



# Sex-dependent expression of microRNA -19b predicts chronic widespread pain and posttraumatic stress disorder development following trauma exposure

Linnstaedt SD<sup>1,2</sup>, Wu A<sup>1,2</sup>, Green P<sup>3</sup>, Levine J<sup>3</sup>, Riker K<sup>1,2</sup>, Rueckels C<sup>1,2</sup>, Yu, S<sup>1,2</sup>, Zimny E<sup>4</sup>, Lewandowski C<sup>4</sup>, Hendry PL<sup>5</sup>, Damiron K<sup>6</sup>, Pearson C<sup>7</sup>, Velilla MA<sup>8</sup>, Jones J<sup>9</sup>, Swor R<sup>10</sup>, Domeier R<sup>11</sup>, McLean SA<sup>1,2,12</sup>

From the <sup>1</sup>TRYUMPH Research Program, <sup>2</sup>Department of Anesthesiology, UNC-CH and <sup>3</sup>Department of Oral and Maxillofacial Surgery, UCSF; <sup>4</sup>Department of Emergency Medicine Henry Ford Hospital; <sup>5</sup>Department of Emergency Medicine Shands Jacksonville Medical Center; <sup>6</sup>Department of Emergency Medicine Albert Einstein Medical Center; <sup>7</sup>Department of Emergency Medicine Detroit Receiving; <sup>8</sup>Department of Emergency Medicine Sinai Grace; <sup>9</sup>Department of Emergency Spectrum Health-Butterworth Campus; <sup>10</sup> Department of Emergency Medicine St. Joseph Mercy Health System; <sup>11</sup>Department of Emergency Medicine William Beaumont Hospital; <sup>12</sup>Department of Emergency Medicine, UNC-CH



## INTRODUCTION

In humans, chronic widespread pain (CWP) and posttraumatic stress disorder (PTSD) are frequent sequelae of trauma that occur more commonly in women. One known trigger of CWP and PTSD is motor vehicle collision (MVC).<sup>1,2</sup> Molecular mechanisms mediating the development of CWP after MVC remain poorly understood. Using *in silico*, human, animal, and molecular studies, we sought to identify microRNA (miRNA), small regulatory RNA, that may contribute to CWP/PTSD vulnerability.

In preliminary studies, using an un-biased *in silico* approach to define miRNA that preferentially target pain/PTSD pathways, we identified miR-19 as a candidate regulatory hub. Interestingly, previous reports have shown that miR-19b (1) modulates the behavioral response to stress<sup>3</sup> and (2) is regulated by the estrogen receptor alpha<sup>4</sup>

## HYPOTHESES

Based on the above data, we hypothesized that (1) circulating levels of miR-19b would predict CWP and PTSD following MVC trauma, (2) miR-19b expression is sex dependent and predicts CWP/PTSD outcomes in a sex-dependent manner, (3) miR-19b regulates gene transcripts known to play pathogenic roles in pain/PTSD.

## METHODS

**IN SILICO:** We first used an unbiased approach to identify miRNA that target gene transcripts that play an important role in pain and PTSD processing. Pain and PTSD genes were identified using three published databases (n = 629 genes)<sup>5,6,7</sup>. Candidate miRNAs were determined via predicted binding to the 3'UTR of these genes (TargetScan); Monte Carlo simulations (x10,000) consisting of randomly selected sets of genes were used to generate a background distribution of the number of predicted targets for each miRNA. This distribution was then used to determine miRNA that preferentially target pain/PTSD genes. **HUMAN:** Next, we examined the association between miR-19b expression (identified via small RNA sequencing) assessed in blood samples (PAXgene RNA tubes, n = 153) collected in the emergency department in the immediate aftermath of motor vehicle collision (MVC) and the presence of CWP (ACR definition) and PTSD (Impact of Events Scale-Revised > 33) at 6 months using logistic regression analysis. **ANIMAL:** Male Sprague Dawley rats (n = 6 Male, 6 Female) were subjected to sound stress exposure as described previously<sup>8</sup>. Whole blood samples were collected using Qiagen RNeasy Protect Animal Blood Tubes before stress exposure, 24 hours, and 2 weeks following stress; total RNA was isolated using RNeasy Protect Animal Blood Kits. miR-19b was quantified using TaqMan stem-loop RT-qPCR normalized to U87. **MOLECULAR:** 3'UTR constructs were made by amplifying 3'UTRs from genomic DNA using PCR, and inserting downstream of a Firefly Luciferase gene in pL-SV40-Fluc using Not1 and EcoR1 restriction enzyme sites. Mutations to predicted binding sites within the cloned 3'UTR were introduced via primers using two step PCR. In dual luciferase reporter assays, miR-19b binding to the specified 3'UTRs was quantified by measuring the level of Luciferin protein produced in HEK293T cells 72 hours after transfection with 20fmol pL-SV40-Fluc (transfection control), 20fmol pL-SV40-Fluc-3'UTR, and 10nM miR-19b or control mimic.

