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Original article

**Effects of chronic ethanol consumption on brain GLP-1R gene expression in mice and humans**

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**Running title:**

GLP-1R: new potential biomarker for AUD

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**Abstract**

The glucagon-like peptide-1 receptor (GLP-1R) has emerged as a promising therapeutic option for alcohol use disorder (AUD), yet the underlying mechanisms and neurocircuitry involved remain unclear. This study aimed to analyze GLP-1R gene expression changes in brain regions associated with alcohol's effects, including the prefrontal cortex (PFC), nucleus accumbens (NAc), and hippocampus (HIP), in mice following 42 days of voluntary ethanol consumption (VEC; 10% v/v) and postmortem samples from 18 patients with AUD. Additionally, we examined the expression of OPRM1 (mu-opioid receptor) and BDNF (brain-derived neurotrophic factor), key targets related to alcohol intake and reward, in the NAc and HIP, respectively.

GLP-1R gene expression was significantly reduced in all brain regions of ethanol-exposed mice and AUD patients. These reductions paralleled decreased OPRM1 and BDNF expression in the NAc and HIP, respectively. Pearson and Spearman correlation analyses revealed no significant associations between gene expression and age, RIN, pH, postmortem interval (PMI), body mass index (BMI), smoking status, age of onset of alcohol use, or years of drinking.

In summary, chronic alcohol consumption in humans or mice was associated with decreased GLP-1R gene expression in brain regions involved in the reinforcing effects of ethanol. These findings open new avenues for further research into how this emerging receptor could serve as a potential biomarker and therapeutic target in AUD.

**Keywords:** postmortem study, mice, AUD, voluntary ethanol consumption, gene expression, GLP-1R.

## 1. Introduction

Alcohol use disorder (AUD) represents a complex psychiatric condition associated with elevated rates of morbidity and mortality on a global scale<sup>1</sup>. The World Health Organization reports that around 400 million individuals worldwide are affected by AUD<sup>2</sup>. Alcohol consumption accounts for about 3 million deaths each year and constitutes a leading cause of premature mortality among individuals aged 15 to 49. Despite this, treatment options remain limited, with only three medications approved by the Food and Drug Administration—namely, acamprosate, disulfiram, and naltrexone—and exhibit limited efficacy<sup>3</sup>. Therefore, there is an urgent need to find new pharmacological treatments that improve the clinical outcome of patients with AUD.

In this regard, preclinical and clinical data indicate that the glucagon-like peptide-1 (GLP-1) system, acting through its receptor (GLP-1R) as part of a gut–brain signaling pathway, plays a critical role in the neurobiology of addictive behaviors<sup>4,5</sup>. The GLP-1R is a class B G protein-coupled receptor that activates cAMP/PKA signaling as well as PI3K/Akt, MAPK/ERK and  $\beta$ -arrestin pathways<sup>6-9</sup>. Notably, it is widely distributed in the brain, including the nucleus accumbens (NAc), hippocampus (HIP), cortical regions, and ventral tegmental area, and is expressed across glutamatergic, GABAergic, and subsets of dopaminergic neurons<sup>10-13</sup>. This signaling and widespread distribution point out its potential to modulate alcohol reinforcing properties.

Specifically, recent studies have shown that GLP-1 receptor (GLP-1R) agonists reduce ethanol intake, motivation to consume ethanol, relapse drinking, and symptoms of abstinence in rodent models<sup>14-17</sup>. Notably, the reduction in alcohol intake caused by GLP-1R agonists is not entirely specific, as earlier studies have also observed simultaneous decreases in food and water intake<sup>18,19</sup>. However, recent studies show a reduction in ethanol intake without changing food or fluid consumption<sup>20-22</sup>. Early clinical studies have shown that GLP-1R agonists reduce alcohol intake in patients with AUD and comorbidities of obesity and type 2 diabetes<sup>23-25</sup>. Moreover, genetic variations in genes encoding for the GLP-1R have been associated with AUD and heavy

drinking<sup>26,27</sup>. Taken together, the evidence provided to date raises important questions about the therapeutic use of GLP-1R agonists in individuals with AUD who are not overweight or diabetic, highlighting the need to distinguish between direct effects on alcohol-related neurocircuitry and broader influences on energy balance and eating behaviors.

To attain a more comprehensive understanding of the interaction between GLP-1 and alcohol, further investigation is urged to examine the potential impact of alcohol on the endogenous GLP-1 system. In rodents, alcohol exposure altered GLP-1 signaling in brain reward regions, including the NAc<sup>28</sup> and the frontal lobe<sup>29</sup>. In humans, indirect evidence provided by neuroimaging and biomarker studies showed that chronic alcohol use alters brain circuits involving GLP-1 pathways<sup>26,30</sup>. However, postmortem brain studies specifically measuring GLP-1R expression after chronic alcohol use are scarce<sup>31</sup>.

