Clasp2 ensures mitotic fidelity and prevents differentiation of epidermal keratinocytes

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INTRODUCTION

Epidermal self-renewal is sustained by the presence of progenitor cells in the basal layer, which asymmetrically divide or delaminate, giving rise to the non-mitotic differentiated stratified layers (Blanpain and Fuchs, 2009; Lechler and Fuchs, 2005). Several molecular mechanisms are instrumental for the control of the finely tuned balance between proliferation and differentiation, including genetic and epigenetic changes, transcriptional regulation, signalling cues and cellular interactions (Blanpain and Fuchs, 2009, Simpson et al., 2011). Moreover, recent reports show that a mitotic block coupled to an increase in ploidy is associated with epidermal differentiation (Gandarillas and Freije, 2014; Zanet et al., 2010). Indeed, a ploidy increase is linked to cell differentiation during the development of multiple organs (Lee et al., 2009; Orr-Weaver, 2015), but despite its relevance, the molecular mechanisms involved remain poorly characterized.

RESULTS AND DISCUSSION

Loss of Clasp2 expression leads to premature differentiation of mouse and human basal keratinocytes

We have previously shown that Clasp2 is enriched in epidermal progenitor cells. This distribution differed from that observed for Clasp1, which appeared to be expressed across all epidermal layers (Fig. S1A). Interestingly, Clasp2 also localizes in the basal compartments of other mouse stratified tissues (Fig. 1A). This localization pattern was validated by performing peptide-competition assays and using alternative antibodies (Fig. S1B,C). Based on these findings, we hypothesized that Clasp2 is required to prevent the differentiation of epidermal keratinocytes.

To test our hypothesis, we used primary mouse and human keratinocytes as models, as they represent powerful in vitro systems that mimic the events of differentiation upon addition of Ca²⁺ to the medium (Hennings et al., 1980). We first knocked down Clasp2 in mouse keratinocytes using specific small hairpin (sh)RNAs. Immunoblot and real-time (RT)-PCR analyses confirmed the specific loss of expression of Clasp2 but not of Clasp1 (Fig. S1D,E).

Morphologically, control cells growing under proliferative low Ca²⁺ (LC) conditions exhibited a polygonal shape that was characteristic of undifferentiated mouse keratinocytes (Fig. 1B). In contrast, Clasp2 knockdown (Clasp2KD) cells displayed a squamous flat morphology and an increase in cell size (Fig. 1B,C); features that are associated with differentiation (Sun
Immunoblot and RT-PCR analyses of the expression of keratins revealed that although Clasp2KD cells still expressed the basal markers *Ker14* (Fig. 1D) and ΔNp63 (an isoform encoded by *Tp63*) (Fig. 1I), high levels of the suprabasal postmitotic markers Ker1, Ker10 and filaggrin were expressed, even under LC conditions (Fig. 1E–G). To mimic the ~50% reduction of *Clasp2* observed previously in the suprabasal epidermal layers in vivo (Shahbazi et al., 2013), we titrated different amounts of small
interfering (si)RNAs specific for Clasp2. The expression of differentiation markers was readily apparent when the Clasp2 mRNA levels were reduced to ∼30% (Fig. 1H; Fig. S1F), suggesting a causative role for Clasp2 in switching the mouse keratinocytes differentiation program. Interestingly, despite the conserved roles between Clasp1 and Clasp2, Clasp1 did not play an equivalent role in preserving mouse keratinocytes in an undifferentiated state (Fig. S1G,H).

The loss of Clasp2 was also accompanied by a significant decrease in cell proliferation (Fig. 1J) and clonogenic potential (Fig. 1K). We further validated our results in an immortalized mouse keratinocyte line, MCA3D (Navarro et al., 1991). Clasp2KD MCA3D cells showed a flat and differentiated morphology (Fig. S2A) and an increase in the expression of differentiation markers (Fig. S2B,C).

To determine whether Clasp2 plays a similar role in human keratinocytes, we first analyzed its localization in human skin samples. This revealed an enrichment of human Clasp2 in the basal progenitor layer (Fig. 2A). *In vitro* studies using primary human keratinocytes showed that Clasp2 levels decreased upon Ca2+ addition (Fig. 2B), indicating that, as in the mouse, Clasp2 expression is intimately coupled to the differentiation status of epidermal cells. Moreover, siRNA-mediated downregulation of Clasp2 in primary human keratinocytes (Fig. 2C) led to an increased expression of differentiation markers (Fig. 2D). Interestingly, Clasp2 has been shown previously to be involved in hematopoietic stem cell maintenance (Drabek et al., 2012), possibly through its role in regulating cell–matrix adhesions (Drabek et al., 2012; Stehbens et al., 2014). Although no alterations in focal adhesion proteins have been observed in Clasp2KD mouse keratinocytes (Fig. S2D–F), these results raise the possibility that Clasp2 sustains progenitor characteristics in different cellular contexts.

**Clasp2 expression ensures mitotic fidelity in primary mouse keratinocytes**

It has been recently shown that an increase in ploidy due to a mitotic block is associated with terminal differentiation in human epidermis (Gandarillas and Freije, 2014; Zanet et al., 2010). Using fluorescence *in situ* hybridization (FISH) assays, we confirmed the presence of some polypliody cells in the suprabasal layers of mouse skin (Fig. 3A), in agreement with previous observations (Karalova et al., 1988; Kartasova et al., 1992). In light of these findings and that a mitotic arrest (e.g. Taxol or Nocodazole treatment) is not sufficient to trigger differentiation (Fig. 3A), unless accompanied by an increase in DNA content (Freije et al., 2012), we hypothesized that the differentiation observed in Clasp2KD mouse keratinocytes stemmed from a mitotic defect leading to a DNA content increase. This is in line with the well-defined role of Clasp2 in the control of mitotic fidelity (Logarinho et al., 2012; Maia et al., 2012; Mimori-Kiyosue et al., 2006; Pereira et al., 2006).

