RESEARCH NOTE

Analysis of morphine responses in mice reveals a QTL on Chromosome 7 [version 1; peer review: 2 approved]

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Abstract

In this study we identified a quantitative trait locus (QTL) on mouse Chromosome 7 associated with locomotor activity and rearing post morphine treatment. This QTL was revealed after correcting for the effects of another QTL peak on Chromosome 10 using composite interval mapping. The positional candidate genes are Syt9 and Ppfibp2. Several other genes within the interval are linked to neural processes, locomotor activity, and the defensive response to harmful stimuli.

Keywords

Opioids, QTL analysis, Locomotor activity, Reward pathway

This article is included in the INCF gateway.

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Introduction
Responses to drugs of abuse vary among individuals and are genetically influenced (Mistry et al., 2014). Such drugs stimulate
the brain reward pathway (Gardner, 2011). Analysis of genetic
variation in the behavioral and neurobiological processes can
reveal molecular mechanisms that regulate or mediate the response
to drugs, and neurobiological changes associated with chronic
drug use. Many of the genes and signaling processes involved
in the reward pathway in humans are conserved in mice (Adinoff,
2004), and mouse genetic methods provide an efficient means
of identifying these genes and loci.

Quantitative trait loci (QTL) analysis of recombinant inbred
mouse strains (RIS) integrates phenotype and genotype data and
is a widely used approach for studying the genetic basis of drug
effects and addiction susceptibility (Spence et al., 2005). The BXD
RIS, derived from C57BL/6J (B) and DBA/2J (D), are a well-
established genetic reference population used in behavioral
neuroscience studies for mapping complex traits associated with
drug use (Crabbe et al., 1996; Dickson et al., 2016; Gora-Maslak
et al., 1991; Peirce et al., 2004; Plomin et al., 1991).

In the present study we reanalyzed data from high throughput
behavioral phenotyping of BXD RIS in the presence of mor-
phine (Philip et al., 2010). Our purpose was to identify additional
morphine response related genetic loci beyond those initially
reported. We employed composite interval mapping for two
behavioral phenotypes, rearing and locomotion in response to
morphine, and identified a QTL on mouse Chromosome 7 that was
masked by a major QTL on Chromosome 10.

Methods
Experimental protocols have been described elsewhere (Philip
et al., 2010). BXD data were generated in the laboratory of
Dr. Charles D. Blaha at the University of Memphis and obtained
from GeneNetwork.org.

QTL mapping
QTL mapping was performed using GeneNetwork 1.0 with a
composite interval mapping function using 2000 permutations.
This is a forward regression approach in which a single locus
with a major effect is included in a mapping model that scans for
additional additive effects and interactions with the major locus.
The technique will miss higher order interactions among loci that
are not detectable as main effects, but is effective when a large,
consistently observed major effect locus is present. Strain mean
scores were Winsorized when statistical outliers were present.
We first determined which marker had the highest LRS value, using a
marker regression analysis and then performed composite interval
mapping, controlling for the Chromosome 10 SNP rs3721803, one of the 3 markers with the highest LRS scores.

Bioinformatics
The MGI database (http://www.informatics.jax.org/) was used to
find information about SNPs and strain polymorphisms occurring
within the Chromosome 7 interval (queried –June 20, 2016). This
database now includes variants detected in the sequencing of 17
mouse genomes (Keane et al., 2011). The 3 SNPs located at the
Chromosome 7 QTL peak (rs13479451, rs3724540, rs6386601) are at ~114.5 Mb in GeneNetwork and ~107.6 Mb in the MGI
and NCBI databases (http://www.ncbi.nlm.nih.gov/gene). In
GeneNetwork, the relevant QTL interval on Chromosome 7 was
110–125 Mb whereas this region corresponds to 103–118 Mb in
the MGI database. As finer mapping methods are developed, the
exact interval location as reported here, may change. DAVID versio
6.8 (https://david.ncifcrf.gov/) was used to obtain functional
annotations and pathway information for the genes within the interval
and GeneWeaver 1.0 (http://www.geneweaver.org/) to identify other
drug-related phenotypes associated with the candidate genes.

Results
Composite interval mapping
As reported by Philip et al. (2010), whole genome scans
produce robust QTLs mapping to Chromosome 10 at 0–30 Mb
(Figure 1A–B). The positional and functional best gene candidate is the
Oprml gene which encodes the opioid G-protein coupled
receptor mu 1 (Philip et al., 2010) which has been previously
detected (Bergeson et al., 2001; Doyle et al., 2014).

We remapped these data for each time point using composite
interval mapping to identify QTLs potentially masked by this large
QTL. This revealed a second significant QTL on Chromosome 7
for locomotion (LRS= 18.0, 114.7 Mb; Figure 1C) and, in an
overlapping position, for rearing (LRS=16.5, 114.3 Mb). We also
observed a time dependent decrease of the peak LRS values for both
traits after the 60–75 minute time interval post-morphine injection.
A suggestive QTL for the rearing trait data was already apparent
on Chromosome 7 from the whole genome scan, but this was not
the case for the locomotion trait data (Philip et al., 2010).

