



## Gene expression changes in conjunctival cells associated with contact lens wear and discomfort

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### ABSTRACT

**Purpose:** This study aimed to analyze the differences in the expression of pain-related genes in conjunctival epithelial cells among symptomatic contact lens (CL) wearers (SCLWs), asymptomatic CL wearers (ACLWs), and non-CL wearers (non-CLWs).

**Methods:** For this study, 60 participants (20 non-CLWs, 40 CLWs) were enrolled. The CLW group comprised 20 ACLWs and 20 SCLWs according to the Contact Lens Dry Eye Questionnaire short form<sup>®</sup>. Conjunctival cells were collected using impression cytology, and RNA was isolated and used to determine the expression levels of 85 human genes involved in neuropathic and inflammatory pain. The effects of CL wear and discomfort were evaluated using mixed-effects ANOVA with partially nested fixed-effects model. Gene set enrichment analysis was performed to assign biological meaning to sets of differentially expressed genes.

**Results:** Six genes (*CD200*, *EDN1*, *GRIN1*, *PTGS1*, *P2RX7*, and *TNF*) were significantly upregulated in CLWs compared to non-CLWs. Eleven genes (*ADORA1*, *BDKRB1*, *CACNA1B*, *DBH*, *GRIN1*, *GRM1*, *HTR1A*, *PDYN*, *PTGS1*, *P2RX3*, and *TNF*) were downregulated in SCLWs compared to ACLWs. These genes were mainly related to pain, synaptic transmission and signaling, ion transport, calcium transport and concentration, and cell-cell signaling.

**Conclusions:** CL wear modified the expression of pain- and inflammation-related genes in conjunctival epithelial cells. These changes may be in part, along with other mechanisms, responsible for CL discomfort in SCLWs.

### 1. Introduction

Contact lenses (CL) can effectively correct visual alterations, but many users cease their use, CL discomfort (CLD) being the main reason [1]. CLD is defined as “a condition characterized by episodic or persistent adverse ocular sensations related to lens wear, either with or without visual disturbance, resulting from reduced compatibility between the contact lens and the ocular environment, which can lead to decreased wearing time and discontinuation of contact lens wear” [2]. However, clear evidence of a correlation between clinical signs and CLD symptoms is lacking [3,4]. Additionally, the cause of CLD is not clear, causing a significant impact on CL wearers and clinicians.

Several studies have reported changes in cytokine, growth factor, and inflammatory mediator levels in tear fluid of CL wearers [5–10] and with CLD [11–13]. These changes may suggest the presence of an underlying inflammation on the ocular surface during CL wear and that this may be a potential cause of CLD. However, contradictory results have been reported. On the one hand, some studies analyzing a considerable number of inflammatory molecules in tears found no differences between asymptomatic and symptomatic CL wearers [10,14]. On the other hand, an upregulation of nerve growth factor (NGF), transforming growth factor- $\beta$ , leukotriene B4 and interleukin (IL)-17 A has been detected in tears of CL wearers with CLD [11–13]. Moreover, conjunctival cells have altered inflammatory gene expression related to ocular surface diseases, e.g., graft-versus-host disease [15], Sjögren's

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## Abbreviations

ACLW	asymptomatic contact lens wearer	HP	Human Phenotype Ontology
CCLRU	Cornea and Contact Lens Research Unit	HPA	Human Protein Atlas
CIC	conjunctival impression cytology	IL	interleukin
CL	contact lens	KEGG	Kyoto Encyclopedia of Genes and Genomes
CLD	contact lens discomfort	MIRNA	miRTarBase
CLDEQ	Contact Lens Dry Eye Questionnaire	OSDI	Ocular Surface Disease Index
CLW	contact lens wearer	PGE2	prostaglandin E2
DED	dry eye disease	REAC	Reactome
DEG	differentially expressed gene	RT-PCR	real-time PCR
GO	Gene Ontology	SCLW	symptomatic contact lens wearer
GO:BP	GO biological process	TBUT	tear film breakup time
GO:CC	GO cellular component	TF	Transfac TRANSCRIPTION FACTOR database
GO:MF	GO molecular function	TNF	tumor necrosis factor
		WP	WikiPathways

syndrome with aqueous tear deficiency [16], and dry eye disease (DED) [17]. These findings highlight the need to identify molecular biomarkers to determine the origin or presence of CLD.

In an exploratory study of our research group [18] we found differences in the expression of several pain-related genes in conjunctival epithelial cells between symptomatic CL wearers (SCLWs), asymptomatic CL wearers (ACLWs) and non-CL wearers (non-CLWs). We identified altered gene expression associated with hydrogel CL wear and CLD. CL wear modified the expression of several genes related to pain and inflammation, specifically those related to analgesia (*PDYN* and *PENK*) and inflammation or pain (*BDKRB1* and *PROK2*). Additionally, SCLWs showed decreased *PENK* and *PDYN* expression and increased *CCL2*, *IL1A*, *IL1B*, *IL2*, and *NGF* expression, all genes associated with pain and inflammation.

Although showing promising results, this study was limited by its small sample size (8 participants/group). An expanded study of ocular surface gene expression in CLWs is warranted to help understand CL-induced changes on the ocular surface and the molecular mechanisms responsible for CLD.

Therefore, the present study aimed to corroborate in a larger population the previous results regarding differences in neuropathic and inflammatory pain-related gene expression in conjunctival epithelial cells among SCLWs, ACLWs, and non-CLWs, thereby identifying alterations in gene expression associated with hydrogel CL wear and CLD.

## 2. Methods

This study was approved by the Institutional Review Board of the Institute of Applied Ophthalmobiology (Universidad de Valladolid) and the Ethics Committee of the Area de Salud Valladolid Este. This study complied with the principles of the Declaration of Helsinki. All participants received detailed information about the study before providing informed consent.

### 2.1. Participants

We enrolled non-CLWs and CLWs. The latter were categorized as ACLWs and SCLWs according to the Contact Lens Dry Eye Questionnaire (CLDEQ) short form© (copyright Begley & Chalmers 2016, with permission) [19,20].

### 2.2. Inclusion and exclusion criteria

The inclusion criteria were age  $\geq 18$  years, astigmatism  $\leq 0.75$  D, and, for the CLWs, use of hydrogel or silicone hydrogel CL for  $\geq 6$  months before study inclusion.

The exclusion criteria were overnight, extended, or continuous CL

wear; any active ocular disease; any previous ocular surgery; any systemic disease that contraindicated CL wear; any topical treatment apart from artificial tears; and DED. DED was defined as an Ocular Surface Disease Index (OSDI) [21] score  $> 12$  and altered results in at least two of the following tests in at least one eye: a fluorescein tear film breakup time (TBUT)  $\leq 7$  s, an extent of fluorescein corneal staining  $\geq 2$  in any area of the cornea (graded 0–4 on the Cornea and Contact Lens Research Unit [CCLRU] scale) [22], and a Schirmer test without anesthesia  $\leq 5$  mm.

### 2.3. Study design

All participants were assessed regarding the inclusion and exclusion criteria. The CLWs were examined with their habitual CLs.

### 2.4. Clinical assessment

The participants wore their habitual correction (e.g., CL) to measure high-contrast visual acuity monocularly on a logMAR scale (Topcon Corporation, Ltd., Tokyo, Japan).

TBUT was measured using fluorescein strips (I-DEW FLO, Entod Research Cell UK, Ltd., Tottenham Lane, London, UK) wetted with 25  $\mu$ L sodium chloride and applied into the inferior fornix, after shaking the excess fluid off the strip [23]. Participants were examined immediately after fluorescein instillation using a slit lamp (SL-D7, Topcon Corporation) with a blue filter (Topcon Corporation) and a Wratten #12 yellow filter (Eastman Kodak, Rochester, NY, USA). Three measurements of the time interval between the last of three blinks and the appearance of the first dry spot were obtained, and the average was recorded. Two minutes after fluorescein instillation, corneal staining was evaluated using the CCLRU scale [22], and the total mean score was determined.