In this study, we performed a comprehensive analysis of the impact of chronic alcohol consumption on GLP-1R gene expression within PFC, NAc, and HIP in both rodent models and patients diagnosed with AUD. Furthermore, we conducted additional examinations of two pivotal markers associated with alcohol dependence: the mu opioid receptor (OPRM1) in the NAc and brain-derived neurotrophic factor (BDNF) in the HIP. OPRM1, which encodes the mu opioid receptor, has been consistently associated with alcohol reward, craving, and treatment response, making it one of the most studied candidate genes in the context of AUD<sup>32-34</sup>. Similarly, BDNF plays a crucial role in synaptic plasticity and neuroadaptation processes underlying alcohol dependence and relapse, and altered BDNF signaling has been reported in both clinical and preclinical models of AUD<sup>35-37</sup>. The HIP was prioritized for BDNF, given its critical role in learning, memory, and neuroplasticity—processes directly affected by chronic alcohol exposure<sup>38,39</sup>. On the other hand, OPRM1 expression was examined in the NAc due to its well-established involvement in reward processing and alcohol reinforcement, where mu-opioid receptor signaling is particularly relevant<sup>40,41</sup>. While both genes are functionally relevant in additional brain regions,

the selection was guided by their strongest mechanistic and experimental links with the HIP and NAc, respectively.

## **2. Materials and methods**

### **2.1 Animals**

Male C57BL/6J mice from Charles River in Lille, France, aged six weeks and weighing 20- 25 grams, were housed in groups of five in enclosures (40 × 25 × 22 cm) under controlled conditions (temperature  $21 \pm 2^{\circ}\text{C}$ , humidity  $60 \pm 10\%$ , 12-hour light/dark cycle from 08:00 to 20:00). Behavioral tests started one week after acclimation. All procedures complied with Spanish Royal Decree 1201/2005, Law 32/2007, and EU Directive 2010/2010/E.

### **2.2. Voluntary Ethanol Consumption in a Two-Bottle Choice Paradigm (VEC)**

This paradigm was carried out according to a protocol previously described<sup>42,43</sup>. All mice were housed individually in cages with two water bottles to facilitate acclimatization and reduce stress. After a week, the two-bottle choice paradigm began: one bottle contained water, and the other contained a solution of increasing ethanol concentrations (2%, 4%, 6%, 8%, 10%) or water (controls), administered every 3 days. Once the ethanol concentration reached 10% for three consecutive days, consumption and preference were measured over a period of six weeks. Solutions were prepared and changed daily between 18:00 and 19:00, with bottles being alternated to avoid bias. Daily intake was recorded, and ethanol intake was calculated in grams per kilogram body weight per day (g/kg/day). The ethanol preference ratio was calculated as ethanol intake divided by total intake.

### **2.3. Gene expression studies by real-time PCR (qPCR) in mice**

Mice were sacrificed at the end of VEC. Briefly, brains were removed from the skull, frozen on dry ice, and stored at -80°C until the testing day. Brain sections measuring 500 µm were cut at various levels, including the regions of interest (PFC, NAc and HIP), according to the Paxinos and Franklin atlas<sup>44</sup>. The sections were then mounted on slides and stored at -80°C. A section from each level was dissected according to the method outlined by Palkovits<sup>45</sup>. Total RNA was isolated from brain punctures using Biozol® Total RNA Extraction Reagent (Bioflux, Inilab, Madrid, Spain) in the PFC, NAc and HIP regions. Following DNase digestion, reverse transcription was performed to generate complementary DNA (cDNA) according to the manufacturer's instructions (High-Capacity cDNA Reverse Transcription Kit with RNase Inhibitor, Applied Biosystems, Madrid, Spain). Quantitative analyses of relative gene expression for GLP-1R (Mm00445292\_m1), OPRM1(Mm01188089\_m1), and BDNF (Mm00432069\_m1) were conducted using the Taqman Gene Expression Assay (Applied Biosystems, Madrid, Spain), which uses a specific fluorescent dye for double-stranded DNA. These analyses were performed on the StepOnePlus™ Real-Time PCR System (Applied Biosystems, Madrid, Spain). The reference gene employed was 18S rRNA (Mm03928990\_g1), detected with Taqman ribosomal RNA control reagents. Briefly, data for each target gene were normalized to the endogenous reference gene, and changes in target gene abundance were determined using the  $2^{-\Delta\Delta CT}$  method

<sup>46</sup>.

## 2.4. Human samples

Postmortem frozen brain samples obtained from patients with AUD (n=18) and their corresponding control subjects (C) (n=18) were kindly provided by the New South Wales Tissue Resource Centre (NSWBTRC) at the University of Sydney in Australia. This brain bank nation has a significant population of individuals experiencing alcohol dependence without the co-abuse of other substances. Thus, this population with AUD of Australia represents a unique resource for



researchers exploring the long-term effects of alcohol on the brain. The brain regions available were the prefrontal cortex (PFC) (Brodmann area 9), NAc, and HIP.

The patients met the criteria established in the Diagnostic and Statistical Manual of Mental Disorders, 4th edition (DSM-IV) for AUD. Details on the methods used at the NSWBTTC to collect demographic, alcohol-related, and other behavioral data have been previously reported <sup>47</sup>. Mean age of beginning drinking is  $19.9 \pm 4.5$  years, and years of consumption are  $35.9 \pm 8.9$ . Additional demographic and postmortem data for all subjects included in the present study are described in Table 1. None of the AUD cases were receiving treatment at the time of death.