FIGURE 1. *In silico* analyses indicate that miR-19 is a strong candidate regulatory hub for both CWP and PTSD

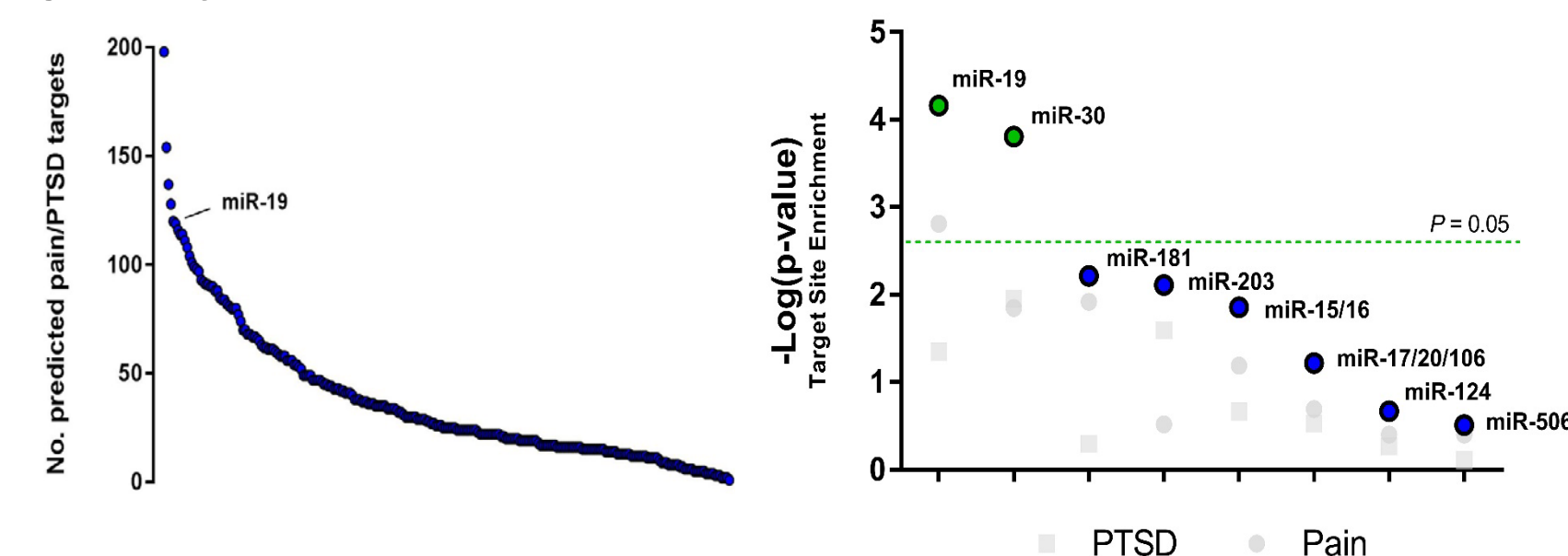


TABLE 1 and FIGURE 2. Participants and Study sites

Characteristic	
Participants, n	153
Females, n (%)	95 (62)
Age, years, mean (SD)	35 (12)
Education, n (%)	
High school or less	56 (37)
Some college	68 (44)
College	22 (14)
Post-college	6 (4)
BMI, mean (SD)	29 (7)

TABLE 2 and FIGURE 3. Circulating miR-19b expression levels predicts CWP and PTSD development following MVC and does so in a sex dependent manner