Tear production was evaluated without topical anesthesia by placing a Schirmer sterile strip (Tearflo; Alcon Laboratories Inc., Fort Worth, TX, USA) in the external canthus of the inferior lid margin. The participants kept their eyes closed, and the strip wetting length was measured after 5 min.

### 2.5. Conjunctival impression cytology

Conjunctival impression cytology (CIC) under topical anesthesia (Colircusí Anestésico Doble; Alcon Laboratories) was used to collect conjunctival cells using one-half of a polyethersulfone filter (Supor 200, pore size: 0.20  $\mu$ m, diameter: 13 mm; Gelman Laboratory, Ann Arbor, MI, USA). The filters were placed with moderate pressure on the upper temporal bulbar conjunctiva. The filters were carefully removed and transferred to 350  $\mu$ L of RLT Buffer (Qiagen, Hilden, Germany) containing 1 % 2-mercaptoethanol. CIC samples were kept frozen at  $-80$  °C

until analysis [15].

## 2.6. Gene expression analysis

Total RNA was obtained from each CIC using an RNeasy Micro Kit (Qiagen, Redwood City, CA, USA) following the manufacturer’s instructions. DNase (Qiagen) digestion was performed to remove genomic (g)DNA traces. RNA concentrations were determined using the Quant-it RNA HS Assay kit (Life Technologies, Carlsbad, CA, USA) and a Qubit Fluorometer (Life Technologies). Total RNA was reverse-transcribed into cDNA using a commercial iScript cDNA Synthesis Kit (BioRad Laboratories Inc., Hercules, CA, USA) to synthesize 12 ng of cDNA from each sample.

Gene expression was analyzed using a commercial real-time PCR (RT-PCR) array (Pain, Neuropathic, and Inflammatory; SAB target list, BioRad Laboratories Inc.) that uses SYBR Green dye detection, according to the manufacturer’s recommendations. Eighty-five human genes related to pain and inflammation were analyzed (Table 1) along with the six housekeeping genes beta-actin (*ACTB*), beta-2-microglobulin (*B2M*), glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*), TATA-binding protein (*TBP*), hypoxanthine phosphoribosyltransferase 1 (*HPRT1*), and ribosomal protein lateral stalk subunit P0 (*RPLP0*). Moreover, the array included the following controls per sample: 1) one control to monitor gDNA contamination, 2) two RNA quality controls to monitor RNA integrity, 3) one reverse transcription control for first-strand synthesis, and 4) one positive PCR control for RT-PCR efficiency. The RT-PCR was performed using a 7500 Real-Time PCR System (Applied Biosystems, Madrid, Spain) as follows: 10 min at 95 °C, 40 cycles of 15 s at 95 °C, and 1 min at 60 °C.

Descriptions of the 85 analyzed genes were obtained from the NCBI gene database (<https://www.ncbi.nlm.nih.gov/gene/>; Appendix A).

## 2.7. Statistical analysis

Statistical analysis was performed by a licensed statistician (co-author IF) using R statistical software [24] and packages from the Bioconductor project [25,26].

The sample size was estimated based on data from our pilot study [18]. The effect sizes of all genes with significant differences between ACLW and SCLW groups were calculated, and the smallest one, corresponding to PTGS1 ( $d = 1.245$ ), was used. Statistical power was established at 80%, and the level of significance was 0.00029 (0.05 divided by 170 to account for multiple testing of 85 genes with two comparisons per gene). Considering these data and the paired design, a minimum sample size of 20 participants per group was estimated.

**Table 1**

Genes analyzed by qPCR using the commercial PCR array profiler “Pain, Neuropathic, and Inflammatory (SAB Target List)”.

Category	Genes
Synaptic transmission	Glutamate receptors <i>GRIN1, GRIN2B, GRM1, GRM5</i>
	Serotonin receptors <i>HTR1A, HTR2A</i>
	Calcium channel <i>CACNA1B</i>
Pain conduction	Cannabinoid receptors <i>CNR1, CNR2</i>
	Ion channel <i>TRPA1, TRPV1, TRPV3</i>
	Opioid receptors <i>OPRD1, OPRK1, OPRM1</i>
	Potassium channels <i>KCNIP3, KCNJ6, KCNQ2, KCNQ3</i>
	Purinergic receptors <i>ADORA1, P2RX3, P2RX4, P2RX7, P2RY1</i>
	Sodium channels <i>SCN10A, SCN11A, SCN3A, SCN9A, SLC6A2</i>
	Eicosanoid metabolism <i>PLA2G1B, PTGER1, PTGER3, PTGER4, PTGES, PTGES2, PTGES3, PTGS1, PTGS2</i>
Modulation of pain responses	Inflammation <i>ACE, ALOX5, BDKRB1, CALCA, CCK, CCKBR, CCL2, CCR2, CD200, CD4, CHRNA4, CSF1, CX3CR1, DBH, EDN1, EDNRA, FAAH, GCH1, IL10, IL18, IL1A, IL1B, IL2, IL6, ITGAM, ITGB2, MAPK1, MAPK14, MAPK3, MAPK8, PROK2, TAC1, TACR1, TLR2, TLR4, TNF</i>
	Neurotransmitters <i>ADRB2, COMT, DBH, MAOB, PDYN, PENK, PNOC</i>
	Neurotrophins <i>BDNF, GDNF, NGF, NTRK1</i>

The ACLW and SCLW groups were paired 1:1 for age, sex, and habitual number of CL-wearing hours, whereas non-CLWs were matched for age and sex. The propensity score [27] was calculated using the MatchIt package [28] in R.

### 2.7.1. Clinical and demographic characteristics

Clinical and demographic characteristics were compared between groups. For quantitative variables, comparisons between two groups were performed using paired Student’s *t*-test or the Wilcoxon test, depending on whether the data were parametric or nonparametric (Shapiro-Wilk test), respectively. For the statistical comparison of three groups, repeated measures ANOVA or the Friedman test, depending on whether the data were parametric or nonparametric (Shapiro-Wilk test), respectively. Pairwise comparison of significant results was performed using paired Student’s *t*-test or the Wilcoxon test, applying the Bonferroni correction. For qualitative variables, comparisons between groups were performed using the McNemar test (two groups) or the Cochran test (3 groups). Additionally, the characteristics of the pilot and newly enrolled samples were also compared. For quantitative variables, the unpaired Student’s *t*-test or Mann-Whitney *U* test were used, depending on whether the data were parametric or nonparametric (Shapiro-Wilk test), respectively. For qualitative variables, the chi-square test was used. Statistical significance was set at  $p \leq 0.05$ .

### 2.7.2. Analysis of differentially expressed genes (DEGs)

mRNA expression was imputed for non-detected values ( $Ct > 35$ ) using the method by McCall et al. [29] which is based on the expectation-maximization algorithm and implemented in the nondetects package of the Bioconductor project. Relative gene expression data were calculated using the Ct method after choosing reference genes (*ACTB*, *GAPDH*, and *RPLP0*) with the geNorm algorithm [30] using the ReadqPCR and NormqPCR packages [31].

Differences between non-CLW and CLW, as well as ACLW and SCLW, groups were compared using a mixed-effects ANOVA with partially nested fixed effects. Models were adjusted on a gene-by-gene basis with  $\Delta Ct$  as the dependent variable using the HTqPCR [32], lme4 [33], and lmerTest [34] packages. The family-wise error rate was controlled using the method by Westfall and Young [35]. Based on the mean estimates provided by our model, effects were quantified using the emmeans package [36]. Statistical significance was set at  $p \leq 0.05$ .