Patients did not present any infectious disorders, including Hepatitis B and C, HIV and AIDS, or Creutzfeldt-Jakob disease.

All participants were Caucasian males and were matched as closely as possible regarding age (AUD:  $55.8 \pm 9$ ; C:  $56.3 \pm 9.4$ ), postmortem interval (AUD:  $39.7 \pm 16.9$  h; C:  $31.8 \pm 13.2$  h) and pH (AUD:  $6.6 \pm 0.2$ , C:  $6.7 \pm 0.2$ ).

## 2.5. RNA integrity number (RIN) evaluation

RNA quality in human samples is crucial for reliable qPCR results. Total RNA was isolated from PFC, NAc, and HIP tissues using TRI Reagent (Applied Biosystems). RNA integrity was assessed with the 2100 Bioanalyzer, which detects 18S and 28S ribosomal bands. The ratio of 28S to 18S yields the RNA Integrity Number (RIN), which ranges from 1 to 10, with lower values indicating greater RNA degradation. Electropherograms and gel images of RNA from control and experimental subjects (Fig. 1) showed a mean RIN of about 7 (PFC C:  $6.85 \pm 0.105$ , AUD:  $6.905 \pm 0.125$ ; NAc C:  $6.876 \pm 0.079$ , AUD:  $6.829 \pm 0.105$ ; HIP C:  $6.867 \pm 0.009$ , AUD:  $6.861 \pm 0.014$ ), indicating good RNA quality for gene expression analysis.

## 2.6. Gene expression studies by real-time PCR (qPCR) in humans

Relative gene expression analyses of GLP-1R, OPRM1 and BDNF in the PFC, NAc, and HIP were conducted in A and C following the same methodology as previously described for mice using the TaqMan Gene Expression Assays (GLP-1R: Hs00157705\_m1, OPRM1: Hs1053957\_m1, BDNF: Hs02718934\_s1). Two reference genes, cyclophilin (PPIA, Hs99999904\_m1) and synaptophysin (SYP, Hs00300531\_m1), were employed to ensure the validity and reproducibility of the results. For each sample, the results are presented as the average derived from each reference gene.

The number of samples analyzed in the human qPCR studies varies based on the number of samples available.

## **2.7. Statistical analysis**

Normality of numeric variables was assessed using the Shapiro–Wilk test (given the sample size below 50 patients). For normally distributed variables, results are presented as mean  $\pm$  standard deviation, and comparisons between groups were performed using the Student's t-test. For non-normally distributed variables, results are presented as median (25th–75th percentile), and comparisons were carried out using the Mann–Whitney U test. Categorical variables are expressed as absolute frequencies and percentages. A p-value  $< 0.05$  was considered statistically significant.

Two-way ANOVA with repeated measures followed by Student-Newman-Keuls was used to analyze body weight in ethanol-exposed mice and their corresponding control group through the VEC.

### **2.7.1. Correlation analysis**

For normally distributed numeric variables, correlations were assessed using Pearson's correlation coefficient, while Spearman's rank correlation coefficient was applied for non-normally distributed variables.

### 2.7.2. Linear Regression

To analyze gene expression, linear regression models were developed to analyze gene expression, incorporating globally significant variables identified through statistical significance ( $p < 0.20$ ) and correlation analyses. Rather than performing separate regressions for each biomarker, all variables that showed significance in at least one marker were included together in a unified model. Three models were tested:

1. Model 1 included only the group variable.
2. Model 2 included age, group, clinical history, cause of death, smoking history and BMI.
3. Model 3 included the same variables as Model 2, with the addition of an age  $\times$  group interaction term.

All statistical analyses were conducted using R (version 4.5.0), employing the following packages: *dplyr* (1.1.4), *readr* (2.1.5), *tidyr* (1.3.1), *gtsummary* (2.3.0), *ggplot2* (3.5.2), and *ggpubr* (0.6.1). SigmaPlot 11 software (Systat Software Inc., Chicago, IL, USA) was used to create figures. The code used in this study is available in the [GitHub](https://github.com/Samantao93/Biomarkers_AUC) repository ([https://github.com/Samantao93/Biomarkers\\_AUC](https://github.com/Samantao93/Biomarkers_AUC)).

## 3. Results

### 3.1. Voluntary Ethanol Consumption (VEC) of C57BL6J male mice

As illustrated in Figure 2A, animals subjected to VEC demonstrated ethanol consumption levels of approximately 5 g/kg per day, along with an ethanol consumption preference ranging from 50% to 60% (Figure 2B).

A two-way ANOVA with repeated measures with group as a between-subject factor and week as a within-subject factor revealed no significant main effect of group ( $F_{(1, 18)} = 0.61$ ,  $p = 0.446$ ) and no significant group  $\times$  week interaction ( $F_{(5, 90)} = 0.98$ ,  $p = 0.436$ ), indicating that body weights did not differ between groups during VEC. As expected, there was a significant main effect of week ( $F_{(5, 90)} = 337.49$ ,  $p < 0.001$ ), reflecting normal weight gain over time (Figure S1).

