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PROGRAMA DE MAESTRÍA Y DOCTORADO EN CIENCIAS MÉDICAS,
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**ESTUDIO DE LAS RESPUESTAS NEUROINFLAMATORIAS EN EL GANGLIO
TRIGÉMINO DE RATONES CON ENFERMEDAD DEL OJO SECO Y ANÁLISIS
PROSPECTIVO DEL EFECTO TERAPÉUTICO DEL SECRETOMA DE CÉLULAS
TRONCALES MESENQUIMALES EN EL COMPORTAMIENTO DEL DOLOR
OCULAR**

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**Study of neuroinflammatory responses in the mouse trigeminal ganglion associated with
dry eye disease and prospective analysis of therapeutic effect of mesenchymal stem cell
secretome on ocular pain behavior**

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ABSTRACT

Dry eye disease (DED) is one of the main causes of ophthalmology office visits and accompanying ocular pain affects the quality of life in patients suffering from. Today, no single therapeutic approach of drug is satisfactory, and no topical analgesic are available to alleviate chronic ocular pain. In first, we used a well characterized aqueous and lipid deficient DED model in order to characterize the neuroinflammatory response on trigeminal ganglion (TG) from DED mice through genetic strategies. In a second time, using the same preclinical model of DED, we also start a prospective analyze of therapeutic effect of mesenchymal stem cell secretome on ocular pain behavior. Indeed, mesenchymal stem cells (MSCs) are adult pluripotent stem cells with neuroprotective, neurotrophic and neuroregenerative properties. MSCs produce a set of proteins and growth factors with various properties such as anti-inflammatory, antifibrotic, anti-apoptotic or even immunomodulatory, and constituting their secretome, which can then exert a beneficial impact on the damaged tissue notably in ocular pain induced by dry eye.

1. Background

Dry eye disease (DED) is one of the main causes of ophthalmology office visits with a prevalence ranged from 5 to 40% in population over 40 years old ^{1, 2}. In 2017, the last TFOS DEWS II® report redefined DED as “a multifactorial disease of the ocular surface characterized by a loss of homeostasis of the tear film, and accompanied by ocular symptoms, in which tear film instability and hyperosmolarity, ocular surface inflammation and damage, and neurosensory abnormalities play etiological roles” ³. One of the main symptoms of DED is ocular pain, which varies in intensity and duration, affecting the quality of life in around 60% of patients suffering from DED ^{1, 4}. Today, no single therapeutic approach of drug is satisfactory, and no topical analgesic are available to alleviate chronic ocular pain.

Cornea is the most densely innervated tissue in mammals, its sensory and autonomic innervation is supplied by the subepithelial plexus, made of thinly myelinated (A) or unmyelinated (C type) ciliary nerves. Corneal neurons are located in the ophthalmic branch of the trigeminal ganglion (TG). These sensory neurons represent about 1.3% to 2% of all TG neurons. Throughout the progress of DED severity, many significant biological processes occur at the peripheral nervous system leading to cellular and molecular changes in the TG. These changes include modulations of intracellular signal transduction, inflammation, glial-inflammatory cells communication and synaptic transmission ⁵.

Inflammation is the core mechanism of DED ⁶, and this has been supported by previous reports where inflammatory and immunomodulatory markers have been found in the epithelium of cornea and conjunctiva samples of patients suffering from DED ⁷.

Mesenchymal stem cells (MSCs) are adult pluripotent stem cells, present in all organism, distinguished by the expression of surface markers as CD73, CD90, CD29, and CD105 and with the capability of differentiation in several cell types (in vitro) ^{8, 9}. Today, cell therapies are considered a promising approach in the treatment of pain ¹⁰. Indeed, increasingly evidence reported that MSCs exhibit neuroprotective, neurotrophic, neuroregenerative and immunomodulatory properties. The success of stem cells treatment has been described in rodent models of neuropathic pain¹¹ after nerved injury of peripheral nerves ^{12, 13, 14} and spinal cord ¹⁵.

One objective of cell therapy is to reduce the inflammatory response. MSCs produce a set of proteins and growth factors with various properties such as anti-inflammatory, antifibrotic, anti-apoptotic or even immunomodulatory, and constituting their secretome. In addition, they are little or non-immunogenic, this property facilitating their use in cell therapy studies. In ophthalmology, the first preclinical studies with MSCs began in 2007, in models of retinal degeneration. Since then, studies have extended to many ophthalmological pathologies: glaucoma, pathologies of the ocular surface or inflammatory and immune pathologies¹⁶. Evidence pointed that the modulatory activity of MSCs is owing to their ability to secrete several factors that can then exert a beneficial impact on the damaged tissue. These secretions include a broad spectrum of factors, collectively called secretome and extracellular vesicles containing functional proteins and RNAs, present in the medium where the stem cells are cultured¹⁶. Therapeutic approach of MSCs in the eye is very promising and have already been used in hypertension and glaucoma models^{17,18}, as well as for retinal degeneration pathologies (as retinitis pigmentosa)^{19, 20}. However, its effect on ocular pain hasn't been evaluated until then.

The aim of this study is first to determine mRNA genes expression implicated in pain and inflammation process in preclinical model of Dry eye obtained by the excision of extraorbital lachrymal gland (ELG) and Harderian gland (HG) of adult male C57BL/6 mice. Then evaluate the clinical relevance of the effect of topical MSC secretome administration on corneal pain behavior induced by severe DED in mice. To depict the effect of bone marrow-derived MSCs secretome on ocular pain, stem cells were previously stimulated (or not) with TNF- α and INF- γ (100ng/ml) to obtain an anti-inflammatory profile.

2. Methods

2.1 Experimental Animals

Six to eight weeks-old C57BL/6 male mice were used (Janvier Labs, Le Genest Saint Isle, France) and housed in secure cages with free food and water gates, under controlled day-night 12/12 hours cycles, $22 \pm 1^{\circ}\text{C}$ temperature and $60 \pm 10\%$ relative humidity. The study was performed in rigorous accordance with the institutional regulations on the care of animals used for research, approved by

the European Communities Council Directive 2010/63/UE (APAFIS #15012015081815454885 v2).

2.1.1 Surgical procedures

Unilateral (right side) ELG and HG gland excisions were performed under ketamine (80 mg/kg intraperitoneal, i.p.) and xylazine (8 mg/kg i.p.) anesthesia as previously described ²¹. Before the surgery, a drop of lacrimal gel (Lubrital TM laboratory Dechra) was applied to both eyes. Under an operative microscope (Leica-Alcon II, Germany), an 8-mm skin incision on the temporal side was made to expose and remove the ELG. After dissociating the conjunctival tissue above the orbital cavity near the internal canthus, the HG was carefully removed. Complete removal was verified by inspecting the surgical area for any remaining glandular tissue. The skin incision was then sutured using 6.0 braided silk sutures (Vicryl 6-0, Ethicon, Scotland). A drop of iodine solution was applied onto the incision to avoid bacterial infection. For sham animals, an incision was made in the same zone without touching the glands. The mice were placed in warm (30°C) cages to recover from the surgery. A dose of 0.03µL of buprenorphine (1:10) was given to all mice on the surgical day and the first postsurgical day.