### 2.7.3. Gene set enrichment analysis

To assign a biological meaning to groups of DEGs differing between non-CLWs and CLWs or SCLWs and ACLWs and to facilitate the interpretation of our findings, gene set enrichment analysis was performed

with the R package gProfileR [37]. Each gene was placed in the following biological annotations: Gene Ontology (GO biological process [GO:BP], molecular function [GO:MF], and cellular component [GO:CC]), Kyoto Encyclopedia of Genes and Genomes (KEGG), Reactome (REAC), WikiPathways (WP), Transfac: TRANScriptioN FACTor database (TF), miRTarBase (MIRNA), Human Protein Atlas (HPA), CORUM protein complexes (CORUM), and Human Phenotype Ontology (HP). p-values were calculated for each biological category based on the hypergeometric distribution and adjusted for multiple comparisons using the method of Benjamini and Hochberg [38] where  $p \leq 0.05$  was considered statistically significant.

### 3. Results

#### 3.1. Study population and clinical data

In total, 60 Caucasian participants (44 women, 16 men; mean age  $26.1 \pm 6.1$  [range: 19–46] years) were included. In addition to 37 newly enrolled participants, data from 23 participants from the pilot study (one subject obtained an invalid result) were included [18]. The characteristics of both samples are presented in Table 2. The study population comprised 20 non-CLWs and 40 CLWs. The mean CL-wearing time of CLWs was  $8.13 \pm 4.36$  years, and they used CLs for  $4.85 \pm 2.42$  days/week and  $8.28 \pm 6.93$  h/day. Conventional hydrogel and silicone hydrogel CLs were used by 15 and 25 CLWs, respectively (Table 3). CLWs were further divided into two groups (20 ACLWs and 20 SCLWs) based on the CLDEQ short form© [19,20]. The characteristics of the three groups are presented in Table 4.

#### 3.2. Differentially expressed genes

The expression levels of the 85 analyzed genes in the four study groups (non-CLW, CLW, ACLW, and SCLW) are shown in Appendix B.

##### 3.2.1. Effect of CL wear (non-CLW vs CLW)

Of the 85 examined genes, six (*GRIN1*, *P2RX7*, *PTGS1*, *CD200*, *EDN1*, and *TNF*) were significantly upregulated in CLWs compared to non-CLWs (Table 5). The fold changes for these genes ranged from 5.76 (*EDN1*) to 72.58 (*PTGS1*).

Additionally, in CLWs compared to non-CLWs, six DEGs differed with borderline statistical significance of which five (*CACNA1B* [ $p = 0.054$ ], *CCK* [ $p = 0.072$ ], *HTR1A* [ $p = 0.057$ ], *PROK2* [ $p = 0.059$ ], and *P2RX3*

**Table 2**  
Characteristics of the pilot study and newly enrolled samples.

	Pilot study	Newly enrolled	p-value
Age (years)	$25.8 \pm 4.1$	$26.3 \pm 7.2$	0.380
Sex (male/female)	7/16	9/28	0.826
CL type (conventional hydrogel/silicone hydrogel)	6/9	9/16	1.000
CL replacement schedule (daily/frequent)	7/8	6/19	0.257
CL refraction (diopters)	$-3.25 \pm 2.00$	$-2.99 \pm 1.55$	0.768
Visual acuity (logMAR)	$-0.10 \pm 0.05$	$-0.09 \pm 0.08$	0.457
CL use (years)	$8.2 \pm 4.3$	$8.1 \pm 4.5$	0.963
Weekly frequency of CL wear (days/week)	$4.8 \pm 2.1$	$4.9 \pm 1.9$	0.875
Daily frequency of CL wear (h/day)	$8.3 \pm 2.6$	$8.3 \pm 2.4$	0.987
CL wear on the day of the visit (h)	$6.3 \pm 1.9$	$5.7 \pm 2.7$	0.357
OSDI questionnaire (score 0–100)	$8.8 \pm 5.8$	$7.6 \pm 7.0$	0.301
Fluorescein tear film breakup time (s)	$8.4 \pm 7.9$	$9.7 \pm 5.8$	0.075
Total corneal staining (score 0–4)	$0.2 \pm 0.4$	$0.2 \pm 0.3$	0.959
Schirmer test without anesthesia (mm)	$20.9 \pm 12.1$	$20.8 \pm 10.8$	0.908

Data are presented as mean  $\pm$  standard deviation or frequencies. CL: contact lens; OSDI: Ocular Surface Disease Index.

[ $p = 0.065$ ] were upregulated and one (*PLA2G1B* [ $p = 0.058$ ]) was downregulated (Table 5).

##### 3.2.2. Effect of CLD (ACLW vs SCLW)

Regarding CLD effects, 11 out of the 85 genes (*GRIN1*, *GRM1*, *HTR1A*, *CACNA1B*, *ADORA1*, *P2RX3*, *PTGS1*, *BDKRB1*, *TNF*, *DBH*, and *PDYN*) were significantly downregulated in SCLWs compared to ACLWs (Table 5). Their fold change ranged from  $-4.81$  (*TNF*) to  $-38.98$  (*HTR1A*).

Furthermore, in SCLWs compared to ACLWs, four genes (*CALCA* [ $p = 0.095$ ], *CNR1* [ $p = 0.063$ ], *GDNF* [ $p = 0.089$ ], and *KCNIP3* [ $p = 0.055$ ]) were downregulated with borderline statistical significance. No gene was upregulated in SCLWs compared to ACLWs.

##### 3.2.3. Gene set enrichment

More than a thousand terms were significantly overrepresented in the gene set enrichment analysis on significant or borderline significant DEGs in CLWs compared to non-CLWs. Table 6 shows the top 20 most significantly overrepresented terms which were principally found in the GO:BP annotation and were related to transport, concentration, and homeostasis of calcium ions.

Regarding significant or borderline significant DEGs in SCLWs compared to ACLWs, thousands of significantly overrepresented terms were found. The 20 most significantly overrepresented terms (Table 7) were also principally found in the GO:BP annotation. These terms involved synaptic signaling and transmission, sensory perception of pain, cell-cell signaling, and ion and cation transport.

Additionally, the term “neuroactive ligand-receptor interaction” was overrepresented in the KEGG annotation in both CLW and CLD groups (Tables 6 and 7, respectively).

## 4. Discussion

CLD is the main cause of CL cessation, but the causes of CLD remain unclear. Alterations in ocular surface neurobiology have been identified as important mechanisms contributing to dry eye symptoms and may play a considerable role in CLD [39]. In 2019, the findings of our pilot study [18] identified DEGs associated with CL wear and CLD. The results of this exploratory study required confirmation in a larger population. The current study confirmed some of the previously obtained results and described new genes altered in both CLWs and CLDs.

#### 4.1. Effects of CL wear

In this study, *GRIN1*, *P2RX7*, and *PTGS1*, *CD200*, *EDN1*, and *TNF* were significantly upregulated in CLWs compared to non-CLWs (Fig. 1).

##### 4.1.1. Synaptic transmission

Synaptic transmission and neurotransmission are involved in pain perception. *GRIN1* encodes a subunit of the glutamate receptor channel superfamily which plays an important role in synaptic plasticity [40]. *GRIN1* is expressed in the conjunctiva [41] however, the biological significance of *GRIN1* increases in the conjunctival epithelium of CLWs is unknown.