### **3.2. GLP-1R, OPRM1 and BDNF gene expression in the PFC, NAc and HIP of C57BL/6J male mice subjected to VEC**

GLP-1R gene expression decreased in the PFC (Figure 3A; Student t-test:  $t = 2.351$ , 16df,  $p = 0.032$ ) ( $n = 8-10$ /group), NAc (Figure 3B; Student t-test:  $t = 2.219$ , 17df,  $p = 0.040$ ) ( $n = 9-10$ /group), and HIP (Figure 3C; Student t-test:  $t = 2.851$ , 15df,  $p = 0.012$ ) ( $n = 7-10$ /group) of mice exposed to VEC in comparison to the control group.

Analysis of OPRM1 gene expression showed a significant reduction in the NAc (Figure 3D; Mann–Whitney U test;  $U = 89$ ,  $p = 0.004$ ) ( $n = 10-11$ /group) of mice exposed to ethanol compared to the control group.

Besides, a significant reduction of BDNF was also found in the HIP (Figure 3D; Student t-test:  $t = 4.646$ , 15 df,  $p < 0.001$ ) ( $n = 7-10$ /group) of mice exposed to ethanol compared to their control group.

Correlation analyses were conducted to examine the relationship between alcohol intake and the expression of GLP-1R, OPRM1 and BDNF across the different brain regions in the rodent model. No statistically significant correlations were observed. A moderate, non-significant correlation was found between alcohol intake and GLP-1R in the HIP (Spearman's  $\rho = 0.59$ ,  $p = 0.07$ ). Correlation coefficients for all markers are presented in Table S1 and the overall pattern is illustrated in Figure S2 (correlation heatmap).

### 3.3. GLP-1R, OPRM1 and BDNF gene expression in the PFC, NAc and HIP of humans with AUD

Notably, GLP-1R gene expression was reduced in all the brain areas analyzed, the PFC (Figure 4A; Mann–Whitney U test;  $U = 235$ ,  $p < 0.001$ ) ( $n=14-18$ /group), NAc (Figure 4B; Student t-test:  $t = 3.208$ ,  $29df$ ,  $p=0.003$ ) ( $n=15-16$ /group) and HIP (Figure 4C; Student t-test:  $t = 4.998$ ,  $30df$ ,  $p<0.001$ ) ( $n=14-18$ /group), of AUD in comparison to C.

OPRM1 gene expression revealed a significant reduction in the NAc (Figure 4D; Student t-test:  $t = 2.801$ ,  $30df$ ,  $p=0.009$ ) ( $n=15-17$ /group) in AUD compared to C. Similarly, the analysis of BDNF gene expression revealed a significant reduction in the HIP (Figure 4E; Student t-test:  $t = 2.895$ ,  $30df$ ,  $p=0.007$ ) ( $n=14-18$ /group) in AUD compared to C.

Pearson's and Spearman product–moment correlation analyses revealed no significant associations between GLP-1R, OPRM1, and BDNF gene expression and age, postmortem interval (PMI), pH, RNA integrity number (RIN). Only a small, significant correlation was observed between GLP-1R in the PFC and PMI ( $r=0.71$ ,  $p<0.01$ ).

For BMI, Pearson's correlations were applied for all genes except GLP-1R in the PFC, where Spearman's method was used due to non-normal distribution. Moreover, Spearman's correlation analyses showed no significant associations between gene expression levels and either age of onset or years of alcohol consumption for GLP-1R, OPRM1, and BDNF, in cases A (Table 2).

Pairwise correlation analyses between GLP-1R, OPRM1, and BDNF gene expression within each brain region and in each group revealed no statistically significant correlations in the AUD group (Figure S3, panel A). Interestingly, in the C group, significant correlations were found between GLP-1R expression in the PFC and BDNF expression in the HIP ( $r = 0.60$ ,  $p < 0.05$ ), and between GLP-1R expression in the NAc and BDNF expression in the HIP ( $r = -0.58$ ,  $p < 0.05$ ) (Figure S3, panel B). Other correlations were weaker and not statistically significant.

Linear regression analyses were performed for each brain region. Adding group and significant descriptive variables increased the explained variance in several models. Inclusion of the age x

group interaction term did not materially improve model fit, except for GLP-1R expression in the NAc, where the explained variance showed a modest increase to 36%, which remains relatively low, accounting for less than half of the total variance. Full model results are available in Table S2.

#### 4. Discussion

This study further supports the strong link between alcohol exposure and the GLP-1R. The following evidence supports this finding: 1) chronic ethanol exposure reduces GLP-1R gene expression in the PFC, NAc, and HIP, brain areas closely associated with alcohol's reinforcing effects, in mice. 2) Interestingly, human postmortem studies revealed a significant reduction of the GLP-1R in these brain areas in individuals with AUD. 3) In both samples, GLP-1R alterations align with the changes found in OPRM-1 and BDNF in NAc and HIP, respectively.

The GLP-1R is widely expressed across the brain, including reward processing areas such as the VTA and NAc<sup>10,48-50</sup>. The cumulative evidence gathered in recent years indicates that the GLP-1R plays a significant role in modulating dopaminergic responses associated with alcohol within these brain regions<sup>28,51,52</sup>. This has led to the exploration of the potential efficacy of GLP-1R agonists in reducing alcohol consumption, with promising results in animal models<sup>14,16,53-56</sup> and human clinical studies<sup>23-25</sup>.

