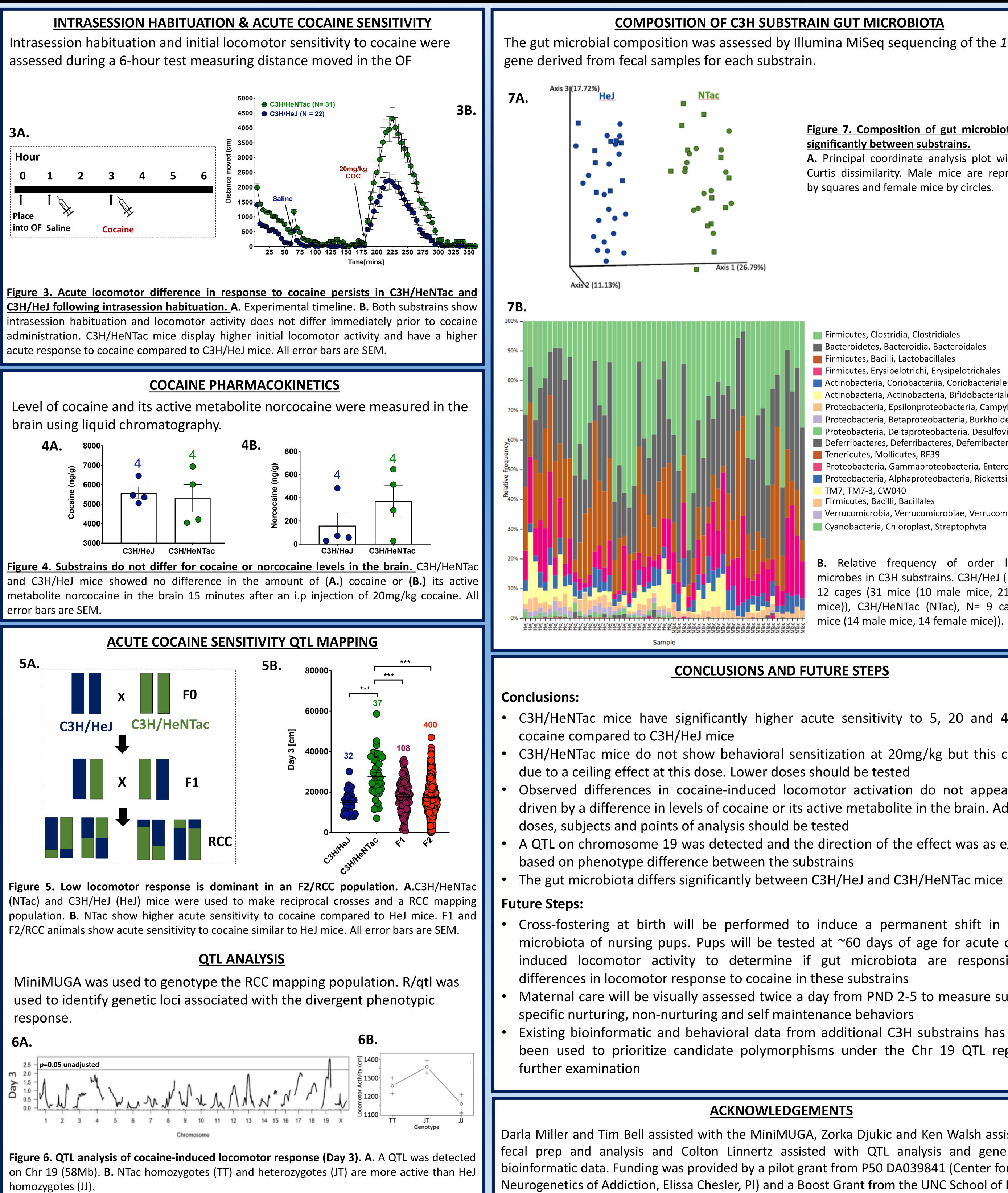
ACUTE COCAINE SENSITIVITY & BEHAVIORAL SENSITIZATION