##### 4.1.2. Pain conduction

Nociceptors transmit information to the central nervous system via action potentials, where various ion channels and receptors play important roles conducting pain signals. *P2RX7* encodes the purinergic receptor *P2RX7*, which is related to chronic inflammatory and neuropathic pain [42–44] and participates in the secretion of interleukins, cytokines (e.g., tumor necrosis factor [TNF]- $\alpha$ ), chemokines, and prostaglandin E2 (PGE2) [45–47]. *P2RX7* has been also related to chronic DED [48,49]. Furthermore, the complex *P2RX7*-NLRP3 inflammasome mediates the release of the pro-inflammatory cytokines IL-1 $\beta$  and IL-18, which may be involved in Sjögren’s-derived ocular dryness [50]. In the



**Table 3**  
Contact lenses (CLs) used by the CL wearers group.

CL type	Replacement	Material	Diameter	Base curve	Laboratory	Number of participants
Conventional hydrogel	Monthly	Omafilcon B	14.2	8.6	CooperVision	3
		Hilafilcon B	14.2	8.6	Bausch & Lomb	2
		Nesofilcon A	14.2	8.6	Bausch & Lomb	3
	Daily	Nelfilcon A	14.0	8.7	Alcon	2
		Omafilcon A	14.2	8.7	CooperVision	2
		Etafilcon A	14.2	8.5	Johnson & Johnson	1
		Filcon IV 1	14.2	8.6	Servilens	1
		Ocufilecon D	14.2	8.6	CooperVision	1
		Silicone hydrogel	Monthly	Comfilcon A	14.0	8.6
Lotrafilcon B	14.2	8.6	Alcon	5		
	Fanfilcon A	14.2	8.4	CooperVision	2	
	Polymacon	14.2	8.6	Bausch & Lomb	1	
Biweekly	Senofilcon A	14.8	8.4	Johnson & Johnson	2	
	Galyfilcon A	14.0	8.7	Johnson & Johnson	1	
Daily	Delefilcon A	14.1	8.5	Alcon	2	
	Somofilcon A	14.1	8.6	CooperVision	1	

**Table 4**  
Characteristics of the study groups.

	Non-CLW	ACLW	SCLW	p-value
<b>Age (years)</b>	25.9 ± 7.8	26.9 ± 5.1	25.5 ± 5.4	0.102
<b>Sex (male/female)</b>	5/15	7/13	4/16	0.584
<b>CL type (conventional hydrogel/silicone hydrogel)</b>	–	6/14	9/11	0.366
<b>CL replacement schedule (daily/frequent)</b>	–	5/15	8/12	0.405
<b>CL refraction (diopters)</b>	–	–3.25 ± 1.50	–2.75 ± 2.00	0.267
<b>Visual acuity (logMAR)</b>	–0.11 ± 0.06	–0.08 ± 0.06	–0.11 ± 0.08	0.312
<b>CL use (years)</b>	–	9.1 ± 4.8	7.1 ± 3.7	0.063
<b>Weekly frequency of CL wear (days/week)</b>	–	5.8 ± 1.5	3.9 ± 1.9	<b>0.009</b>
<b>Daily frequency of CL wear (h/day)</b>	–	8.8 ± 2.2	7.7 ± 2.5	0.134
<b>CL wear on the day of the visit (h)</b>	–	5.8 ± 3.2	6.1 ± 1.3	0.721
<b>OSDI questionnaire (score 0–100)</b>	4.1 ± 2.9	6.1 ± 4.1	13.2 ± 7.0	<b>&lt;0.001*</b>
<b>Fluorescein tear film breakup time (s)</b>	11.1 ± 7.0	9.0 ± 7.6	9.0 ± 7.6	0.638
<b>Total corneal staining (score 0–4)</b>	0.1 ± 0.2	0.3 ± 0.4	0.1 ± 0.2	0.500
<b>Schirmer test without anesthesia (mm)</b>	22.1 ± 12.0	18.6 ± 9.8	22.2 ± 11.7	0.394

Data are presented as mean ± standard deviation or frequencies. ACLW: asymptomatic contact lens wearer; CL: contact lens; CLW: contact lens wearer; OSDI: Ocular Surface Disease Index; SCLW: symptomatic contact lens wearer. \* pairwise comparisons with Bonferroni correction, p-value <0.05 in the symptomatic group compared with all other groups.

cornea, P2RX7 participates in wound healing by regulating corneal integrity and epithelial cell migration [51]. Therefore, purinergic receptors may participate in the regulation of inflammation in DED. Our results suggest that the upregulation of P2RX7 in CLWs may indicate changes in the inflammatory state and increased pain sensitivity.

#### 4.1.3. Modulation of pain responses

The transduction of pain signals can be modulated by different inflammatory and pain mediators (including growth factors, cytokines, and chemokines) released by neurons and immune cells, among others.

In this category, *PTGS1* expression was the highest with a 72.58-fold change. *PTGS1* encodes an enzyme that participates in the biosynthesis of prostaglandins which participate in the development of the inflammatory response and allodynia [52,53]. Prostaglandins potentiate the effects of other inflammatory mediators (e.g., bradykinin and histamine) which directly induce inflammation [52] and can be released with

cytokines after stimulation of the ocular surface by tear hyperosmolarity [54,55]. The increased *PTGS1* expression in CLWs could be a consequence of the hyperosmolarity on the ocular surface provoked by CLs [56], similar to the increased tear PGE2 levels observed in DED subjects [54,57].

*CD200* encodes the glycoprotein CD200. The interaction between CD200 and its inhibitory receptor CD200R modulates pro-inflammatory responses [58,59], and several studies have demonstrated the anti-inflammatory effects of CD200/CD200R interactions [60–62]. Therefore, the high *CD200* levels in CLWs could be a protective response to the pro-inflammatory state caused by CL wear, protecting cells against CL-induced tissue damage.

We also found higher *EDN1* expression in CLWs. This gene, associated with somatic pain, inflammation, and nerve injury [63–65] encodes endothelin 1, which is involved in nociceptive signaling [63,66]. *TNF* expression was also increased in CLWs. In addition to its well-known pro-inflammatory role, *TNF-α* induces neuropathic pain and hyperalgesia [67]. Gu et al. [68], proposed that *EDN1* and *TNF* participate linked in different pathways, including *TNF* signaling pathway. Thus, the increases in *EDN1* and *TNF* expression in CLWs may be related to upregulated *TNF* signaling and, therefore, may be involved in altered conjunctival inflammation and pain during CL wear. However, increased *TNF-α* levels in tear fluid have been described for reusable hydrogel CLWs [69] and also in CLWs exposed to adverse environmental conditions [7]. Moreover, the upregulation of both *PTGS1* and *TNF* in CLWs may indicate that the inflammatory state is further activated or that the presence of CLs modifies the basal conditions of the conjunctival epithelium. Additionally, the abovementioned increased P2RX7 receptor might lead to the observed increases in *PTGS1* and *TNF* expression [45,46].

#### 4.2. Effects associated with CLD

Regarding CLD-associated changes in gene expression between SCLWs and ACLWs, *GRIN1*, *GRM1*, *HTR1A*, *CACNA1B*, *ADORA1*, *P2RX3*, *PTGS1*, *BDKRB1*, *TNF*, *DBH*, and *PDYN* were significantly downregulated in SCLWs (Fig. 2).

##### 4.2.1. Synaptic transmission

All genes downregulated in SCLWs in this category (*GRIN1*, *GRM1*, *HTR1A*, and *CACNA1B*) encode proteins or receptors related to neuronal excitability or neurotransmitter release.