The results revealed that the expression of GLP-1R was significantly decreased in all the brain regions analyzed (NAc, HIP and PFC) in male mice exposed to chronic ethanol consumption for 45 days, with a mean ethanol intake of 5 g/Kg body weight per day. Few previous studies have examined the impact of ethanol on GLP-1R, finding differences depending on the brain region analyzed, the type of alcohol exposure (acute vs. chronic), and the sex of the rodent. In these studies, no alterations in GLP-1R expression were detected in the PFC, VTA, amygdala, HIP, or striatum after ethanol exposure<sup>28</sup>. An increase of GLP-1R was found in the NAc and lateral septum of high alcohol-consuming rats in comparison to low alcohol-consuming rats<sup>21,28</sup>.

Discrepancies between our results and those previously published may be related to the species used (mice vs. rats), the chronic ethanol consumption paradigm (two-bottle choice vs. intermittent access), or the duration of ethanol intake (45 days vs. 12 weeks). Our findings, therefore, expand upon prior work by examining multiple brain regions in mice under VEC, providing additional evidence for GLP-1R alterations associated with long-term ethanol exposure.

For instance, our study demonstrated a significant reduction in GLP-1R gene expression across corticolimbic brain regions in individuals with AUD. Specifically, we observed a downregulation of GLP-1R in the HIP, NAc, and PFC of patients with a long-term history of alcohol use. These results indicate similar changes in both types of samples (mice and humans) across all the analyzed areas.

Only one previous study examined changes in human postmortem brain tissues of male individuals diagnosed with severe AUD according to DSM-5, who also smoked<sup>31</sup>. In this study, an increase in GLP-1R was found in the HIP of individuals with AUD, with no differences in the PFC or NAc. The discrepancy in the changes of GLP-1R gene expression in the brain between both studies may be related to differences in alcohol patterns and consumption, the years of alcohol consumption, and/or the pharmacological treatment, among other potential factors.

Our findings support and expand upon previous preclinical evidence indicating that GLP-1R signaling influences alcohol-related behaviors. Animal studies have demonstrated that central activation of GLP-1R decreases alcohol intake and alcohol-seeking behaviors by lowering dopamine release in the NAc<sup>15,53</sup>. In this context, the reduced GLP-1R expression observed here may reflect a disturbance in endogenous inhibitory mechanisms regulating alcohol reward, which could potentially contribute to compulsive alcohol use. However, as we did not assess GLP-1R coupling or cell-type-specific expression, this interpretation should be considered hypothesis-generating, and future studies using functional and cellular approaches will be required to clarify the underlying mechanisms.

In the HIP and PFC, GLP-1R signaling contributes to neuroprotection and executive function<sup>57-61</sup>. The downregulation of GLP-1R gene expression in these brain regions may, at least in part, underlie alcohol-related cognitive deficits and impairments in decision-making and inhibitory control. Some human postmortem studies suggested a compensatory increase in brain GLP-1R expression<sup>31</sup>, however, our results may reflect later-stage neuroadaptive or degenerative changes.

Interestingly, this study revealed that changes in GLP-1R are consistent with those found in two key neurobiological markers of alcohol addiction, the OPRM-1 and BDNF in the NAc and HIP. The mu opioid receptor (encoded by OPRM1) plays a central role in alcohol reward by modulating the hedonic and motivational effects of alcohol through the mesocorticolimbic circuit<sup>62-64</sup>. In our study, we observed reduced OPRM1 in the NAc in mice subjected to chronic ethanol exposure and in patients with AUD. Previous studies on this topic, however, reported heterogeneous findings: while several studies have described decreased OPRM1 in the NAc of mice exposed to ethanol<sup>65-69</sup> and in patients with AUD<sup>70</sup>, others have reported increased expression or have focused on functional alterations (e.g., receptor coupling, signaling) rather than the gene expression per se<sup>67,68</sup>. This variability likely reflects the complex regulation of the mu opioid receptor, involving transcriptional, translational, and functional mechanisms. The reduced OPRM1 expression observed in our samples may reflect either receptor downregulation following chronic stimulation or neuroadaptive loss of opioid tone. Notably, lower OPRM1 expression has been associated with blunted reward sensitivity and an altered response to naltrexone treatment<sup>71</sup>.

Interestingly, the analysis of BDNF gene expression, closely related to cognitive processes affected by alcohol consumption<sup>72-76</sup>, revealed a significant reduction in mice and patients with AUD. These findings are consistent with prior studies showing that chronic alcohol exposure suppresses BDNF signaling, contributing to cognitive impairments and increased vulnerability to consume alcohol<sup>77-80</sup>. Despite further research is needed, the concurrent downregulation of both



BDNF and GLP-1R in the HIP may represent a convergent mechanism leading to hippocampal dysfunction in AUD.