2.1.2 Drugs and topical instillation

MSCs secretome was obtained from MSCs Long Evans rat femurs. After culturing the MSCs until passage 5 and characterizing them, 2 types of secretomes were prepared: one without stimulation of MSCs (MEM, 1% Penicillium/Streptomycin) and the other one with MSCs priming by TNF- α and INF- γ (100ng/ml) in order to obtain an anti-inflammatory profile. Secretomes were concentrated X20 using the Amicon Filter Ultra-15 Ultracel 3K by centrifugation at 4000rpm for 1 hour. Both were instilled topically, 5µL twice a day, for 14 days (between days 8 and 21 post-surgery) in right eye.

There were four groups: sham group without treatment, instilled as the control treatment group with MEM-1% P/S, one treated group instilled with non-stimulated MSCs secretome (SNS) and one treated group with stimulated TNF-alfa /INF-gamma MSCs secretome (SSti).

2.2 Corneal Fluorescein Staining

In order to evaluate corneal integrity, fluorescein staining was performed on day 7 after surgery and before starting the treatment and on day 21, after the last instillation. A drop of 1% fluorescein sodium (Fluorescein Faure 0.5%; Novartis France) was applied in the right eye of lightly anesthetized mice. Eyes were examined under cobalt blue light, using slit lamp biomicroscopy. Digital images of corneal surface was captured by a digital camera using EyeSuite™ software (Koeniz, Switzerland) and the defects were classified based on the Oxford Grading System and previous reports²¹: 0, no staining; 0.5, slight punctate staining; 1, diffuse punctate staining; 2, diffuse staining covering less than one third of the cornea; 3, diffuse staining covering more than one third of the cornea; and 4, staining covering more than two thirds of the cornea.

2.3 Eye closing ratio measurement

Spontaneous eye closure is a good index for monitoring spontaneous eye pain²¹. Spontaneous eye closure or the eye ratio is one of the quantitative measures of the grimace scale, which is used to monitor spontaneous pain behavior^{23,24}. The eye closing ratio was calculated based on photographs and corresponds to the ratio height/width. The width is the distance between the internal and external canthus and height the distance between the edge of the upper eyelid and lower eyelids, going through the center of the cornea. Images were captured by a digital camera using EyeSuite™ software (Koeniz, Switzerland). The same millimetric scale was used in all the measurements.

2.4 Confocal microscopy

A laser-scanning *in vivo* confocal microscopy (IVCM, Heidelberg Retina Tomography (HTR) II/Rostock Cornea Module (RCM; Heidelberg Engineering GmbH, Heidelberg, Germany) was used to examine the entire corneal integrity of anesthetized mice²⁵. A minimum of 100 serial TIFF images, covering an area of 400 x 400 μm, was acquired per animal. The first acquisition was in the superficial center of the tissue, determined manually as 0-40 μm for epithelium, 40-140 μm for the stroma and 140-150 μm for the endothelium, as previously described²⁶.

2.5 Measurement of mechanical corneal sensitivity

To evaluate mechanical corneal sensitivity, von Frey filaments test was performed at D0, D7 and D21. To achieve this purpose, various forces of calibrated von Frey filaments (0.008 to 0.04g) were applied to the center of the cornea of immobilized mice. The mechanical threshold corresponded to the eye-blink response ²⁷.

2.6 Gene expression analysis of TG at day 21

2.6.1 Tissue preparation

21 days after lachrymal gland excision, anesthetized mice were transcardially perfused with 10 mL 0.9% NaCl solution. TG were carefully removed and stored at – 80°C until use.

2.6.2 RT-qPCR analysis

RNA extraction from the ipsilateral TG was performed with a NucleoSpin RNA Purification II kit (NucleoSpin RNA S, Germany). RNA quality and concentration were then measured by the NanoDrop method (Thermo Scientific, England). Then, reverse transcription was performed by iScript cDNA Synthesis Kit (BIO-RAD) according to the manufacturer's instructions. RT-qPCR was performed with SsoAdvanced Universal SYBR® Green supermix (Bio-Rad) and pain, neuropathic and inflammatory (SAB Target List) M96 well plate (Bio-Rad ref: 10034393). The GAPDH gene was used as the endogenous reference for each reaction; mRNA levels were calculated after normalization of the results for each sample with those for GAPDH mRNA. The $2^{-\Delta\Delta C_t}$ method was used to analyze the relative differences in specific mRNA levels between groups.

2.7 Statistical analysis of data

Statistical values are reported as mean \pm standard error of the mean (SEM) and analyzed with Graph-Pad Prism version 7.00 (GraphPad Software, La Jolla California USA). The level of significance (α) was set to 0.05 in all cases. Data were evaluated by unpaired and two-tailed

Student's t test (two independent groups), or one-way ANOVA test (multiple independent groups) in case of equal variances, followed by post hoc Bonferroni test when $p < 0.05$. When variable "time" was considered, a bifactorial analysis was performed by two-way ANOVA.

3. Results

3.1 Extraorbital lachrymal gland and Harderian gland excision induce superficial corneal epitheliopathy and reduced spontaneous eye opening

The oxford grade was measured with fluorescein staining at D7 after surgery, using a slit-lamp ophthalmoscope with cobalt blue filter and image analysis to determine corneal epithelium injury. Slit-lamp examination and fluorescein staining showed a significant difference on superficial punctate keratitis in operated animals ($n = 14$) (2.54 ± 0.14) compared sham group ($n = 4$) (1 ± 0) and at day 7 day after the surgery, ($***P < 0.001$) (**Fig.1 and 2A**).

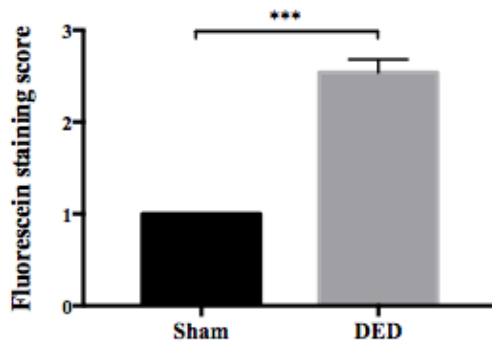


Figure 1: Corneal fluorescein test quantified at day 7 after surgery in sham and operated animals without treatment. Sham group $n = 4$, DED group $n = 14$. Results are expressed as the mean \pm SEM.

The analysis of the *in vivo* confocal microscopy images showed no alteration in sham group during the study. In contrast, we reported some alterations in the corneal tissue in DED mice at day 7, before starting the treatment, notably in the epithelium corneal level (red asterisk), with the presence of dendritic cells (red arrows) and immune cells (yellow arrows) in the sub-basal plexus, and the presence of activated cells in their stroma (black arrows) (**Fig.2B**).