*GRIN1* and *GRM1* encode G-protein-coupled glutamate receptors that mediate fast excitatory synaptic transmission (*GRIN1*) and modulate neurotransmission (*GRM1*) [70]. *GRM1* also appears to regulate inflammation, as its silencing is related to *CXCL1*, *IL6*, and *IL8/CXCL8* upregulation [71]. The downregulation of *GRIN1* and *GRM1* in SCLWs

**Table 5**  
Differentially expressed genes in individuals with contact lens (CL) wear and CL discomfort (CLD).

Category	Gene	CL wear				CLD				
		Non-CLW (n=20) mean $\Delta$ Ct (95% CI)	CLW (n=40) mean $\Delta$ Ct (95% CI)	Fold change	Adjusted p-value	ACLW (n=20) mean $\Delta$ Ct (95% CI)	SCLW (n=20) mean $\Delta$ Ct (95% CI)	Fold change	Adjusted p-value	
Synaptic transmission	Glutamate receptors	<i>GRIN1</i>	18.29 (8.446, 28.138)	15.05 (9.522, 20.583)	9.44	<b>0.006</b>	14.52 (9.270, 19.769)	18.83 (9.104, 28.546)	-19.77	<b>0.003</b>
		<i>GRM1</i>	16.49 (8.937, 24.039)	15.20 (10.815, 19.576)	2.45	0.194	14.67 (10.290, 19.040)	17.02 (9.442, 24.595)	-5.11	<b>0.037</b>
	Serotonin receptors	<i>HTR1A</i>	17.35 (7.082, 27.613)	14.79 (8.587, 20.986)	5.90	0.057	13.42 (7.428, 19.421)	18.71 (8.087, 29.331)	-38.98	<b>0.001</b>
	Calcium channel	<i>CACNA1B</i>	16.63 (8.736, 24.528)	14.65 (9.876, 19.418)	3.96	0.054	14.12 (9.507, 18.732)	17.16 (8.986, 25.333)	-8.23	<b>0.006</b>
Pain conduction	Purinergic receptors	<i>ADORA1</i>	15.07 (7.487, 22.658)	14.84 (10.463, 19.216)	1.18	0.824	13.41 (9.029, 17.785)	16.50 (8.923, 24.086)	-8.56	<b>0.007</b>
		<i>P2RX3</i>	16.71 (8.758, 24.656)	14.73 (9.974, 19.487)	3.94	0.065	14.41 (9.707, 19.122)	17.02 (8.871, 25.176)	-6.10	<b>0.035</b>
		<i>P2RX7</i>	12.61 (4.161, 21.058)	9.76 (4.919, 14.61)	7.19	<b>0.029</b>	11.50 (6.648, 16.359)	10.87 (2.461, 19.28)	1.55	0.548
Modulation of pain responses	Eicosanoid metabolism	<i>PTGS1</i>	17.98 (10.240, 25.729)	11.80 (7.323, 16.282)	72.58	<b>&lt;0.0001</b>	12.39 (7.897, 16.884)	17.40 (9.646, 25.148)	-32.16	<b>&lt;0.001</b>
	Inflammation	<i>BDKRB1</i>	14.46 (6.573, 22.343)	15.03 (10.307, 19.748)	-1.48	0.626	13.25 (8.325, 18.176)	16.24 (8.196, 24.274)	-7.92	<b>0.010</b>
		<i>CD200</i>	14.19 (5.069, 23.312)	11.33 (5.9, 16.755)	7.28	<b>0.020</b>	13.28 (8.309, 18.249)	12.24 (2.851, 21.627)	2.06	0.341
		<i>EDN1</i>	10.08 (2.497, 17.667)	7.56 (3.189, 11.924)	5.76	<b>0.025</b>	8.36 (3.993, 12.728)	9.28 (1.706, 16.849)	-1.89	0.359
		<i>TNF</i>	14.59 (6.010, 23.174)	10.63 (5.815, 15.455)	15.54	<b>&lt;0.001</b>	11.48 (6.905, 16.055)	13.75 (5.275, 22.220)	-4.81	<b>0.044</b>
	Neurotransmitters	<i>DBH</i>	15.85 (5.046, 26.659)	14.55 (8.017, 21.075)	2.47	0.346	13.27 (6.955, 19.591)	17.13 (5.941, 28.310)	-14.45	<b>0.010</b>
		<i>PDYN</i>	17.42 (9.015, 25.819)	15.55 (10.525, 20.581)	3.16	0.108	14.88 (9.627, 20.124)	18.09 (9.531, 26.658)	-9.31	<b>0.011</b>

Data are presented as the estimated mean  $\Delta$ Ct (Ct gene of interest – Ct housekeeping) values (95% CI) for each gene; significant p-values are denoted in bold font. The up- and downregulated genes in these groups are highlighted in orange and green, respectively. Differences between groups were compared using a mixed-effects ANOVA with partially nested fixed effects. Statistical significance was set at p-value  $\leq 0.05$ . ACLW: asymptomatic contact lens wearer; CI: confidence interval; CLD: contact lens discomfort; CLW: contact lens wearer; SCLW: symptomatic contact lens wearer.

may disrupt neuronal or cellular excitability and could be involved in the upregulation of pro-inflammatory cytokines related to ocular discomfort. However, we did not find any significant increase in the expression of *IL6* or any other cytokine gene analyzed (*CCL2*, *IL1A*, *IL1B*, *IL2*, *IL10*, and *IL18*) in SCLWs compared to ACLWs. *CXCL1* or *IL8/CXCL8* expression might be altered in these patients; however, these cytokines were not included in our gene panel.

*HTR1A* had the greatest negative fold change (–38.98). This gene encodes a serotonin receptor (5-hydroxytryptamine receptor 1 A) that is associated with pain sensitivity [72,73]. *HTR1A* also regulates pain-related serotonin functions and plays a neuroprotective role [74, 75]. According to these results, the discomfort experienced by SCLWs might be partly due to altered neuroprotective mechanisms involving *HTR1A* receptors. Dysregulation of serotonergic pathways in SCLWs is also possible, altering their pain sensitivity, resulting in discomfort.

*CACNA1B* encodes a subunit of the N-type voltage-gated calcium channel which is associated with chronic pain and controls neurotransmitter release [76,77]. Changes in *CACNA1B* expression might be linked to the observed downregulation of *HTR1A*, *GRIN1*, and *GRM1*, as the neuroprotective effects of *HTR1A* involve a reduction in calcium influx and the release of glutamate [75,78,79].

#### 4.2.2. Pain conduction

*ADORA1* encodes the adenosine A1 receptor *ADORA1*, [80,81]. Adenosine receptors are involved in pain and inflammation [82–84] and T. Yang et al. [84], reported decreased TNF- $\alpha$ , IL-6, IL-1 $\beta$ , and IL-12 levels in aged *Adora1* knockout mice. The downregulated *ADORA1* expression in SCLWs compared with that in ACLWs could be a protective effect to decrease *ADORA1* expression and the secretion of pro-inflammatory cytokines.

Like *P2RX7*, *P2RX3* encodes a purinergic receptor (*P2RX3*), which

participates in the development of hyperalgesia owing to its activation by ATP released from damaged or inflamed tissues. De Oliveira Fusaro et al. [85], demonstrated in rats that activation of *P2RX3* and *P2RX2/3* receptors by ATP mediates bradykinin-induced mechanical hyperalgesia. According to our results, CLD observed in SCLWs may be related to hyperalgesia triggered by the upregulation of *P2RX3* signaling. Thus, *P2RX3* downregulation in SCLWs compared to that in ACLWs may be a protective response to decrease *P2RX3* levels and reduce the hyperalgesic state in SCLWs.

#### 4.2.3. Modulation of pain responses

Modulation of pain responses was the most-altered CLD-related category, with five significantly downregulated genes in SCLWs compared to ACLWs.