Correlation analysis of gene-gene interactions within each brain area and across groups revealed distinct patterns between controls and AUD. In the control group, a positive correlation between GLP-1R expression in the PFC and BDNF expression in the HIP was observed, which may reflect a physiological interaction between cortical GLP-1 signaling and hippocampal neurotrophic pathways. In the AUD group, this relationship showed an inverse, although non-significant, trend, which could indicate a possible alteration in these cross-regional interactions in the context of chronic alcohol exposure. Although these findings should be interpreted cautiously, they suggest that the functional coupling between GLP-1 and BDNF pathways may differ between groups.

These differences may reflect alterations in the functional coupling between GLP-1 and BDNF pathways. Previous experimental evidence has suggested that GLP-1 signaling can influence BDNF expression and activity through intracellular pathways such as cAMP/CREB, which are involved in neuronal survival, synaptic plasticity, and neurogenesis<sup>81-84</sup>. For example, agonists of the GLP-1 receptor have been shown to upregulate BDNF and its downstream signaling cascades in neuronal cultures and animal models, contributing to neuroprotection and cognitive improvement in various pathological contexts, including models of neurodegeneration and psychiatric disorders<sup>85,86</sup>. Furthermore, GLP-1 and BDNF have been proposed to act synergistically to support cortical–hippocampal communication and regulate energy balance and stress responses in the brain<sup>87-89</sup>.

Although the precise mechanisms underlying these interactions remain to be fully elucidated, the existing literature provides a biologically plausible framework linking GLP-1 signaling and BDNF pathways. The differences in gene–gene correlations observed between controls and individuals with AUD in the present study could reflect adaptive or maladaptive changes in these neurobiological systems associated with chronic alcohol exposure.

In summary, our results showed that chronic alcohol consumption, whether in humans or murine models, reduces GLP-1R gene expression in brain areas closely related to the reinforcing properties of ethanol. The simultaneous decrease in GLP-1R, OPRM-1, and BDNF across key mesocorticolimbic brain regions underscores a multifaceted neurobiological deficit in AUD. This finding opens new alternatives for further research into how this emerging receptor, GLP-1R, can be helpful as a potential biomarker for AUD, further supporting its therapeutic potential in this drug use disorder.

### **Limitations of the study**

This study presents limitations. First, it was only conducted in males, suggesting that future studies should also assess potential alterations in GLP-1R gene expression in female subjects. Second, we measured gene expression but did not assess protein levels or receptor function. Finally, assessment of GLP-1R in other patterns of consumption (e.g., binge drinking) and ethanol relapse and abstinence will further contribute to characterizing the role of GLP-1R in AUD.

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### **Data availability**

The data generated during the current study are available from the corresponding author upon reasonable request.

**Author Contributions**

ABT performed gene expression analyses, acquired the data, assisted with data interpretation, and drafted the manuscript. MSGG assisted with data interpretation and formal analysis, and contributed to writing the original draft as well as reviewing and editing the final version. SOM conducted the linear regression and correlation analyses and provided statistical support. JM contributed to the study concept and design, and reviewed and edited the final version of the manuscript. All authors reviewed and approved the final version of the manuscript.

**Ethics approval and consent to participate**

All methods were performed in accordance with the relevant guidelines and regulations.

All animal procedures were approved by the Ethics and Research Integrity Committee of Miguel Hernández University (approval number: UMH.IN.JM.01.21) and were conducted in accordance with institutional and national guidelines for the care and use of laboratory animals.

Human samples were obtained from the New South Wales Tissue Resource Centre (NSWBTRC) at the University of Sydney, Australia. The use of these samples was approved by the Ethics and Research Integrity Committee of Miguel Hernández University (approval number: IN-JM-001-11), in accordance with the biobank's governance procedures.

Written informed consent was obtained from all participants prior to sample collection.

**Conflict of interest**

The authors declare that they have no conflict of interest.

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### Figure and legends

**Figure 1. Total RNA integrity number (RIN) evaluation in the prefrontal cortex (PFC), nucleus accumbens (NAc) and hippocampus (HIP) of AUD subjects (n=18) and controls (n=18).** Representative electropherograms and gel images of the mean RIN value from LPFC (A), NAc (B) and HIP (C) brain regions. (D) The grey box contains the global mean value from all the studied samples in the RIN values summary table.

**Figure 2. Voluntary ethanol consumption in male C57Bl/6J mice.** A) Ethanol intake is measured in g/kg/day, with data collected on the volume consumed every 24 hours. B) The preference for ethanol intake is calculated as the ratio of ethanol consumption to total intake [ethanol preference = ethanol consumption/(ethanol consumption + water consumption)]. The dots indicate the means, with vertical lines representing the  $\pm$ SEM for each parameter assessed.

**Figure 3. Relative gene expression of GLP-1R, OPRM1 and BDNF in mesocorticolimbic brain areas of mice exposed to chronic voluntary ethanol consumption.** A) Changes in the relative gene expression of GLP-1R in the prefrontal cortex (PFC), B) nucleus accumbens (NAc), and C) hippocampus (HIP) of mice exposed to the two-bottle choice test. D) Changes in the relative gene expression of OPRM1 in the NAc of mice exposed to the two-bottle choice test. E)

Changes in the relative gene expression of BDNF in the HIP of mice exposed to the two-bottle choice test. The dots indicate the means, with vertical lines representing the  $\pm$ SEM for each parameter assessed. \*Indicates values from mice exposed to VEC that significantly differ from the vehicle group.