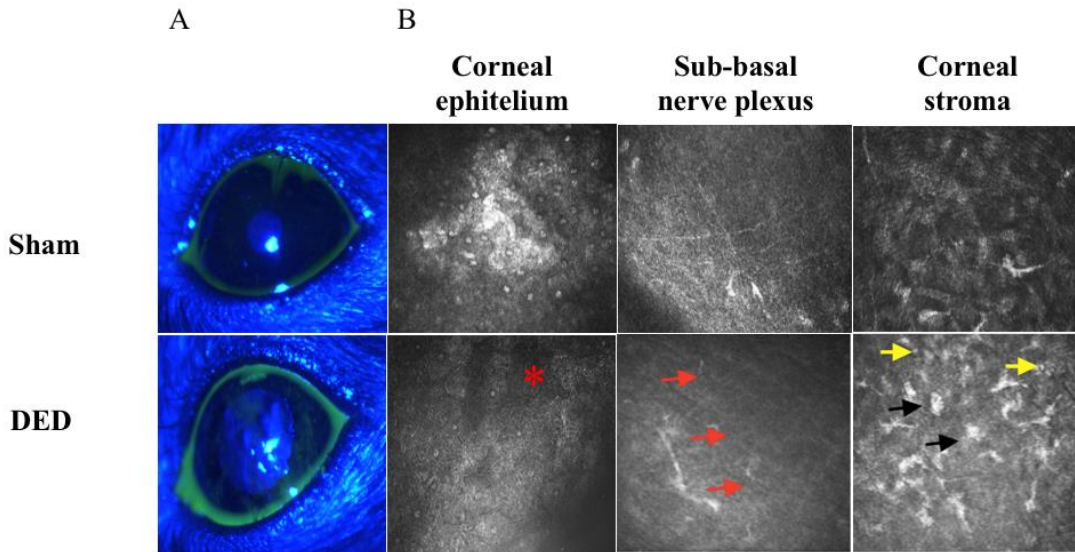
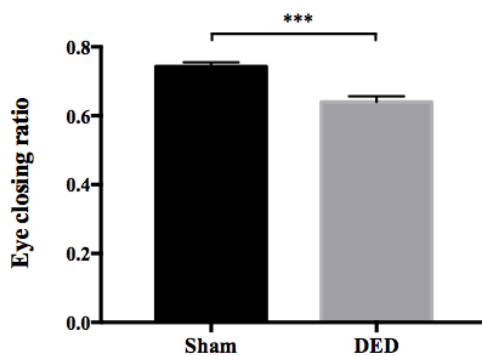


Figure 2. Corneal images acquired 7 days after surgery in sham and DED groups. (A) Corneal surface observed under slit lamp biomicroscopy examination with fluorescein. Superficial keratitis observed in DED mouse. (B) In vivo confocal microscopy. Note the alterations of the corneal epithelium (red asterisk), the long thin irregular dendritic cells in the sub-basal plexus (red arrows), small round hyper-reflective immune cells (yellow arrows), and the activated cells (black arrows) in the stroma of the DED mice.

The spontaneous eye closing ratio refers to the relation height/width in an open eye. Based on ocular photographs of lightly anesthetized mice, we considered the height as the distance between the eyelids' edges and the width as the distance between both medium and lateral canthus. The value for the sham animal was 0.74 ± 0.006 , whereas for all the DED mice, at day 7, was $0.64 \pm$

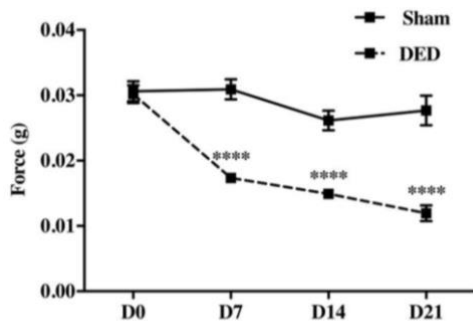


0.004 , showing a lower ratio in DED mice, which is considered an indicator of ocular pain (Fig.3).

Figure 3. Eye closing ratio of sham group and DED animals measure at day 7 after the surgery. A significant decrease in the ratio is showed in DED mice (***) $P < 0.001$.

The corneal mechanical sensitivity was measured with von Frey filaments. At the beginning of the study (D0) we found not significantly difference between the sham animals and the DED group (0.031 ± 0.002 g vs 0.030 ± 0.001 g, $P > 0.05$). Sham animals remained stable during the study.

The DED group showed a decreased in the corneal mechanical sensitivity by day 7 after surgery



and continued to decline until the end of the study (at D21: 0.028 ± 0.002 vs 0.012 ± 0.001 g, $P < 0.0001$), which reflected mechanical hypersensitivity (Fig. 4).

Figure 4. Corneal mechanical sensitivity (g). The threshold was measured with von Frey filaments **** $P < 0.0001$ relative to the sham group. Results are expressed as the mean \pm SEM.

3.2 Extraorbital lachrymal gland and Harderian gland excisions induce upregulation of different pain and inflammatory related genes in the ipsilateral trigeminal ganglion 21 days after surgery

We evaluated by RT-qPCR analysis the expression of genes implicated in inflammatory and pain process at 21-day post-surgery in sham and DED mice. Thus, our data showed that 28 of the 96 genes studied are significantly regulated by DED in the TG of DED mice when compared with sham mice.

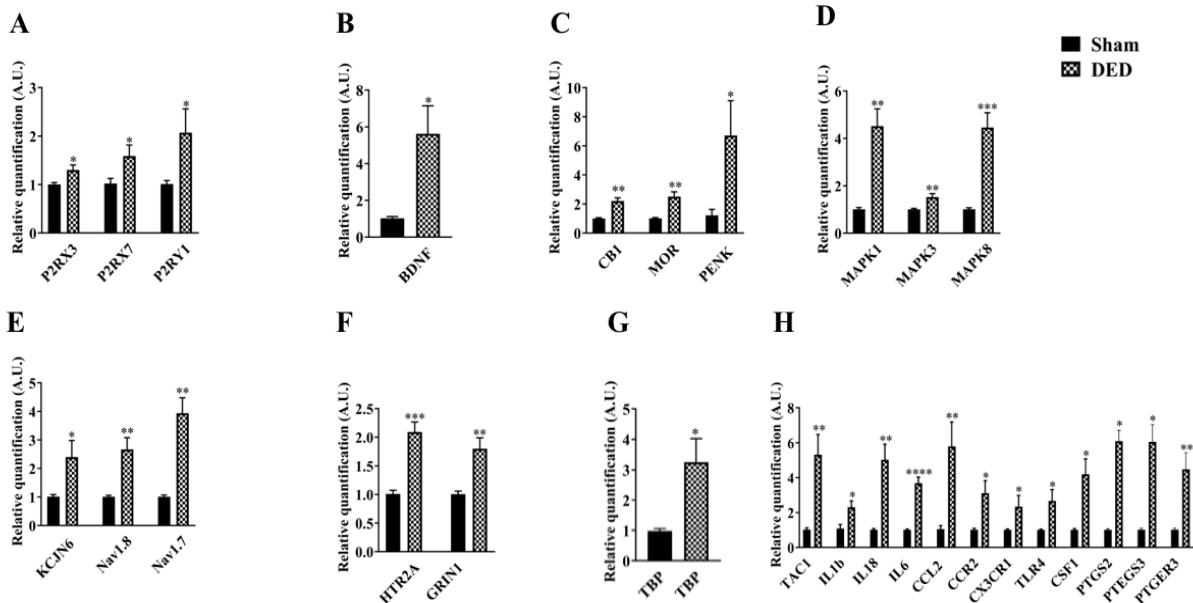


Figure 5: Real time qPCR analysis of TG from sham and DED animals at day 21 after surgery. (A), (B) Glial-inflammatory cell communications genes. (C) Pain inhibition related genes. (D) Intracellular signal transduction genes. (E) Voltage gated ion channels genes