*PTGS1* is an enzyme involved in the biosynthesis of prostaglandins that can exhibit pro- and anti-inflammatory and immunomodulatory properties [53]. Some prostaglandins have concentration- and time-dependent cumulative effects causing pain even at low levels [52]. *PTGS1* may be downregulated in SCLWs via a feedback mechanism due to high prostaglandin levels, which cause discomfort. However, low *PTGS1* levels may be related to a decreased synthesis of anti-inflammatory prostaglandins, causing CLD. Although some studies found increased PGE2 levels in tears of individuals with DED [54,57,86], prostaglandin levels in tears of participants with and without CLD were not found significantly different [87].

The expression of bradykinin receptor gene *BDKRB1* was lower in SCLWs than in ACLWs. Bradykinin is an endogenous peptide associated with inflammation [88]. The bradykinin receptors *BDKRB1* and *BDKRB2* are involved in the initiation and maintenance of inflammatory processes [89]. *BDRKB1* can be highly and rapidly upregulated following inflammatory stimuli [90]. As mentioned above, ATP-induced

**Table 6**  
Gene set enrichment analysis of the top 20 differentially expressed genes in contact lens wearers (CLWs).

Category	Term ID	Term description	CLW	
			Count	p-value
GO:BP	GO:0043269	Regulation of ion transport	7	<0.001
GO:BP	GO:0007204	Positive regulation of cytosolic calcium ion concentration	6	<0.001
GO:BP	GO:0051480	Regulation of cytosolic calcium ion concentration	6	<0.001
GO:BP	GO:0006816	Calcium ion transport	6	<0.001
GO:BP	GO:0010524	Positive regulation of calcium ion transport into cytosol	4	<0.001
GO:BP	GO:0055074	Calcium ion homeostasis	6	<0.001
GO:BP	GO:0006874	Cellular calcium ion homeostasis	6	<0.001
GO:BP	GO:0072503	Cellular divalent inorganic cation homeostasis	6	<0.001
GO:BP	GO:0051049	Regulation of transport	8	<0.001
GO:BP	GO:0010243	Response to organonitrogen compound	7	<0.001
GO:BP	GO:0072507	Divalent inorganic cation homeostasis	6	<0.001
GO:BP	GO:1901698	Response to nitrogen compound	7	<0.001
GO:BP	GO:0006875	Cellular metal ion homeostasis	6	<0.001
GO:BP	GO:0043270	Positive regulation of ion transport	5	<0.001
GO:BP	GO:0006812	Cation transport	7	<0.001
GO:BP	GO:0030003	Cellular cation homeostasis	6	<0.001
GO:BP	GO:0006873	Cellular ion homeostasis	6	<0.001
GO:BP	GO:0055065	Metal ion homeostasis	6	<0.001
GO:BP	GO:0019233	Sensory perception of pain	4	<0.001
KEGG	KEGG:04080	Neuroactive ligand-receptor interaction	6	<0.001

The 20 most significantly overrepresented terms are shown. p-values were calculated based on the hypergeometric distribution and adjusted for multiple comparisons using the method of Benjamini and Hochberg [38] where  $p \leq 0.05$  was considered statistically significant. GO:BP: Gene Ontology biological process; KEGG: Kyoto Encyclopedia of Genes and Genomes; Count: number of altered genes present in the term.

**Table 7**  
Gene set enrichment analysis of the top 20 differentially expressed genes in symptomatic contact lens wearers (SCLWs).

Category	Term ID	Term description	CLD	
			Count	p-value
GO:BP	GO:0043269	Regulation of ion transport	11	<0.001
GO:BP	GO:0098916	Anterograde <i>trans</i> -synaptic signaling	10	<0.001
GO:BP	GO:0007268	Chemical synaptic transmission	10	<0.001
GO:BP	GO:0099537	<i>Trans</i> -synaptic signaling	10	<0.001
GO:BP	GO:0099536	Synaptic signaling	10	<0.001
GO:BP	GO:0019233	Sensory perception of pain	7	<0.001
GO:BP	GO:0007267	Cell-cell signaling	11	<0.001
GO:BP	GO:0006811	Ion transport	12	<0.001
GO:BP	GO:0007610	Behavior	9	<0.001
GO:BP	GO:0045776	Negative regulation of blood pressure	5	<0.001
GO:BP	GO:0003008	System process	12	<0.001
GO:BP	GO:0006812	Cation transport	10	<0.001
GO:BP	GO:0051049	Regulation of transport	11	<0.001
GO:BP	GO:0044057	Regulation of system process	8	<0.001
GO:CC	GO:0045202	Synapse	10	<0.001
KEGG	KEGG:04080	Neuroactive ligand-receptor interaction	9	<0.001
GO:BP	GO:0051480	Regulation of cytosolic calcium ion concentration	7	<0.001
GO:BP	GO:0050877	Nervous system process	10	<0.001
GO:CC	GO:0036477	Somatodendritic compartment	8	<0.001
GO:CC	GO:0150034	Distal axon	6	<0.001

The 20 most significantly overrepresented terms are shown. p-values were calculated based on the hypergeometric distribution and adjusted for multiple comparisons using the method of Benjamini and Hochberg [38] where  $p \leq 0.05$  was considered statistically significant. GO:BP: Gene Ontology biological process; GO:CC: Gene Ontology cellular component; KEGG: Kyoto Encyclopedia of Genes and Genomes; Count: number of altered genes present in the term; CLD: contact lens discomfort.

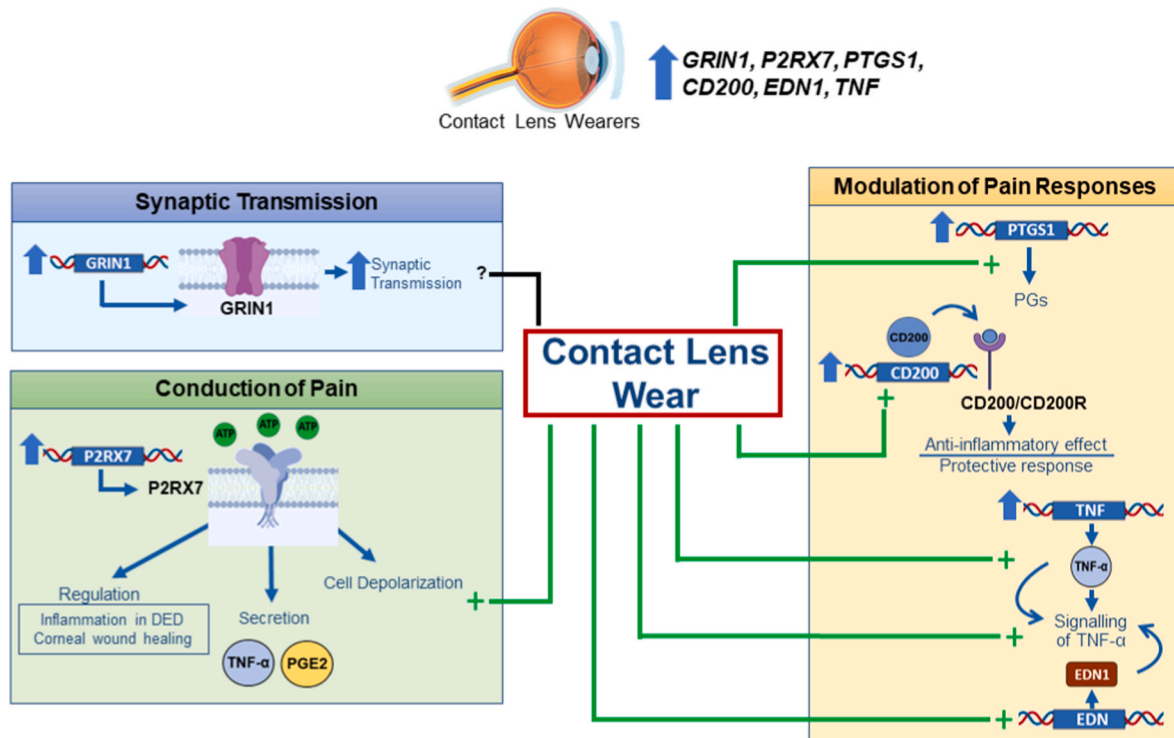
P2RX3 and P2RX2/3 activation mediates bradykinin-induced mechanical hyperalgesia [85]. In SCLWs, decreased expression of *BDKRB1*, as well as that of *P2RX3*, might be a protective mechanism to reduce P2RX3 levels and alleviate the hyperalgesic state in SCLWs. Kininogen (the precursor of bradykinin) had increased levels in the tears of CLWs [91]; however, bradykinin levels in tears were not significantly different between CLWs and non-CLWs [92].