**Figure 4. Relative gene expression of GLP-1R, OPRM1 and BDNF in mesocorticolimbic brain areas of patients with AUD.** A) Changes in the relative gene expression of GLP-1R in the prefrontal cortex (PFC), B) nucleus accumbens (NAc), and C) hippocampus (HIP) of individuals with AUD. D) Changes in the relative gene expression of OPRM1 in the NAc of individuals with AUD. E) Changes in the relative gene expression of BDNF in the HIP of individuals with AUD. The dots indicate the means, with vertical lines representing the  $\pm$ SEM for each parameter assessed. \*Indicates values from AUD patients that significantly differ from controls.

**Table 1. Demographic and clinical data of patients with AUD and their corresponding control group**

Subject	Age	PMI (hours)	Brain pH	Began drinking	Drinking years	COD category	Clinical History	Smoking	BMI
AUD1	67	48	6.40	25	42	Respiratory/Toxicity	None	Current	21.5
AUD2	41	54	6.70	25	16	Neurological	None	Current	21.7
AUD3	64	39	6.76	25	39	Toxicity	Depression	Current	20.3
AUD4	45	18.5	6.57	14	31	Respiratory	Depression	Current	29.1
AUD5	65	7	6.47	25	40	Stroke	Depression	Current	20
AUD6	61	59	6.57	16	45	Cardiac	Depression	Current	25.2
AUD7	49	44	6.41	16	33	Cardiac	None	Current	25.8
AUD8	49	16	6.19	14	35	Cardiac	None	Current	32.7
AUD9	62	40	6.59	25	37	Cardiac	Depression	Ex-smoker	34.6
AUD10	44	59	6.87	18	26	Cardiac	Depression	Current	24.5
AUD11	60	28	6.48	17	43	Infection	None	Current	42.3
AUD12	50	34.5	6.93	16	34	Respiratory/Toxicity	Depression	Ex-smoker	28.2
AUD13	70	62	6.82	25	45	Cardiac	Depression	Current	26.8
AUD14	43	29	6.29	25	18	Hepatic/Blood Loss	None	Current	31.8
AUD15	58	21.5	6.65	20	38	Infection	None	Current	23.9
AUD16	55	17	6.85	25	30	Respiratory	Depression	Never	29.7
AUD17	58	44.5	6.47	15	43	Cardiac	None	Current	19.9

<b>AUD18</b>	63	28	6.89	19	44	Respiratory	None	Current	19.2
<b>C1</b>	50	30	6.37	-	-	Cardiac	None	Current	28.2
<b>C2</b>	59	40	6.53	-	-	Cardiac	None	Ex-smoker	25.8
<b>C3</b>	55	12	6.39	-	-	Cardiac	None	Never	28.7
<b>C4</b>	50	40	6.87	-	-	Cardiac	None	Current	28.6
<b>C5</b>	69	52	6.95	-	-	Cardiac	None	Never	21.6
<b>C6</b>	67	25	6.70	-	-	Cardiac	None	Ex-smoker	32.4
<b>C7</b>	48	17	6.62	-	-	Cardiac	None	Never	33.2
<b>C8</b>	59	28	6.77	-	-	Cardiac	None	Current	35
<b>C9</b>	64	41	6.73	-	-	Cardiac	None	Never	25.3
<b>C10</b>	47	27	6.66	-	-	Cardiac	None	Current	29.2
<b>C11</b>	61	22	6.41	-	-	Cardiac	None	Current	29.9
<b>C12</b>	61	30	6.69	-	-	Cardiac	None	Never	34.5
<b>C13</b>	66	32	6.66	-	-	Cardiac	None	Never	33.7
<b>C14</b>	53	26	6.36	-	-	Cardiac	None	Ex-smoker	29.6
<b>C15</b>	66	63	6.91	-	-	Cardiac	None	Never	27.5
<b>C16</b>	62	46	6.95	-	-	Cardiac	None	Ex-smoker	32.8
<b>C17</b>	37	14.5	6.46	-	-	Cardiac	None	Never	24.7
<b>C18</b>	40	27	6.79	-	-	Cardiac	None	Never	34.9

AUD: alcohol use disorder; C: controls; PMI: postmortem interval; COD: cause of death.