3.2.1 Glial-inflammatory cells communication is increased in chronic DED

The mRNA expression levels of *P2RX3*, *P2RX7* and *P2RY1* in TG at 21 post-surgical day, dramatically increased by 29 %, 54.9 % and 103.96 % (*P2RX3* : 1.00 ± 0.03 vs $3.93 \pm 1.29 \pm 0.10$; *P2RX7*: 1.02 ± 0.10 vs 1.58 ± 0.22 ; *P2RY1*: 1.01 ± 0.07 vs 2.06 ± 0.49 , $P < 0.05$; **Fig. 5A**) in the TG of DED animals compared to sham animals. These data suggest that severe DED might provoke hyperalgesia mechanism by inducing an upregulation of these purinergic receptors.

Brain-derived neurotrophic factor (BDNF) plays a role in nociceptive hypersensitivity in the central nervous system. Its expression is induced by ATP which is controlled by purinergic receptors ²⁸. We showed that mRNA BDNF levels increased by 465 % in the TG of DED animals compared to sham animals (1.01 ± 0.09 vs 5.62 ± 1.52 , $P < 0.05$; **Fig. 5B**).

3.2.2 Pain inhibition genes are upregulated in chronic DED

Mu opioid receptor (MOR), cannabinoid receptor 1 (CB1) and proenkephalin (PENK) are known to inhibit severe acute pain and modulate nociception ^{29, 30}. Thus, we observed that the mRNA levels of MOR, CB1 and PENK increased by 149 %, 121 % and 149 % in the TG of DED animals compared to sham animals (MOR : 1.00 ± 0.05 vs 2.49 ± 0.33 ; CB1 : 1.00 ± 0.05 vs 2.21 ± 0.21 , $P < 0.01$ and PENK: 1.00 ± 0.05 vs 2.49 ± 0.33 , $P < 0.05$; **Fig 5C**).

3.2.3 Increase of intracellular signal transduction at TG of DED animals

The mitogen-activated protein kinase (MAPK) are essential mediators of signal transduction and their activation leads to pain hypersensitivity³¹. MAPKs 1, 3 and 8 mRNA levels increased by 342 %, 49 % and 340 % (MAPK1: 1.02 ± 0.07 vs 4.51 ± 0.73 , MAPK3: 1.02 ± 0.04 vs 1.52 ± 0.14 , $P < 0.01$ and MAPK 8: 1.01 ± 0.06 vs 4.45 ± 0.62 , $P < 0.001$; **Fig. 5D**) in TG of DED animals compared to sham animals.

3.2.4 Overexpression of KCJN6, Nav1.8 and Nav 1.7 voltage gated ion channels mRNA levels in the TG of DED mice

Electrical excitation of peripheral somatosensory nerves is controlled by potassium and sodium ion channels^{32,33}. The level of mRNA coding for potassium channel 2 (KCJN6) increased by 136.63 % the TG of DED animals compared to sham animals (KCJN6: 1.01 ± 0.07 vs 2.39 ± 0.58 , $P < 0.05$; Fig. 6). In addition, the levels of sodium channel 1.8 (Nav 1.8) and 1.7 (Nav 1.7) mRNA increased by 166 % and 293 % (Nav1.8: 1.00 ± 0.05 vs 2.66 ± 0.40 ; Nav1.7: 1.00 ± 0.06 vs 3.93 ± 0.53 , $P < 0.01$; **Fig. 5E**) in the TG of DED animals compared to sham animals.

3.2.5 Markers of synaptic transmission increases in chronic DED

An increase of electrical excitation increases synaptic transmission. We investigated serotonin and glutamate receptors expression in the TG of DED and sham animals. Therefore, the levels of 5-Hydroxytryptamine Receptor 2A (HTR2A) and Glutamate [NMDA] receptor subunit zeta-1 (GRIN1) mRNA increased by 109 % and 79 % (HTR2A: 1.00 ± 0.06 vs 2.09 ± 0.17 , $P < 0.001$; GRIN1: 1.00 ± 0.05 vs 1.79 ± 0.18 , $P < 0.01$; **Fig. 5F**) in TG of DED animals.

3.2.6 TATA box binding protein gene is overexpressed in DED mice

The levels TATA-binding protein (TBP) mRNA increased by 235.05 % in TG of DED animals compared to sham animals (0.97 ± 0.08 vs 3.25 ± 0.77 , $P < 0.01$; **Fig. 5G**).

3.2.7 Genes related to Inflammation are highly expressed in TG of DED animals

The mRNA levels of prostaglandin-endoperoxide synthase 2 (PTGS2) also known as cyclooxygenase-2 (COX-2), prostaglandin E synthase 3 (PTGES3) and prostaglandin E receptor 3 (PTGER3) increased by 501 %, 501 % and 342 % (PTGS2: 1.01 ± 0.07 vs 6.08 ± 0.62 ; PTGES3: 1.01 ± 0.09 vs 6.05 ± 0.98 , $P < 0.05$ and PTGER3: 1.01 ± 0.08 vs 4.47 ± 0.94 , $P < 0.01$; Fig. 5H) in TG of DED animals compared to sham animals.

Moreover, the levels of tachykinin Precursor 1 (TAC1), colony stimulating factor 1 (CSF1) and toll like receptor 4 (TLR4) mRNA increased by 421 %, 315 % and 163 % (TAC1: 1.02 ± 0.10 vs 5.31 ± 1.15 , $P < 0.01$; CSF1: 1.01 ± 0.06 vs 4.19 ± 0.87 , $P < 0.05$ and TLR4 : 1.00 ± 0.04 vs 2.66

± 0.65 , $P < 0.05$; **Fig. 5H**) in TG of DED animals compared to sham animals. Besides, the levels of interleukins IL1B, IL18 and IL6 mRNA increased by 113 %, 398 % and 263 % (IL1B: 1.08 ± 0.23 vs 2.30 ± 0.36 , $P < 0.05$; IL18: 1.01 ± 0.07 vs 5.03 ± 0.89 , $P < 0.01$ and IL6 : 1.00 ± 0.05 vs 3.67 ± 0.35 , $P < 0.0001$; **Fig. 5H**) in TG of DED animals. Furthermore, the levels of the chemokine (C-C motif) ligand 2 (CCL2), C-C chemokine receptor type 2 (CCR2) and CX3C chemokine receptor 1 (CX3CR1) mRNA expression increased by 450%, 207 % and 132 % (CCL2: 1.05 ± 0.19 vs 5.78 ± 1.39 , $P < 0.01$; CCR2: 1.01 ± 0.07 vs 3.10 ± 0.71 , $P < 0.05$; CX3CR1: 1.00 ± 0.05 vs 2.34 ± 0.64 , $P < 0.05$; **Fig. 5H**) in TG of DED animals.

