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Connexin 43 deficiency accelerates skin wound healing and extracellular matrix remodeling in mice

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ABSTRACT

Background: Cellular channels composed of connexin 43 are known to act as key players in the life cycle of the skin and consequently to underlie skin repair.
Objective: This study was specifically set up to investigate the suite of molecular mechanisms driven by connexin 43-based channels on wound healing.
Methods: To this end, a battery of parameters, including re-epithelialization, neovascularization, collagen deposition and extracellular matrix remodeling, was monitored over time during experimentally induced skin repair in heterozygous connexin 43 knockout mice.
Results: It was found that connexin 43 deficiency accelerates re-epithelialization and wound closure, increases proliferation and activation of dermal fibroblasts, and enhances the expression of extracellular matrix remodeling mediators.
Conclusion: These data substantiate the notion that connexin 43 may represent an interesting therapeutic target in dermal wound healing.

1. Introduction

Intercellular communication mediated by gap junctions is major driver of skin differentiation and remodeling. Gap junctions consist of 2 hemichannels of adjacent cells, which in turn are built up by 6 connexin (Cx) proteins. As many as 10 different connexin family members have been identified in human and rodent skin, all of which are named after their molecular weight and are expressed in a cell type-specific and developmental stage-specific way [1–4]. Thus, keratinocytes in the epidermal *stratum basale* and *stratum spinosum* as well as dermal fibroblasts and endothelial cells abundantly express Cx43, while keratinocytes in the *stratum granulosum* mainly produce Cx26. Not surprisingly, connexin expression in the epidermis undergoes drastic modifications during skin repair and disease [5,6]. In fact, epidermal Cx43 expression decreases after initial skin injury at wounded margins, but increases in dermal fibroblasts [7]. The importance of Cx43 in skin repair is evidenced by the fact that heterozygous Cx43 knockout mice exhibit early wound closure associated with higher proliferation and mobilization of keratinocytes in wound healing [8]. Furthermore, animals treated topically with Cx43 antisense oligodeoxynucleotides display improved closing of skin lesions with significantly lower deposits of granulation tissue and subsequent reduction in scar formation [9]. Likewise, wounded and burned murine skin treated with Cx43 antisense oligodeoxynucleotides presented accelerated wound healing, enhanced keratinocyte proliferation, and increased migration of fibroblasts and more pronounced collagen deposits [5,10]. Lu and group [11] demonstrated that fibroblasts derived from keloids or hypertrophic scars have considerably lower quantities of Cx43 compared with counterparts derived from normal skin. In addition, diabetic rats exhibit delayed wound re-epithelialization and abnormal expression of Cx43 in the epidermis of the wound edges [12]. Altogether, these observations point to a clear-cut role for Cx43 in skin repair. In this context, the present study was set up to further identify the molecular mechanisms related to wound healing affected by Cx43. For this purpose, several parameters, including re-epithelialization, neovascularization, collagen deposition and extracellular matrix remodeling, were monitored over time during

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experimentally induced skin repair in heterozygous Cx43 knockout mice.

2. Materials and methods

2.1. Animals

Eight-week-old male wild-type (WT, $n = 18$) and heterozygous knockout ($Cx43^{+/-}$, $n = 18$) mice with a CD1 background were used in this study. $Cx43^{+/-}$ mice were obtained from the International Agency for Research on Cancer (France) and were generated by replacing exon 2 of the Cx43 gene with the neomycin resistance gene [13]. Mice were housed under controlled conditions (*i.e.* temperature, 22 ± 2 °C, relative humidity 65 ± 15%, and 12 h light/dark cycle). All mice had access to commercial diet and filtered water *ad libitum*. These management conditions were in accordance with the recommendations of National Research Council (2010) and animal studies were performed with the approval of the Committee on Care and Use of Animal Resources of the School of Veterinary Medicine and Animal Science, University of São Paulo, Brazil (protocol no. 1525008).

2.2. Genotyping

Genotyping was performed according to standard procedures using tail-derived DNA as previously described [14]. Primer pairs used for detection of the endogenous Cx43 gene were 5′-CCCCACTCTCACCTATGTCTCC-3′ and 5′-ACTTTTGCCGCCTAGCTATCCC-3′, generating a polymerase chain reaction (PCR) product of 520 base pair (bp). Primer pairs used for detection of the neomycin resistance gene were 5′-GGCCACAGTCGATGAATCCAG-3′ and 5′-TATCCATCATGGCTGATGCAA-3′, generating a PCR product of 294 bp. The amplicons were loaded onto a 1.5% agarose gel in Tris-buffered saline.