The area under the QTL peak contains 280 protein coding genes
(MGI Chromosome 7: 103–118 Mb, GeneNetwork Chromosome 7:
110–125 Mb; database query-June 20, 2016, Supplementary
worksheet 2). Of these genes, 162 are associated with olfactory
receptors. Of the other genes with functional annotations, 11 are
connected with neural processes (Adm: neural tube development,
Appb1, Tab, Calca, Cckbr, Cnas4: sensory perception and
and cognition, Insc, Arml: neurogenesis, Tpp1: neuromuscular control,
Rras2: regulation of neuron death and Pde3b: morphine addiction
(KEGG pathway 05032).

There are 3 SNPs mapped at the location of the LRS peak
and two positional candidates: Synaptogamin 9 (Syt9: rs13479451,
rs3724540) and PPFIA binding protein 2 (Ppfibp2, rs6386601).
Both of these genes differ between the parental strains (MGI
database query – June 20, 2016). Syt9 functions in vesicle traffic
and Ca2+ triggered exocytosis (Ncbi, 2016b) and Ppfibp2 is
involved in the regulation and development of neuronal synapses
(Ncbi, 2016a). These two candidates are also differentially
expressed in the striatum of the brains of mice from strains with
distinct opioid sensitivity (Korostynski et al., 2006; GeneWeaver:
Syt 9, geneset #86830; Ppfibp2, geneset #86906).
Conclusions

Genetic analysis of the BXD RIS resulted in the detection of an additional locus for morphine induced locomotor activity and rearing on Chromosome 7 which may be associated with activation of the reward system pathway in response to morphine treatment. Whether this effect is opioid-specific or also occurs with other classes of drugs is not yet clear. Alternatively, this QTL may also be related to general locomotor activity or nociception, a central nervous system response to potentially harmful stimuli. The best gene candidates within the QTL interval, besides the positional candidates Srr9 and Pf5hp2, are Calca and Cckbr (sensory perception of pain) and Pde3b (morphine addiction).

Data availability

All data are available in GeneNetwork (www.genenetwork.org; see supplementary worksheet 1 for trait-ids and descriptions). Trait
ID: Locomotion: 11843, 11833, 11844, 11834, 11845, 11835, 11846, 11847, 11851, 11832, 11837, 11838, 11839, 11840, 11841, 11842, 11843, 11834, 11845, 11835, 11836, 11887, 11888, 11878, 11854.

Data are also available in the Supplementary material.

Author contributions
WEC assisted in interpreting the results and writing the manuscript; ED performed the functional annotation analysis; EJC provided the original data and assisted with interpreting the results and writing the manuscript; AD conceived the study, supervised the analyses, and wrote the manuscript. All authors approved the final submitted draft.

Competing interests
No competing interests were disclosed.

Grant information
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The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Supplementary material
GeneNetwork traits used in the QTL analysis.

List of genes within the Chromosome 7 interval.

References


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I have only minor comments, listed below.

1. “In the present study we reanalyzed data from high throughput behavioral phenotyping of BXD RIS in the presence of morphine (Philip et al., 2010).” Although it is clear what the authors are trying to say, strictly speaking this sentence implies that the authors had morphine present (on their desks? Or in their bloodstream??) when they were analyzing the data. Please make the sentence less ambiguous.

2. “Strain mean scores were Winsorized when statistical outliers were present”. Please elaborate on this and/or cite references to support the decision to modify as opposed to exclude data.

3. “We remapped these data for each time point using composite interval mapping to identify QTLs potentially masked by this large QTL.” Please clarify what “time point” refers to here.

4. “protein coding genes” this is a redundant expression. Please use either “protein coding sequences” or “genes”.

In the discussion, perhaps a few words could be mentioned about why in general reanalysis of prior phenotyping data may yield useful new pieces of information about QTLs..

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
The manuscript from Crusio \textit{et al.} describes the use of GeneNetwork to identify QTLs associated with morphine response in a genetic reference mouse population. The authors highlight many strengths afforded by both GeneNetwork and the BXD recombinant inbred mice. Specifically, they used composite interval mapping to reanalyze publicly available phenotypic and genotypic data in the BXDs to identify a QTL on chromosome 7 that had been masked by a major QTL on chromosome 10. Next, they employed a bioinformatics approach to prioritize among candidate genes within the QTL interval. This resulted in the identification of promising candidate genes that may be associated with drug-abuse phenotypes.

One step that would strengthen the manuscript would be to use QTLminer in GeneNetwork to examine \textit{cis}-regulation of the genes located within the QTL support interval (or even just the most promising candidate genes) and to see if any of those genes were expression QTLs in BXD mice.

In addition, the authors raise an interesting question when they ask whether the chromosome 7 QTL is opioid-specific, or if it also occurs with other classes of drugs. They could use GeneNetwork to search for genetic correlations between the expression levels of their top candidate genes and drug-related traits.

Minor Points:
On the GeneNetwork website, Trait ID 11851 is defined as the number of beam breaks after morphine injection, but is described as “distance traveled” and “locomotion” in the Figure 1 legend of the manuscript.

\textbf{Competing Interests:} No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.
could use GeneNetwork to search for genetic correlations between the expression levels of their top candidate genes and drug-related traits."

Correlation analyses do not rule out or support association with other drugs. The few significant correlations that we found were based on less than 10 common strains.

**Competing Interests:** No competing interests were disclosed.

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