These results highlight an upregulation of the genes implicated in pain conduction and modulation of pain responses in TG of DED animals.

3.3 Analysis of therapeutic effect of MSC secretome topical treatment on severe DED mice cornea

Twice daily topical instillations of MSC secretome or MEM 1% P/S was applied topically from 7 days after extraorbital and Harderian lacrimal glands excision, during 14 consecutive days. Sham group, with healthy corneas, was not treated. DED animals were separated into 3 treatment groups: the control treatment group with MEM-1% P/S, one group instilled with non-stimulated MSCs secretome (SNS) and one group treated with stimulated TNF-alfa and INF-gamma MSCs secretome (SSti).

By slit-lamp examination with fluorescein staining after 14 days of treatment, at D21 we observed a statistically difference in all treated DED animals according to the Oxford score, compared with the first measurement at D7, before starting the treatment (SSti 1.20 ± 0.020 , SNS 1.00 ± 0.27 and MEM P/S 1.25 ± 0.25 ; $***P > 0.001$) and compared with DED animals without treatment (2.55 ± 0.33 ; $*P < 0.05$, $**P < 0.01$, $***P < 0.001$) (**Fig.6**).

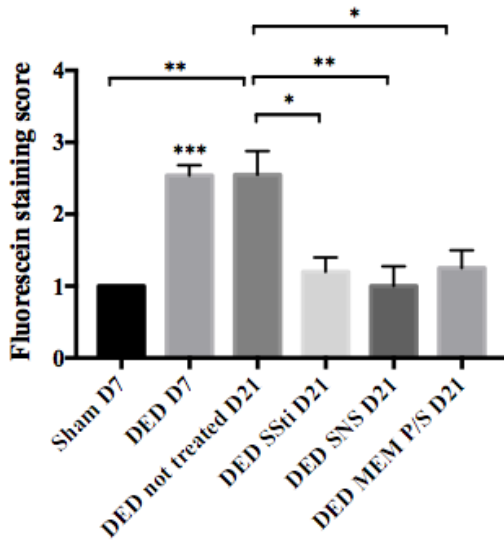


Figure 6. Fluorescein staining was examined at D7 after surgery, before starting treatment in DED mice (Sham group $n = 4$ (0.88 ± 0.13), DED group $n=14$ (2.54 ± 0.14)); (** $P < 0.001$) and also at D21 (14 days after treatment) showing a remarkable decrease in all treated mice (DED not treated $n = 10$ (2.55 ± 0.33), SSti $n = 5$ (2.6 ± 0.25), SNS $n = 5$ (2.4 ± 0.25), MEMP/S $n = 4$ (2.5 ± 0.29)). Results are expressed as the mean \pm SEM.

The eye closing ratio of sham animals (0.75 ± 0.010) showed an improve in the different DED treated groups at the end of the study (SSti 0.76 ± 0.003 , SNS 0.73 ± 0.006 and MEM group 0.703 ± 0.011) when comparing with the previous measurement at day 7, showing a statistically difference between day 7 and day 21 measures (** $P < 0.001$) and also compared with DED animals not treated at day 21 (0.65 ± 0.022 ; * $P < 0.05$, ** $P < 0.01$) (**Fig. 7**).

The mechanical allodynia was tested using von Frey filaments on treated mice. At D7 after surgery, DED mice showed mechanical hypersensitivity compared with sham animals. After the topical administration of treatment, the three groups showed an increase in the mechanical threshold, what can be interpreted as a recovery on normal corneal sensitivity (** $P < 0.01$). Although we reported no difference between SSti, SNS and MEM groups, the statistical significance was higher in relation to DED mice not treated at day 21 (** $P < 0.001$, **** $P < 0.0001$) (**Fig. 8**).

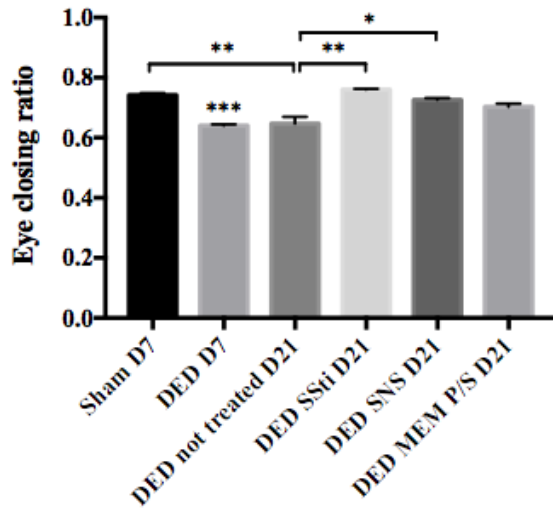


Figure 7. Eye closing ratio. Measurement on D7 showing a significant difference between sham group and DED animals (sham 0.74 ± 0.006 and DED mice 0.64 ± 0.004); (** $P < 0.001$) Note the raise on the ratio of treated groups at D21 (Ssti 0.76 ± 0.003 , SNS 0.73 ± 0.006 and MEM group 0.703 ± 0.011); compared with DED not treated animals (0.65 ± 0.022 ; * $P < 0.05$, ** $P < 0.01$).

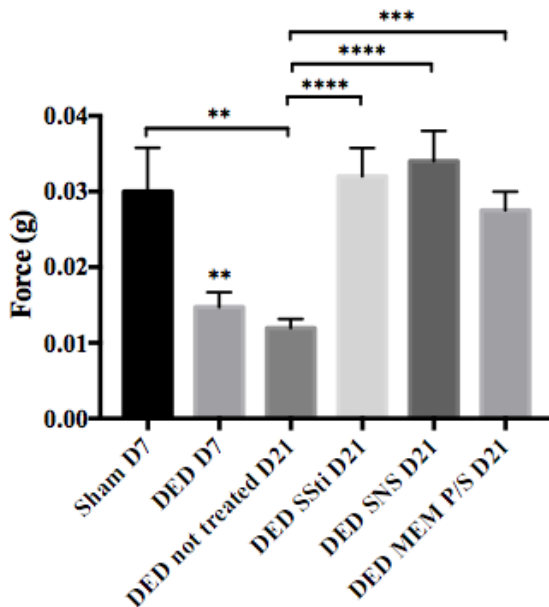


Figure 8. Corneal mechanical sensitivity. The threshold was measured with von Frey filaments (A) At day 7 after surgery, DED animals showed an important increase in the mechanical threshold when compared with sham animals (sham 0.275 ± 0.005 and DED mice 0.015 ± 0.005); (** $P < 0.001$). (B) At day 21, after 14 days of treatment, note the improvement on the corneal sensitivity of all treated DED mice (Ssti 0.032 ± 0.004 , SNS 0.034 ± 0.004 and MEM P/S 0.039 ± 0.006); (** $P < 0.01$) when compared with not treated DED animals (0.011 ± 0.001 ; ** $P < 0.001$, **** $P < 0.0001$). Results are expressed as the mean \pm SEM.