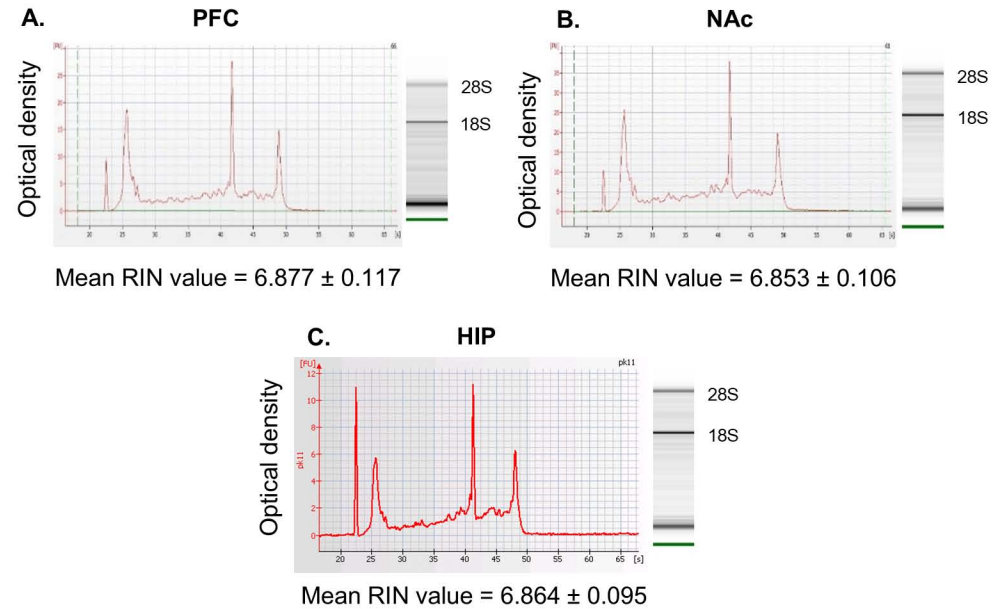
**Table 2. Pearson's and Spearman's rank correlation coefficients for GLP-1R, OPRM1, BDNF gene expressions and age, PMI, pH, RIN, Began Drinking, Drinking years for controls and AUD cases**

			Age	PMI	pH	RIN	BMI	Began Drinking	Drinking Years
<b>PFC</b>	<b>C</b>	<b>GLP-1R</b>	r= -0.07** p= 0.82	r= -0.28** p= 0.34	r= -0.18** p= 0.55	r= -0.2** p= 0.5	r=0.02** p=0.95		
	<b>AUD</b>	<b>GLP-1R</b>	r= 0.12** p= 0.62	<b>r= 0.71**</b> <b>p= &lt;0.01</b>	r= -0.32** p= 0.19	r= -0.25** p= 0.31	r=0.04** p=0.87	r= -0.1** p= 0.7	r= 0.33** p=0.19
<b>NAC</b>	<b>C</b>	<b>GLP-1R</b>	r= 0.41 p= 0.14	r= 0.14 p= 0.64	r= 0.06 p= 0.85	r= -0.26 p= 0.36	r=-0.10 p=0.74		
	<b>AUD</b>	<b>GLP-1R</b>	r= -0.14 p= 0.59	r= 0.26 p= 0.33	r= 0.29 p= 0.28	r= -0.39 p= 0.14	r=-0.20 p=0.45	r= -0.03** p= 0.91	r= -0.07** p= 0.79
	<b>C</b>	<b>OPRM1</b>	r= -0.41 p= 0.11	r= -0.09 p= 0.73	r= 0.01 p= 0.96	r= 0.19 p= 0.47	r=-0.15 p=0.59		
	<b>AUD</b>	<b>OPMR1</b>	r= -0.21 p= 0.46	r= 0.23 p= 0.41	r= -0.13 p= 0.65	r= 0.26 p= 0.34	r= 0.01 p=0.96	r= 0.27** p= 0.33	r= -0.34** p=0.21
<b>HIP</b>	<b>C</b>	<b>GLP-1R</b>	r= 0.48 p= 0.08	r= 0.26 p= 0.37	r= 0.42 p= 0.13	r= 0.42 p= 0.14	r=0.31 p=0.27		
	<b>AUD</b>	<b>GLP-1R</b>	r= 0.15 p= 0.54	r= -0.11 p= 0.67	r= 0.45 p= 0.06	r= -0.24 p= 0.34	r=-0.27 p=0.28	r= 0.28** p= 0.25	r=0.01** p= 0.97
	<b>C</b>	<b>BDNF</b>	r= -0.47 p= 0.09	r= -0.08 p= 0.79	r= 0.03 p= 0.92	r= 0.12 p= 0.68	r=0.09 p=0.77		
	<b>AUD</b>	<b>BDNF</b>	r= -0.04 p=0.87	r= -0.14 p= 0.57	r= -0.17 p= 0.51	r= -0.28 p= 0.26	r=0.02 p=0.92	r= 0.27** p= 0.29	r= -0.24** p= 0.33

C: controls; AUD: alcohol use disorder; GLP-1R: glucagon-like peptide-1 receptor; PMI: postmortem interval; RIN: RNA integrity number.

For normally distributed numeric variables, correlations were assessed using Pearson's correlation coefficient, while Spearman's rank correlation coefficient was applied for non-normally distributed variables (\*\*).

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**D. RIN values summary (mean  $\pm$  SEM)**

	DLPFC	NAc	HIP	Mean
CONTROL	$6.850 \pm 0.105$	$6.876 \pm 0.079$	$6.867 \pm 0.081$	$6.865 \pm 0.009$
AUD	$6.905 \pm 0.125$	$6.829 \pm 0.127$	$6.861 \pm 0.110$	$6.864 \pm 0.014$
Mean	$6.877 \pm 0.117$	$6.853 \pm 0.106$	$6.864 \pm 0.095$	