Variable <sup>a</sup>	CWP		PTSD	
	OR (95% CI) <sup>b</sup>	p value	OR (95% CI) <sup>b</sup>	p value
miR-19b	0.20 (0.04, 0.95)	0.043	0.16 (0.04, 0.75)	0.020
Sex	<0.01 (0.00, 0.35)	0.027	<0.01 (0.00, 0.06)	0.009
miR-19b*sex	16.46 (1.53, 177.67)	<b>0.021</b>	35.67 (3.02, 422.02)	<b>0.005</b>
Age	1.01 (0.98, 1.05)	0.417	0.99 (0.95, 1.03)	0.959

<sup>a</sup>Site was also included in the model as a categorical variable. <sup>b</sup>OR = odds ratio, CI = confidence interval

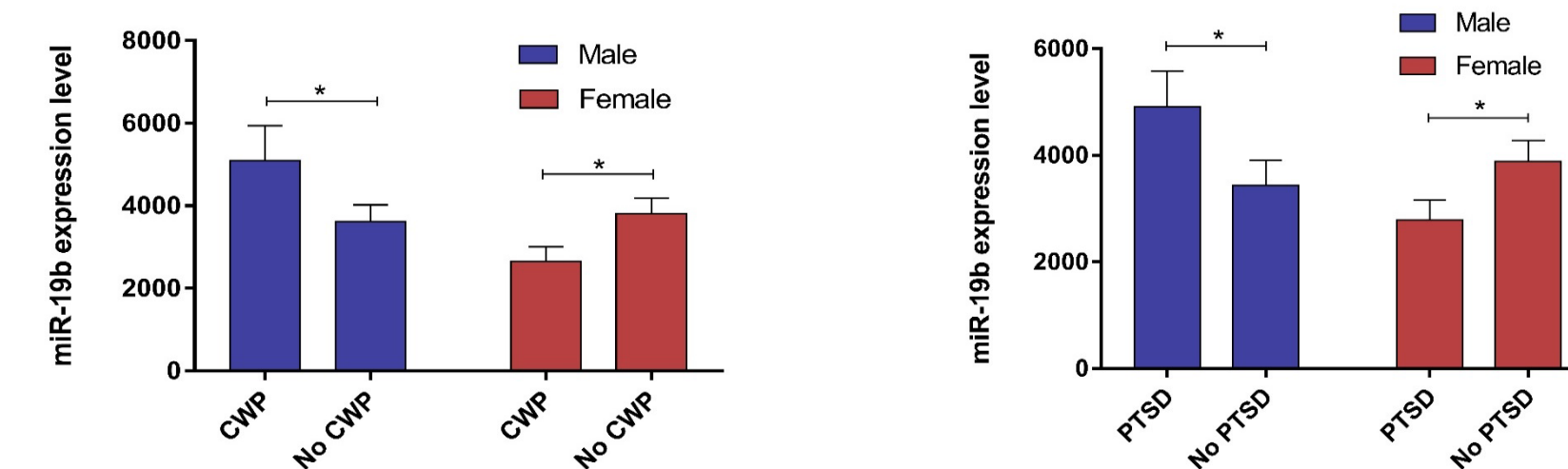


FIGURE 4. Circulating miR-19b expression differs in male and female rats and changes in a sex dependent manner following sound stress exposure