4. DISCUSSION

4.1 Effect of the excision of ELG and HG glands compared with a sham group

DED symptomatology has a broad range of complaints in addition to visual ones, that includes dysesthesias, referred as “dryness”, “burning” and “aching”, between others³⁴. The clinical

manifestations of DED are well known as factors that impact quality of life, assessed in severe cases, as debilitating as angina pectoris³⁵.

Different rodent models of DED have been studied, for example with the topical use of benzalkonium chloride³⁶, the intraglandular administration of botulinum toxin³⁷ and the excision of extra and intraorbital lacrimal glands³⁸.

In this study, clinically, we observed that the excision of ELG and HG glands triggered an increased in behavioral pain when measured with eye closing ratio and corneal mechanical threshold, as well as a rise on the corneal fluorescein staining scale.

It has been considered that inflammation plays a main role in the physiopathology of DED, held by research on different tissue culture, animal models and patients results³⁹. We observed a significative difference on the fluorescein score since the day 7 after surgery when compared sham and DED animals. We also found important differences in DED animals on the *in vivo* confocal microscopy as early as the 7 day after surgery²¹ according to previous studies: epithelial alterations, dendritic cells in sub-basal nerve layer and activated and immune cells in the anterior stroma. In accordance with previous DED models, the immune and inflammatory response has been described with IVCN findings like activated keratocytes and cell infiltration⁴⁰. The increased number of hyper-reflective structures in the stroma is thought that correspond to inflammatory cell infiltration and activation that could be triggered by the epithelial injury⁴¹.

4.2 Effect of DED on the expression of gene implicated in inflammatory and pain process in TG at D21 after surgery in mice

In this study, we systematically investigated the gene expression related to neuropathic pain and inflammation on TG of a mice model of pain induced by severe DED, at day 21. Once we evaluated the different mRNA expression between sham and DED group, our data showed that 28 of the 96 genes studied might play a pivotal role in neuroinflammatory mechanisms related to this specific type of chronic pain. Thus, a better understanding of pain biomarkers is required not only to

improve the evaluation and diagnosis techniques, but to develop prognosis supports and to reach new and better therapeutic targets related to the expression of genes manipulation.

4.2.1 Glial inflammatory cells communication

Adenosine triphosphate (ATP) connects with to the purinergic signaling system including P2X and P2Y receptors and activates inflammatory cells. Besides, activation of purinergic receptors contributes to acute nociception and maintaining of nociceptive sensitivity⁴². Therefore, we investigated the mRNA levels of P2RX3, P2RX7 and P2RY1 in the TG of DED animals and sham animals. Our data showed that the excision of ELG and HG generates a severe aqueous deficient dry eye that increase some markers associated with inflammation and pain at day 21 after the surgery on the TG of those animals. In the family of P2X purinoreceptors, P2X3 receptors were firstly characterized in dorsal root ganglia neurons, and it was reported an important role in neuropathic and inflammatory pain transduction⁴³. It has been found that the signaling from different soluble factors, such as BDNF, is effective in rising P2X3 receptor function and promoting phosphorylation ⁴⁴. The P2RX7 receptor is a member of a family of extracellular ATP (eATP)-gated ion channels expressed in immune cells, where its function is to activate the inflammatory cascade. This receptor is found documented in pain processes and has been investigated as a target in the treatment of infectious and inflammatory diseases⁴⁵.

4.2.2 Pain inhibition genes

CB1 or type 1 cannabinoid receptor (CB₁) is a primary constituent of the endocannabinoid system. Its receptor abundance, as well as its function, are dynamically regulated according the CB₁ gene expression when there is a pathological condition or in response to drug exposure, including cannabinoids themselves⁴⁶. Activation of cannabinoid receptors (CB₁R and CB₂R) induces potent anti-allodynic effects in rodent models of pain ^{47,48}. However, it is little known about regulation of CB₁ gene expression. This increase expression of CB₁, MOR and PENK genes may cause an increase of their receptor's activation, although in the other hand it may not explain why analgesia is decreased during neuropathic pain.

The mu opioid receptor (MOR) plays a key role in mediating the major clinical effects of analgesics, such as the effects of morphine ⁴⁹. In contrast to a previous study that reported a

decrease MOR mRNA in dorsal root ganglia following a chronic nerve injury^{†50}, we found an increase in MOR mRNA expression. The study of different neuropathic models may explain and underlie those differences.

Proenkephalin (PENK) -derived peptides are involved in responses as pain and neuromodulation, as they control the expression of endogenous opioid peptide⁵¹. This is the first study that describes the mRNA levels of PENK in TG in a DED model. The increased expression in the results suggest it as a promising therapeutic target.

4.2.3 Intracellular signal transduction

Signaling pathways for neuropathic pain related to DED include the gene mitogen-activated protein kinase (MAPK) family⁴. The gene mitogen-activated protein kinase-1 (*MAPK1*), which belongs to the MAP kinase family and is also known as extracellular signal-regulated protein kinase-2 (ERK2), a pain response modulation gene MAPK3, and the cell apoptosis closed related MAPK8 were evaluated in this study. Quantification of MAPK1, MAPK3 and MAPK8 gene expression showed a significant increase in pathologic tissue of DED mice compared with normal tissue of sham, suggesting that the regulation of MAPK signaling has a potential therapeutic target for the treatment of neuropathic pain in DED, since the stimulation of endocannabinoids receptors is associated with the activation of MAPKs pathways with increased activity of different transcription factors⁵².

4.2.4 Voltage ion channels

G protein-gated inwardly rectifying potassium channel (GIRK) are associated in regulation of excitatory and inhibitory neurotransmission by decreasing cell excitability through the membrane hyperpolarization with the outward potassium current induced by their opening⁵³. GIRK 2 or KCNJ6[‡] is a G protein coupled channel that mediates a significant component of analgesia as it has been associated with opioid antinociception on postsynaptic inhibition⁵⁴.

[†] This decreased expression of the MOR may partially explain why opioid analgesia is decreased during neuropathic pain.

[‡] KCNJ6: potassium inwardly rectifying channels, subfamily J, member 6.

It has been reported that KCNJ6 is expressed in dorsal root ganglia (DRG), where is selective for small unmyelinated non-peptidergic and large myelinated neurons⁵⁵. Genetic analyses suggest that GIRK2 gene variation may predict analgesic effectiveness (GIRK2)⁵⁶. In our study, the genetic expression of KCNJ6 was significantly increased in TG of DED mice at D21 when compared with sham group.