2.3. Excisional wounding procedures

Excisional punches were made as described previously with slight modification [15]. Mice (±30 g) were anesthetized by intraperitoneal injection of 100 mg/kg ketamine and 20 mg/kg xylazine. Their dorsal skin was cleaned, shaved and sterilized with iodine solution. Two 5 mm full-thickness excisional punches were created through the skin and *panniculus carnosus* on the upper paravertebral region. Wounds were photographed daily and visually monitored for possible signs of infection. The wound areas were standardized by comparison on day *N* with the original wound size on day 0 and expressed as a percentage of wound closure using the formula [(day 0 area − day *N* area)/day 0 area] × 100. The extent of wound contraction was visualized as the edge of scar and was easily distinguishable from the extent of re-epithelialization.

2.4. Histological analysis

Wound beds surrounded by a margin of non-wounded skin were collected at days 3, 7 and 14 post-injury ($n = 6$/genotype/day). Wounds were divided in half in the least healed portion. Half of the wound was fixed overnight at 4 °C in 60% methanol, 30% chloroform and 10% acetic acid. Tissues were processed through graded ethanol solutions and embedded in paraffin blocks. Tissue sections of 5 μm were stained with hematoxylin/eosin or Sirius red. The other half of the wound was collected in RNAlater (Qiagen, USA), submerged in liquid nitrogen and stored at −80 °C for further analysis.

2.5. Wound re-epithelialization and neovascularization

Hematoxylin/eosin-stained slides were evaluated for the presence of newly formed blood vessels and thickness of the epithelium 3, 7 and 14 days after injury. For the latter, 10 measurements per animal were carried out and averaged, with 5 on each edge of the skin lesion. Quantification of blood vessel formation was performed in 10 wound areas in the dermal region of the lesion. Quantification of collagen deposits during tissue remodeling was performed on Sirius red stained slides. Ten fields in the tissue remodeling area were measured on each slide. The proportion of collagen fibers relative to the total area of remodeling in the dermis after injury was quantified. All analyses were performed using the image analysis Image-Pro Plus system (Media Cybernetics, USA). The average number of newly formed blood vessels was expressed per μm^2 of injured area. The average thickness of the epithelium and the total area of collagen were expressed in mm and percentage, respectively.

2.6. Immunohistochemistry analysis of dermal fibroblast activation and proliferation

For quantification of activation and proliferation of fibroblasts, double immunohistological staining of alpha smooth muscle actin (αSMA) and proliferating cell nuclear antigen (PCNA) was performed. Briefly, histological sections were incubated with primary antibodies raised against αSMA (Sigma, USA; 1:100) and PCNA (Dako, USA; 1:100) revealed, respectively, by Fast red and Diaminobezidine according to the manufacturer's instructions (EnVision Doublestain System, Dako, USA). Morphometric analysis was performed for the quantification of total fibroblasts and proliferating fibroblasts using an image analysis Image-Pro Plus system (Media Cybernetics, USA). Results were expressed as number of cells per μm^2 of injured tissue.

2.7. Immunofluorescence staining of collagens type I and III

During the early stages of wound healing, fibroblasts actively produce type III collagen. During remodeling, type III collagen is replaced by type I collagen to restore the normal dermal collagen composition [16]. Histological sections were unmasked in Tris–ethylenediaminetetraacetic acid solution at pH 9.0 for 20 min in a microwave at 700 W. Sections were then subjected to enzymatic digestion with 0.4% pepsin (Sigma, USA) diluted in 0.5 N acetic acid for 30 min at 37 °C. Thereafter, sections were subsequently rinsed and incubated overnight in a moisturized chamber at 4 °C with primary antibodies raised against collagen type I or type III (Rockland, USA; 1:50). Next, slides were incubated with secondary antibody swine anti-rabbit IgG, FITC-conjugated (Dako, USA, 1:100). After 90 min incubation in moist and dark chamber, the sections were counterstained with propidium iodide (1:1000), which stains the cell nucleus in red. Finally, slides were mounted with Vectashield (Vector Laboratories, USA), sealed with nail polish and photographed using a Nikon E-800 fluorescence microscope (Nikon, Japan).

2.8. Quantitative real-time PCR analysis

The qPCR technique was performed following the MIQE guidelines [17]. Total RNA (*i.e.* 3 μg) was isolated from skin tissue using the RNAspin mini RNA isolation kit (GE HealthCare, USA) and was reverse transcribed to cDNA using random primers and VILO Master Mix kit (Invitrogen). Primers and probes assays for real-time PCR were purchased from Applied Biosystems (USA), including those for: collagen type I (assay ID Mm00801666_g1), collagen type III (assay ID Mm00802332_m1), transforming growth factor beta 1 (TGFβ-1; assay ID Mm00441724_m1), matrix metallopeptidase 2 (MMP-2; assay ID Mm00439508_m1). 18S rRNA (assay ID Mm04277571_s1) and ACTB (assay ID Mm00607939_s1) were used as reference gene to normalize the results. Each sample was analyzed in duplicate and negative