*TNF* was significantly downregulated in SCLWs compared to ACLWs and upregulated in CLWs compared to non-CLW. *TNF- $\alpha$*  levels are increased in CLWs under adverse environmental conditions [93] and in the tears of patients with DED [94]. On one side, the increased *TNF* expression in ACLWs might reflect their higher frequency of CL wear reported. And, on the other, the decreased *TNF* expression in SCLWs might be due to a protective feedback mechanism in which, due to high

*TNF- $\alpha$*  levels, the expression of this gene is downregulated.

Lastly, *DBH* and *PDYN* expression was decreased in SCLWs compared with ACLWs. *DBH* encodes dopamine  $\beta$ -hydroxylase, that converts dopamine to norepinephrine. The sympathetic system plays an important role in tear production [95,96], and dopamine levels affect the spontaneous blink rate [97]. Downregulation of *DBH* in SCLWs may lead to an alteration in dopaminergic metabolism, which may reduce the blink rate, interfering tear dynamics [98] and leading to CLD experienced by these individuals. This hypothesis agrees with the lower blink rate reported in dry eye subjects during the use of visual display terminals [99].

*PDYN* encodes a precursor protein for three opioid neuropeptides [100] being *PDYN* expression critical for pain regulation [101]. The decreased *PDYN* levels in SCLWs could be related to CLD; conversely, the



**Fig. 1.** Summary of differentially expressed genes in conjunctival epithelial cells from contact lens wearers (CLWs) compared to non-CLWs.

Six genes were upregulated in CLWs compared to non-CLWs and were involved in three different categories related to pain or inflammation. **Synaptic transmission:** The glutamate receptor *GRIN1* participates in synaptic transmission. Currently, the role of this gene in the development of pain and inflammation in CLWs remains unknown. **Pain conduction:** *P2RX7* is associated with chronic inflammatory and neuropathic pain. *P2RX7* also contributes to *TNF-α* and prostaglandin E2 secretion, increases pain sensitivity, and induces an inflammatory state on the ocular surface. **Modulation of pain responses:** *PTGS1* participates in the biosynthesis of prostaglandins (PGs), which are involved in the development of inflammatory responses. The increase in the expression of *CD200* might be a protective response against the pro-inflammatory state caused by CL wear. *EDN1* and *TNF* might participate together in *TNF-α* signaling. Therefore, increased *EDN1* and *TNF* expression in CLWs could be involved in the alteration of conjunctival inflammation and pain states. ATP: adenosine triphosphate; CD200R: CD200 receptor; DED: dry eye disease; *EDN1*: endothelin 1; *GRIN1*: glutamate ionotropic receptor NMDA type subunit 1; *P2RX7*: purinergic receptor P2X, ligand-gated ion channel 7; PGE2: prostaglandin E2; PGs: prostaglandins; *PTGS1*: prostaglandin-endoperoxide synthase 1; *TNF*: tumor necrosis factor; *TNF-α*: tumor necrosis factor  $\alpha$ . This figure has been created using [Biorender.com](https://biorender.com) and PowerPoint.

higher *PDYN* levels in ACLWs could be responsible for the lack of symptomatology in these participants.

#### 4.3. Biological meaning

To assess the biological significance of the altered genes, we performed enrichment analysis in both CLW and CLD groups. This analysis revealed that thousands of terms were significantly overrepresented. The 20 top terms that were significantly overrepresented in the CLW and CLD groups were related to calcium and ion transport, synaptic processes sensory pain perception, and behavior (understood as internally coordinated responses of organisms to internal/external stimuli, which involve nervous system activity). This enrichment analysis reinforces our hypothesis regarding molecular changes and alterations in the transmission of pain associated with CL use and the presence of CLD.

#### 4.4. Final considerations

CL wear increased the expression of genes involved in synaptic transmission (*GRIN1*), pain conduction (*P2RX7*), and modulation of pain response (*PTGS1*, *CD200*, *EDN1*, and *TNF*), suggesting that CL use modifies the basal conditions of the ocular surface, with the potential to induce a para-/pro-inflammatory state of the conjunctiva.

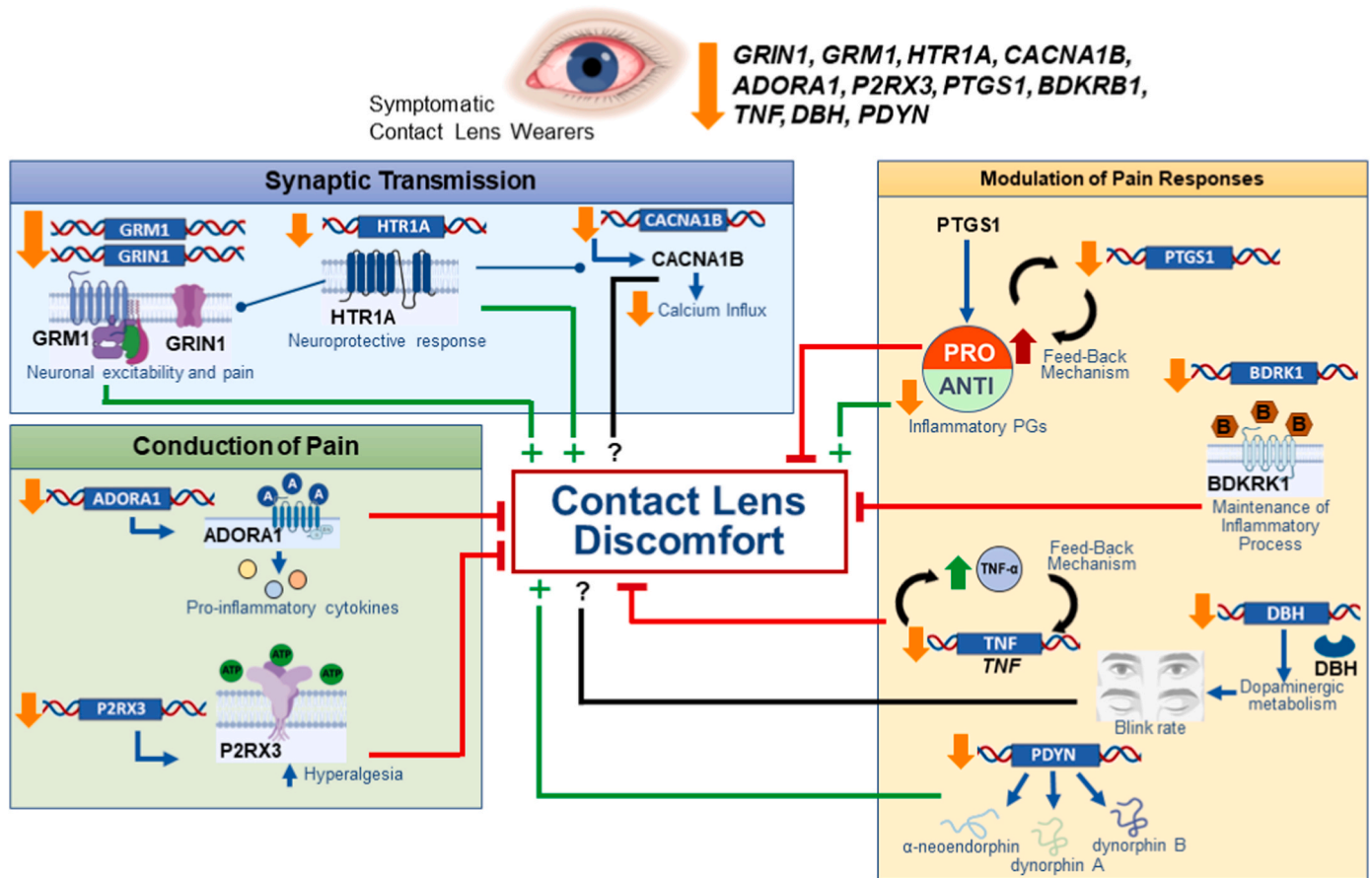
In contrast, the expression of genes involved in synaptic transmission (*GRIN1*, *GRM1*, *HTR1A*, and *CACNA1B*), pain conduction (*ADORA1* and *P2RX3*), and pain response modulation (*PTGS1*, *BDKRB1*, *TNF*, *DBH*, and *PDYN*) was downregulated in SCLWs compared to ACLWs. This