Voltage-gated sodium (Nav) channels are essential contributors for action potentials in excitable cells such as neurons and they are well known for their main role as analgesic targets³³. Nine subtypes of Nav (Nav1.1–Nav1.9) are known, and each one has been described with a different physiological function in dorsal root ganglion neurons⁵⁷. The Nav1.7 channel is highly expressed in small nociceptive neurons while the Nav1.8 channel is mainly expressed by small primary sensory neurons⁵⁸. These channels, Nav1.7 and Nav1.8, play important roles in the development of inflammatory and neuropathic pain and therefore they have been underlined as potential molecular targets for its management ⁵⁸. In contrast to Nav1.7 channels, which may play a role as threshold channels in peripheral sensory neurons, Nav1.8 channels have been found to carry most of the sodium current responsible for the rising phase of the action potentials⁵⁹.

Nerve injury has been found to trigger upregulation of Nav1.7 in DRG neurons and rearrangement of Nav1.7 channels, rising neuropathic pain in mice⁶⁰.

Additionally, endogenous opioids contribute to pain insensitivity in mice with Nav1.7 lack, which suggest the existence of compensatory regulation mechanisms in Nav1.7 deficient mice ⁶¹.

Gain-of-function modifications in Nav1.8 have been described in patients with neuropathic pain, which had an enhanced channel response to depolarization and hyperexcitability in DRG neurons, including reduced current threshold, increased firing frequency, and spontaneous activity⁶².

Both sodium channels genes, Nav1.7 and Nav 1.8, showed a substantial increase in our DED murine model at day 21 after surgery, highlighting them as significant molecular targets.

4.2.5 Synaptic transmission genes

In our study, we found a relevant increase in the measurement of HTR2A and GRIN1 genes. The detection of the mRNA synaptic transmission genes in rodent TG untreated model guided us to

develop new approaches to further define their clinic relevant. Serotonin or 5-hydroxytryptamine (5-HT) has been identified as a central neurotransmitter of the antinociceptive system of the spinal cord⁶³. From the metabotropic serotonin receptor (5-HT₂R) family, which contains three isoforms⁶⁴, the 5-HT_{2A}R is a G protein-coupled receptor (GPCR) that leads a rise in calcium release from intracellular stores⁶⁵. The multiple interactions of 5-HT_{2A} receptors form protein complexes, with molecules such as: the metabotropic glutamate mGlu₂ receptor, dopamine D₂ receptor, cannabinoid CB₁ receptor, 5-HT_{1A} receptor, the ghrelin receptor (growth hormone secretagogue receptor 1 α , GHS1 α R), the melatonin MT₂ receptor, and the N-methyl-D-aspartate (NMDA)-gated ion channel subunit GluN_{2A} ⁶⁶. This biological interaction is not completely elucidated but has led to identify the HT_{2A} as a main participant in allodynia circuits ⁶⁷, and it has been reported the involvement of HTR_{2A} gene polymorphisms on the sensitivity to chronic pain disorders ^{68, 69}.

The GRIN1 gene encodes for the heteromeric glutamate-gated calcium ionotropic channel, the subunit zeta-1 protein of the N-methyl-D-aspartate (NMDA₁) receptor, which has a fundamental role in the brain on synaptic physiology⁷⁰.

Activation of NMDARs has been described as a key for the developed and maintenance of chronic pain, known as central sensitization, due to its capability of increase calcium influx and the consequent trigger of intracellular signaling pathways, which magnify the response to nociceptive stimuli. The overload of calcium has been associated with neuron loss⁷¹, and extra-synaptic NMDAR activation may suppress survival-promoting genes⁷². A recent study reported that NMDAR deletion at dorsal horn synapses offered neuroprotection by blocking the transition from acute to chronic pain and without disturb of nociception⁷³.

4.2.6 TATA box binding protein

The regulation of transcription initiation has been proposed the main way of gene expression control. The pre-initiation complex or PIC assembly is in charge of the loading of RNA polymerase II (Pol II) onto DNA⁷⁴. The TATA-box binding protein (TBP), a single protein of intermediate size but a ubiquitous general transcription factor, was identified as a component of the TFIID factor,

one of the leading eight PIC factors^{§75}. TBP first characterization was as an activity that attaches to TATA mRNA box genes and nucleates the arrangement of the Pol II – PIC, but now is known that transcription from RNA polymerase I, II and III promoters requires TBP in different complexes, even the processes are not well understood⁷⁶.

It has become clear that the increase or decrease in TBP amount will be reflected either in gene expression or gene activity^{39,77}. When neuronal and glial cells were cocultured it was reported that mutant TBP promoted a markedly inflammatory pathways activation in astrocytes, which caused neurotoxicity⁷⁸. Further studies are necessary to explain the implication of this TBP gene rise expression on inflammation and pain on TG due to DED.

4.2.7 Inflammation related genes in DED

In a deep gene analysis reported, six genes were identified as main related with pain: FOS, IL6, TNF, TAC1, IL8, and KNG1⁷⁹. In the present study, 12 genes related to inflammation are reported, two of them were identified as essential in the pain gene analysis and we reported a statistically significant higher value of mRNA in TG of DED mice: IL6, and TAC1.

Interleukin 6 (IL6) was the second central gene consider as a key element of pain⁷⁹. It is one of the main cytokines of acute phase response and its over-expression has been broadly studied in association with a wide range of diseases as well as its regulatory function in many types of pathological pain, including nerve injuries⁸⁰.

TAC1 belong to the tachykinin gene family. It encodes different neuropeptides, such as Substance P, which contributes to neurogenic inflammation process and its presence in C fibers suggest the role of TAC1 onto inflammatory pain⁸¹.

Two important members of the IL-1 cytokine family were found statistically highly expressed in the DED group: IL-18 and IL-1 beta. IL-18 function was firstly described as a factor that induces IFN- γ production from Th1 cells. At present, it is known that has a stimulating role in both innate

[§] TFIIA, TFIIB, TFIID, TFII E, TFII F, TFII H, Pol II, and Mediator.

and acquired immunity⁸². On the other hand, IL-1 beta has already been studied as a potent pronociceptive agent in the periphery and CNS ⁸³. Likewise, its release as result of corneal injury-induced ocular pain has been documented²⁶.

We observed that mice suffering from DED showed at D21 an upregulation of CCL2 and CCR2 proinflammatory markers in the TG, with respect with sham control animals.

Evidence suggest that sensory neurons express the chemokine CCL2 and its receptor CCR2⁸⁴. The CCL2-CCR2 axis has been implicated in the pathogenesis of a broad spectrum of diseases including neurological diseases, where directly excite nociceptive neurons and stimulate pain behavior⁸⁴.

Recently, the microglial activation of TLR4 and CCR2 signaling pathways showed to promote mechanical allodynia during repeated social defeat, a mouse model of psychosocial stress that activates microglia and rise the neuroinflammatory responses⁸⁵. Toll-like receptor 4 (TRL4) has been identified as a receptor in the microglia involved in the induction and preservation of pain in rodent models of neuropathy⁸⁶. We found an increased mRNA expression of TRL4 gene in our murine DED model.