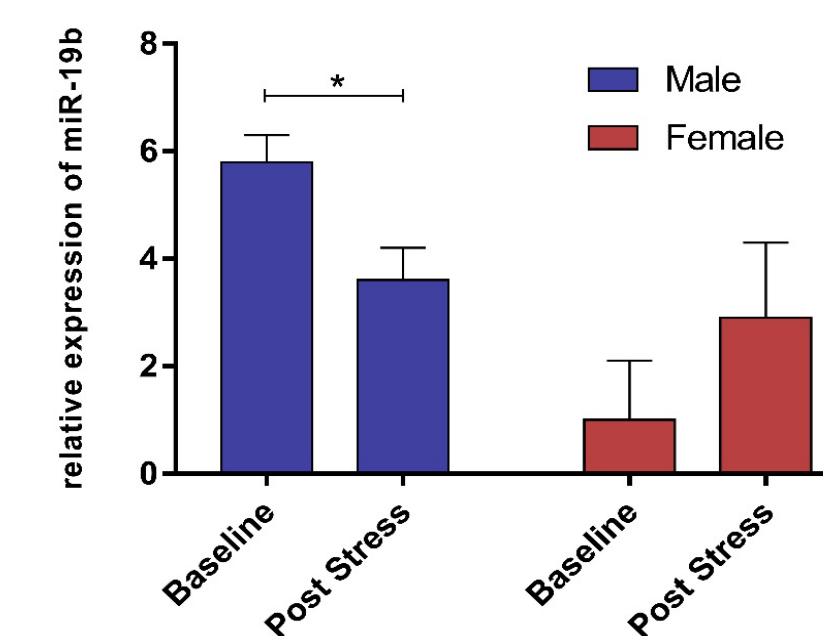
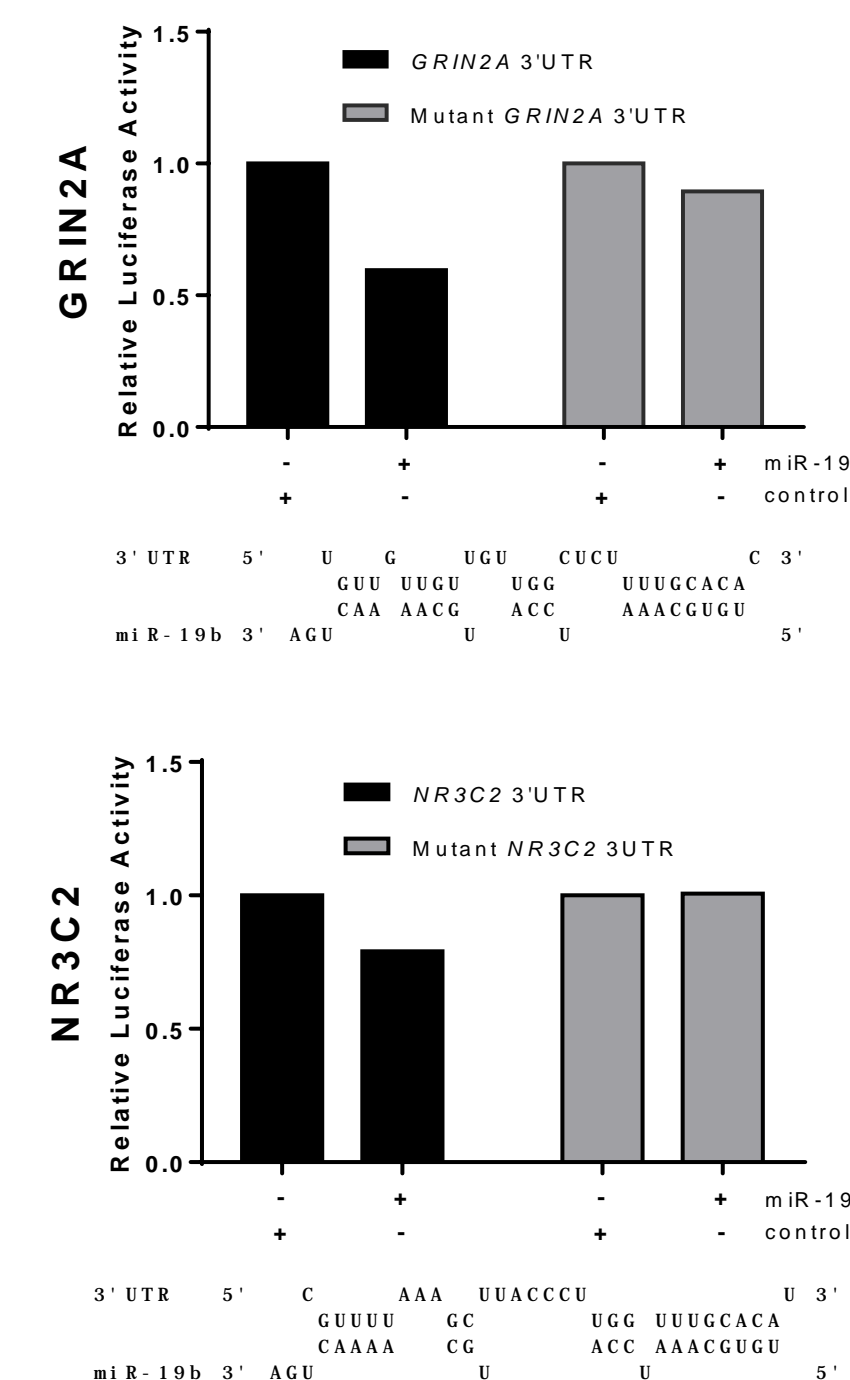


FIGURE 5. GRIN2A and NR3C2 are directly regulated by miR-19b



## RESULTS

**IN SILICO:** *In silico* analyses indicated that miR-19 targets more genes implicated in pain/PTSD pathogenesis than would expected based on chance (n = 112/629, p < 0.05, Figure 1).