downregulation of various receptors and ion channels disrupts neuronal excitability and pain perception, leading to the occurrence of CLD. Additionally, some of these gene alterations have been described in relation to DED, suggesting a common pathological mechanism.

Some authors have suggested that CLD is caused by an imbalance in mechanical adaptation mechanisms [102]. The pattern found in this study comparing CLWs with non-CLWs behaves in a way opposite to that when comparing SCLWs and ACLWs. This suggests that ACLWs are protected by adaptive mechanical mechanisms on the ocular surface, alleviating symptom severity. It is possible that these adaptive mechanisms fail in SCLWs, which is why some CLWs develop CLD. As such, this study establishes a starting point for determining the molecular mechanisms underlying adaptation to CL wear in ACLWs and its failure in SCLWs.

A major objective of this study was to corroborate the results of a pilot study [18]. Based on the differences between non-CLWs and CLWs, increased *PTGS1* expression was observed in CLWs in both studies. *CACNA1B* and *PROK2*, which were previously found to be significantly increased, were also increased in this study but only bordered on statistical significance. *CD200* and *GRIN1* also showed significantly higher expression levels in CLWs; however, they were significantly downregulated in our previous study. Moreover, in this study, we found increased expression of *EDN1*, *P2RX7*, and *TNF* in CLWs, genes that were previously unaltered. Regarding CLD effects, the current results for *ADORA1*, *BDKRB1*, *CACNA1B*, *HTR1A*, *PDYN*, and *PTGS1* confirmed the changes found in the pilot study, whereas *P2RX3* was upregulated in SCLWs in our previous study. The other four genes, *DBH*, *GRIN1*, *GRM1*,





**Fig. 2.** Summary of differentially expressed genes in conjunctival epithelial cells from symptomatic contact lens wearers (SCLWs) compared to asymptomatic contact lens wearers (ACLWs).

Eleven genes were downregulated in SCLWs compared to ACLWs. These genes belong to three categories related to pain or inflammation. **Synaptic transmission:** The decrease in *GRIN1* and *GRM1* expression in SCLWs could alter their neuronal or cellular excitability, increasing CLD. Downregulation of *HTR1A* may attenuate the neuroprotective response of this receptor, which is related to CLD observed in SCLWs. In addition, the downregulation of *HTR1A* could also be associated with the downregulation of *CACNA1B*, *GRIN1*, and *GRM1*, as the neuroprotective effects of *HTR1A* involve a reduction in calcium influx and the release of glutamate. **Pain conduction:** The decrease in the expression of *ADORA1* could be a protective response to reduce the production of pro-inflammatory cytokines associated with *ADORA1* receptor activation. Downregulation of *P2RX3* may be a protective mechanism that decreases mechanical hyperalgesia mediated by the activation of this receptor. **Modulation of pain responses:** The downregulation of *PTGS1* in SCLW could be either a protective feedback mechanism in response to pro-inflammatory prostaglandins or a cause of the CLD observed due to a decrease in the synthesis of anti-inflammatory prostaglandins. The decrease in both *BDKRB1* and *P2RX3* might be a protective mechanism to reduce the inflammatory state present in SCLWs. The downregulation of *TNF* may be also a protective feedback mechanism in response to high levels of the pro-inflammatory cytokine *TNF-α*. The reduction in *DBH* expression might alter the dopaminergic metabolism, which could alter the blink rate in these individuals. Finally, the decrease in the expression of *PDYN* could be one of the causes of the occurrence of CLD in SCLWs, since this gene encodes a precursor protein for different opioid neuropeptides, which are essential for pain regulation. A: adenosine; *ADORA1*: adenosine A1 receptor; ATP: adenosine triphosphate; B: bradykinin; *BDKRB1*: bradykinin receptor B1; *CACNA1B*: calcium voltage-gated channel subunit alpha 1 B; *DBH*: dopamine β-hydroxylase; *GRIN1*: glutamate ionotropic receptor NMDA type subunit 1; *GRM1*: glutamate metabotropic receptor 1; *HTR1A*: 5-hydroxytryptamine (serotonin) receptor 1 A; *P2RX3*: purinergic receptor P2X, ligand-gated ion channel 3; *PDYN*: prodynorphin; PGs: prostaglandins; *PTGS1*: prostaglandin-endoperoxide synthase 1; *TNF*: tumor necrosis factor; *TNF-α*: tumor necrosis factor α.

This figure has been created using [Biorender.com](https://biorender.com) and PowerPoint.

and *TNF*, were significantly downregulated in this study but were not DEGs in the pilot study. The increased sample size in the current study allowed us to obtain results that were statistically more consistent than those obtained in the pilot study.

This study has some limitations. We excluded subjects with DED based on the criteria established in the pilot study [18]; which, although similar, differs from the one proposed by TFOS DEWS II [103]. We only analyzed the effects of hydrogel or silicone hydrogel CLs. Nevertheless, soft CLs represent 86% of CL fittings, and silicone hydrogel was the most commonly fitted CL (76%) in 2022 [104]. We assumed that cells collected by CIC are mainly epithelial, but we cannot completely exclude the presence of a small amount of other cell types present on the ocular surface (e.g., immune cells); therefore, we cannot dismiss the possibility that some of the observed gene expression changes are related to these

cells. It would be interesting to further analyze gene expression in other cell types on the ocular surface to complete our study. Finally, we analyzed gene expression but not the corresponding protein levels. Due to post-translational mechanisms, these changes in mRNA expression might not correspond to the final amount of the expressed protein. To corroborate these results, it would be interesting to analyze the expression of proteins encoded by the genes we found to be altered because, to our knowledge, most of these proteins have not been studied in CLD.

In conclusion, the present study confirms that changes in pain-related gene expression in conjunctival epithelial cells in CLWs may account for or contribute to the occurrence of CLD in SCLWs or its absence in ACLWs.

## Author contributions

AACG participated in the interpretation of data, analysis, and drafting of the manuscript. LVN, CVS, ALdIR, MBV, and CAaA participated in patient recruitment and clinical data collection. CGV performed laboratory experiments. IF performed the statistical analyses. AEdS and MJGG participated in the study design, data collection, data analysis and interpretation, financial support, and manuscript writing. All authors approved the final version of the manuscript.

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## Declaration of competing interest

None.

## Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jtos.2023.12.004>.

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