In this study, the pain induced by DED was accompanied by a significant increase in the levels of CX3CR1 and CSF1. The CX3CL1(fractalkine) is a soluble chemokine produced by neurons and astrocytes⁸⁷, and its receptor CX3CR1, which expression has been reported on microglial cells in the spinal cord of rats with neuropathic pain through a nerve injury induced model⁸⁸.

CSF1 is a cytokine that acts on macrophage-lineage cells. Increased levels of CSF1 are found in different neurologic pathologies including nerve injury⁸⁹. CSF1 over-expression was described to contribute in microglial numbers and inflammatory responses⁹⁰.

Lastly, the mRNA levels of PTGS2, PTGES3, and PTGER3, which contributes to prostaglandin synthesis, were significantly higher in TG of DED animals than to their sham counterparts. COX-2, known as the prostaglandin synthase cyclooxygenase-2, catalyzes the first two steps prostaglandin synthesis and it is encoded by the PTGS2 gene, and even it can be found in both non-

inflammatory and inflammatory environments, the main expression of this gene is controlled by pro-inflammatory stimuli⁹¹. PTGS2 can be induced by cytokines and there are numerous signaling pathways that activates its promoter, which contains binding sites for TATA-box. It has been characterized as a therapeutic target with a basic function in pain response that presents diverse variants that are associated with pharmacodynamics⁹². One of the four known prostaglandin E2 receptor is PTGER3. It has been reported, regarding pain, that its expression provides endogenous antinociception, showing an opposite effect of the other PTGE2 receptors. Furthermore, PTGE3 receptor was found vastly expressed in spinal cord and sensory DRG of rats⁹³.

Chronic neuropathic pain caused by DED remains a major therapeutic challenge and new proposals are been studied; in example, the enhancement of endogenous opioid peptide concentration in anterior segment tissues⁹⁴, and the use of topic cannabinoids⁹⁵. However, the interaction of the genes involved is required, because the final effect not depends only of the aim interaction of the ligands with the proteins, but also the molecular environment. In example, studies suggest that glial cells, mostly microglia, exert a critical task in opioid tolerance and opioid induced hyperalgesia by the activation of TLR4⁹⁶, while ion channels, such as KCNJ6, are also basic for opioids analgesic effects achievements⁹⁷. The injury to nervous system that conducts to neuropathic pain may result in neural cells excitability, where the expression and correct function of ion channels expressed by them is the core of the promising ion channels blockers onto sensory nociceptive neurons⁹⁸. Thus, the opioid binding to MOR ligands is not enough to achieve a satisfactory analgesic response. In this long-sought need for improved pharmacological responses, gathering research in ionic channels physiology had led to potential analgesic treatments.

4.3 Effect of the instillation of MSC secretome twice a day during 14 days in a DED characterized model

This study showed a potential anti- inflammatory effect of MSCs secretome, a set of several factors that have been proved to produce a positive impact on damage tissue, in a rodent model of corneal pain generated by DED. Our data indicates a clinical improvement in mice with DED induced by the excision of ELG and HG lacrimal glands. However, we could not find any significative difference between the groups treated with secretome SSti and SNS when compared with MEM

P/S instillation. This could be explained due to the topical administration of a medium that contributes with aminoacids, glucose and vitamins in addition to supplemented antibiotics (penicillin and streptomycin) in a severely dry corneal surface. Due to Covid-19 pandemic we neither could replicated this study in a new group of animals nor could be able to finish the complete molecular study. Our experiments could be improved with a higher number of mice, taking measurements more frequently and added a MEM without P/S treated DED group; and according to the results, the topical dose could be increased.

Current DED management help to improve the symptoms associated with DED⁹⁹, but antinociceptive treatments for this disease remains a therapeutic challenge. Nowadays, some treatments use anti-inflammatory and immunosuppressive actions of autologous serum which aims to promote tissue repair by providing growth factors¹⁰⁰.

Different reports have demonstrated the effect of MSCs *in vitro* and *in vivo* models of DED, showing in both cases, beneficial outcomes on inflammation. In one *in vitro* model, the stimulation of corneal human cells through pro-inflammatory cytokines TNF-alfa and IFN-gamma in culture with the secretome or in coculture with MSCs showed a decrease in the expression of inflammatory markers ¹⁰¹. Two *in vivo* studies have shown the success of MSCs in decreasing inflammation reaction in DED models ^{102,103}. Several studies have proved the promising effect of MSCs and their secreted factors as the responsible of tissue repair ^{104, 105, 106}.. Hence, our study assessed a new topical treatment by considering the potential effect of MSCs secretome based on the background of precedent acute inflammatory models and a recent study that have focused the value of MSCs drafts in dry eye . Also, there have been reported in severe DED murine models the effect of MSCs when they have been applied through different ways, systemically or periorbital and the improve was significative on the lacrimal gland function in both cases⁴⁴.

Even it has been proved that MSC transplantation significantly improves the regenerative capacity of damaged lacrimal gland structures to 62% of total tissue¹⁰⁷, the risk of side effects of bone marrow transplant hasn't been reported. The higher amount of viable acinar structures after MSC draft corroborates the therapeutic potential of this type of therapy¹⁰⁷.

Using the secretome without the risk of secondary effects of drafts, based on the proposal that the trophic factors on the MSCs secretion are the responsible of the therapeutic effects^{108,109,110}, emerges as a promising approach for the restorative therapy of pain in patients with severe DED.

4.4 Limitations of the current study

Several limitations of this study should be considered. Research of ocular pain as a symptom of DED has lately been started. Therefore, the biomarkers related, and the curative treatment remain unknown. The number of the mice where less than the half of our main model, thus additional validation studies are needed to corroborate our findings.

We are describing for the first time the genes overexpressed in a rodent DED model TG. The molecular mechanism and associated signaling pathways of this pathology still remains largely unknown. What has become evident is that the expression levels of these genes and the protein framework are critical for the neuropathological outcomes. Despite the limitation that the analysis in this study is considered preliminary and exploratory, we present novel meaningful candidate genes associated with chronic pain in dry eye disease.

Considering that gene expression is controlled by a large amount of transcription factors and epigenetic mechanisms, there is a long way to walk, however, we have started analyzing how peripheral nerve injury alters the expression levels of many genes. Moreover, it is well known that chronic pain due to severe DED is associated with neural damage. However, the complete gene expression in the TG is still undetermined. With the increase of injury time, compared with the sham group, the gene expression profile of our mice model exposed to an induced DED, showed on TG significantly upregulation at mRNA level; it is necessary to confirm the protein expression in further studies, to understand if the up and downregulation is consistent to their gene expression at mRNA level.

Finally, the effect of topical administration of MSCs secretome in our DED model was not completely evaluated because of the quarantine due to Covid-19. The therapeutic implications of these outcomes remain to be determined. Finally, the use of topical MSCs secretome has not yet

been officially evaluated in controlled trials as treatments of ocular pain generated by DED, and consequently, it is not possible to discuss the potential therapeutic dose.

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