**HUMAN:** miRNA samples were obtained from study participants enrolled at 10 US Emergency Department sites (Figure 2). All individuals were African Americans between the ages of 18-65, study participant characteristics are shown in Table 1. Circulating expression levels of miR-19b predicted both CWP and PTSD in a sex-dependent manner (Table 2). In males, higher expression of miR-19b predicted CWP/PTSD. In contrast, in females, lower expression of miR-19b predicted CWP/PTSD (Figure 3).

**ANIMAL:** miR-19b expression was sex-dependent. Following sound stress exposure, miR-19b expression levels decreased in male animals and increased in female animals (Figure 4).

**MOLECULAR:** Among initial pain/PTSD genes tested, the glutamate receptor 2A (*GRIN2A*) and Mineralocorticoid receptor (*NR3C2*) are direct targets of miR-19b (Figure 5). Many additional genes predicted to be targeted by miR-19b are in the circadian rhythm pathway (e.g. *RORA*, *CLOCK*, *PER2*, *OPN4*). Testing for miR-19b binding to these additional targets is underway.

## CONCLUSIONS

miR-19b expression influences the development of chronic widespread pain and PTSD after motor vehicle collision. Sex-dependent differences in miR-19b suggest that this miRNA may mediate sex differences in CWP/PTSD vulnerability after common traumatic events.

## REFERENCES

- McLean SA, Ullrich JC, Slade GD, Soward AC, Swor RA, Peak DA, Jones JS, Rathlev NK, Lee DC, Domeier RM, Hendry PL, Bortsov AV, Bair E. Incidence and predictors of neck and widespread pain after motor vehicle collision among US litigants and nonlitigants. *Pain* 2013.
- Wynne-Jones G, Jones GT, Wiles NJ, Silman AJ, Macfarlane GJ. Predicting new onset of widespread pain following a motor vehicle collision. *The Journal of rheumatology* 2006;33(5):968-974.
- Voik N, Paul ED, Haramati S, et al. MicroRNA-19b associates with Ago2 in the amygdala following chronic stress and regulates the adrenergic receptor beta 1. *The Journal of Neuroscience* 2014;34:15070-82.
- Castellano L, Giamas G, Jacob J, et al. The estrogen receptor- $\alpha$ -induced microRNA signature regulates itself and its transcriptional response. *Proceedings of the National Academy of Sciences* 2009;106:15732-7.
- Perkins JR, Lees J, Antunes-Martins A, et al. PainNetworks: A web-based resource for the visualisation of pain-related genes in the context of their network associations. *PAIN* 2013;154:2586. e1- e12.
- LaCroix-Fralish, M.L., Ledoux, J.B. and Mogil, J.S. The Pain Genes Database: an interactive web browser of pain-related transgenic knockout studies. *Pain*, 131:3.e1-3.e4, 2007.
- Maixner, William; Diatchenko, Luda; Hamilton, Michael; Fillingim, Roger; Gracely, Richard; Slade, Gary; Mogil, Jeffrey; Sleptsov, Alex. *Algnomics Pain Research Panel v2.0*. [http://www.algnomics.com/pdf/AlgnomicsPainPanel\\_v2\\_540.pdf](http://www.algnomics.com/pdf/AlgnomicsPainPanel_v2_540.pdf) Accessed 2016
- Khasar SG, Burkham J, Dina OA, Brown AS, Bogen O, Alessandri-Haber N, Green PG, Reichling DB, Levine JD. Stress induces a switch of intracellular signaling in sensory neurons in a model of generalized pain. *J Neuroscience*, 2008

Research reported in this publication was supported by an American Pain Society Future Leaders in Pain Grant, The Mayday Fund, and the National Institute of Arthritis and Musculoskeletal and Skin Diseases of the National Institutes of Health under Award Number R01-AR060852. The content is solely the responsibility of the authors and does not necessarily represent the official views of these funding agencies.