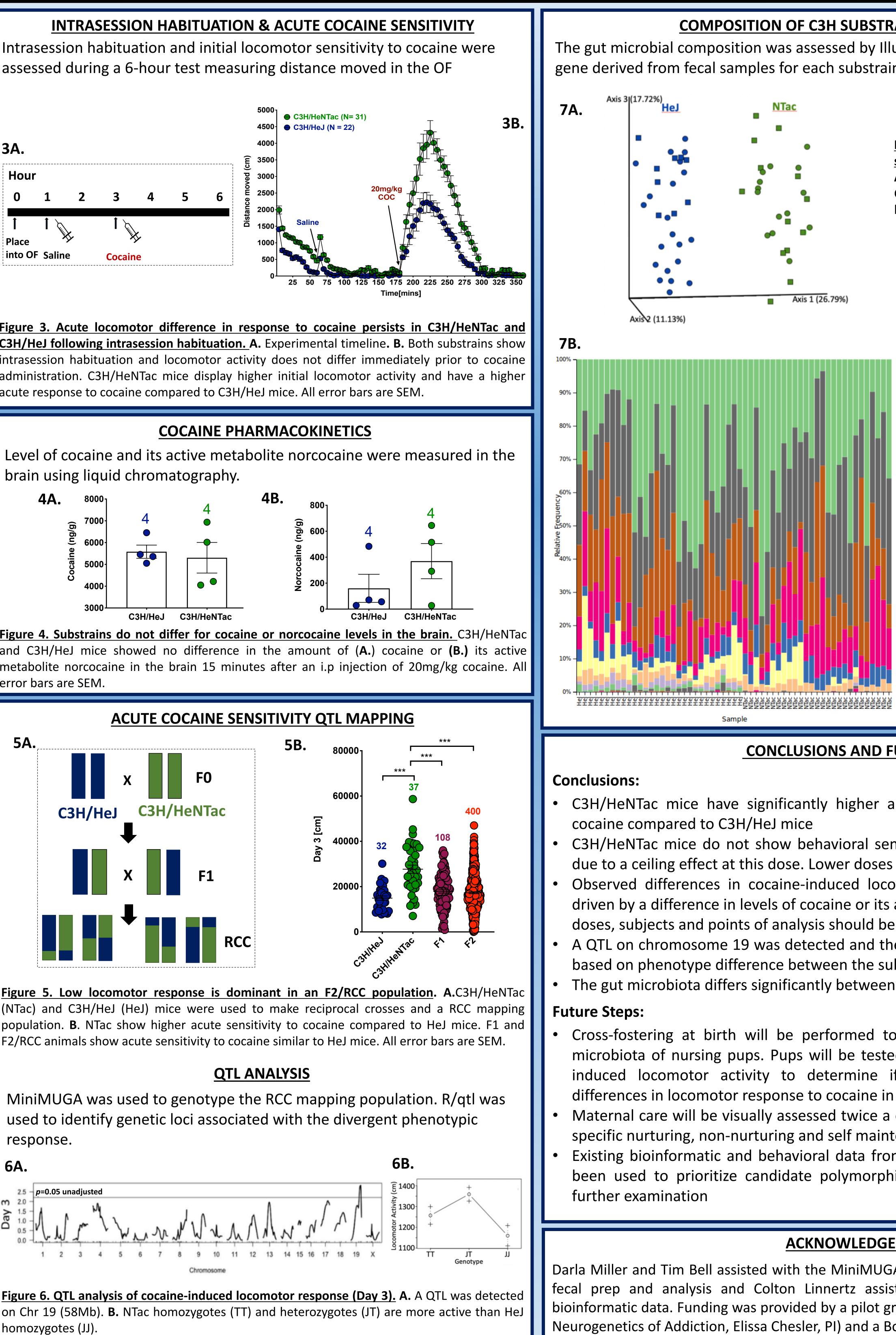
Acute sensitivity to 5, 20 and 40 mg/kg cocaine was assessed using locomotor activity in the open field (OF). Behavioral sensitization was measured using a 19-day protocol during which mice received either an i.p. injection of saline (S) or cocaine (C).



sensitization to cocaine. A. Experimental timeline. B. C3H/HeNTac (NTac) mice have significantly higher locomotor activation in response to 20mg/kg cocaine compared to C3H/HeJ(HeJ) mice (p<0.001), and C. at both lower (5mg/kg) and higher (40mg/kg) doses. **D.** HeJ mice displayed behavioral sensitization while NTac mice do not. For sensitization data, *** represent within substrain differences. All error bars are SEM.

Identification of a genetic locus and environmental factors influencing initial cocaine sensitivity in C3H substrains Christiann H. Gaines^{1,2}, Sarah A. Schoenrock¹, Ian Carroll³, Fernando Pardo-Manuel de Villena¹, Martin Ferris¹, Lisa M. Tarantino^{1,4}





COMPOSITION OF C3H SUBSTRAIN GUT MICROBIOTA

The gut microbial composition was assessed by Illumina MiSeq sequencing of the 16S rRNA

Figure 7. Composition of gut microbiota differ significantly between substrains.

A. Principal coordinate analysis plot with Bray-Curtis dissimilarity. Male mice are represented by squares and female mice by circles.

Firmicutes, Clostridia, Clostridiales Bacteroidetes, Bacteroidia, Bacteroidales Firmicutes, Bacilli, Lactobacillales Firmicutes, Erysipelotrichi, Erysipelotrichales 📕 Actinobacteria, Coriobacteriia, Coriobacteriales Actinobacteria, Actinobacteria, Bifidobacteriales Proteobacteria, Epsilonproteobacteria, Campylobacterales Proteobacteria, Betaproteobacteria, Burkholderiales Proteobacteria, Deltaproteobacteria, Desulfovibrionales Deferribacteres, Deferribacteres, Deferribacterales Tenericutes, Mollicutes, RF39 Proteobacteria, Gammaproteobacteria, Enterobacteriales Proteobacteria, Alphaproteobacteria, Rickettsiales TM7, TM7-3, CW040 Firmicutes, Bacilli, Bacillales Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales Cyanobacteria, Chloroplast, Streptophyta **B.** Relative frequency of order level of microbes in C3H substrains. C3H/HeJ (HeJ), N= 12 cages (31 mice (10 male mice, 21 female mice)), C3H/HeNTac (NTac), N= 9 cages (28

CONCLUSIONS AND FUTURE STEPS

C3H/HeNTac mice have significantly higher acute sensitivity to 5, 20 and 40mg/kg

mice (14 male mice, 14 female mice)).

C3H/HeNTac mice do not show behavioral sensitization at 20mg/kg but this could be

Observed differences in cocaine-induced locomotor activation do not appear to be driven by a difference in levels of cocaine or its active metabolite in the brain. Additional

A QTL on chromosome 19 was detected and the direction of the effect was as expected

Cross-fostering at birth will be performed to induce a permanent shift in the gut microbiota of nursing pups. Pups will be tested at ~60 days of age for acute cocaineinduced locomotor activity to determine if gut microbiota are responsible for

Maternal care will be visually assessed twice a day from PND 2-5 to measure substrain-

Existing bioinformatic and behavioral data from additional C3H substrains has already been used to prioritize candidate polymorphisms under the Chr 19 QTL region for

ACKNOWLEDGEMENTS

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