To test this hypothesis, we first conducted cell cycle analyses and observed an increased proportion of polypliody (Fig. 3B), as well as a high DNA content in Clasp2KD mouse keratinocytes (Fig. 3C; Table S1). This increase in the G2–M population was further validated using the sensors of the fluorescence ubiquitylation-based cell cycle indicator (FUCHI) (Fig. S3B): the monomeric Kusabira Orange (mKO2)–Cdt1 sensor of cells in G1 and the monomeric Azami Green (mAG)–Geminin sensor of cells in S, G2 or M phase (using the human proteins) (Sakaue-Sawano et al., 2008). Importantly, this phenotype was not accompanied by an increase in apoptosis (Fig. 3D; Table S1).

We next analyzed whether the high DNA content observed in Clasp2KD mouse keratinocytes was associated with mitotic spindle alterations. Clasp2KD mouse keratinocytes exhibited a significant increase in centromeres numbers at interphase (Fig. 3E,F), and multiple mitotic spindle alterations, including decreased MT density, and multipolar and disorganized spindles (Fig. 3G,H). Time-lapse microscopy experiments showed that Clasp2KD mouse keratinocytes exhibited longer cell division times (Fig. 3I; Fig. S3C). These results were confirmed using mouse keratinocytes expressing histone-H2B–GFP (H2B–GFP). Several alterations were observed during mitosis, such as misaligned and lagging chromosomes (Fig. 3J), leading to inaccurate chromosome segregation.

**DNA damage and p53 activation are associated with the premature differentiation observed in Clasp2KD mouse keratinocytes**

Alterations in chromosome numbers are known drivers of genomic instability and DNA damage (Passerini et al., 2016). Accordingly, Clasp2KD mouse keratinocytes displayed significantly higher levels of DNA damage, as marked by the presence of phosphorylated (phospho)–γH2AX foci (Fig. 4A). Moreover, cell synchronization experiments revealed a delay in S-phase, in line with the observed increase in phospho–γH2AX and replication stress (Fig. 3D; Table S1). These results were validated by time-lapse microscopy studies of control and Clasp2KD mouse keratinocytes expressing the FUCHI sensors (Fig. 4B). Our results support a model in which Clasp2 deficiency induces mitotic alterations that instead of leading to cell death result in polypliody and subsequent differentiation. Indeed, the induction of other mitotic alterations that result in polypliody, such as inhibition of Aurora kinase A (AurkA) (Fig. S3E,F) or genotoxic agents that trigger a mitotic checkpoint (Freije et al., 2012), also lead to differentiation. Over time, the accumulation of chromosome alterations induces further genomic instability. Interestingly, loss of Clasp2, similar to the loss of AurkA (Katayama et al., 2004) or...
inhibition of other mitotic kinases (Freije et al., 2012) triggered an increase in p53 mRNA levels ($\textit{Tp53}$; Fig. 4C) in response to DNA damage and mitotic checkpoint activation. A role for p53 in limiting the proliferation of polyploid cells has long been recognized (Ganem et al., 2014), and in human keratinocytes its inactivation further potentiates squamous differentiation (Freije et al., 2014). To test if p53 has a similar role in the context of Clasp2 deficiency, we knocked down Clasp2 expression in p53-null mouse keratinocytes (Fig. 4C) and in p53KD human keratinocytes (Fig. 4E). Clasp2KD p53KD human keratinocytes exhibited an increase in differentiation (Fig. 4F). However, Clasp2KD p53 knockout mouse keratinocytes showed a significant decrease in the expression of differentiation markers (Fig. 4D). These results underscore the existence of p53-dependent mechanisms in mouse keratinocytes that promote the differentiation of cells that bypass a mitotic alteration. However, loss of p53 in human keratinocytes triggers additional protective mechanisms that may not be conserved in mouse.

Our findings indicate that loss of Clasp2 in keratinocytes leads to reductions in cell growth due to mitotic alterations, leading to an increase in ploidy and premature differentiation in the absence of cell death, highlighting the presence of surveillance mechanisms in keratinocytes, which prevent the proliferation of cells with high DNA content and DNA damage. Although it is intriguing that the loss of Clasp2 does not cause apparent physiological defects in mouse skin (Drabek et al., 2012), possibly due to compensatory mechanisms, overall our data indicate that Clasp2 is required to maintain the fidelity of cell division and to prevent the differentiation of mouse and human keratinocytes. Future research...
and 29 Clasp2KD cells). (C) mRNA levels of keratinocytes coexpressed mKO2 experiments per panel. (D) mRNA levels of keratinocytes. (E) mRNA levels of deficient human keratinocytes. Data are presented as mean±s.e.m. *p<0.05; **p<0.004, ****p<0.0001; ns, non-significant; (A,B) Mann-Whitney U test, (C) one-way ANOVA test (both for p53 and for Clasp2), (D) one-way ANOVA test, (E) Kruskal-Wallis test, (F) two-tailed Student’s t-test. n=2 independent experiments per panel.

will shed light into how Clasp2 cooperates with cytoarchitectural, transcriptional and translational pathways to prevent keratinocyte differentiation.

MATERIALS AND METHODS
Primary cell culture, transfection, viral infection and treatments
Wild-type mice (C57/BL6) were handled according to the ethical regulations of the CNIO and the Institute of Health Carlos III, Madrid, Spain. Primary mouse keratinocytes were isolated from newborn mouse back-skin, as previously described (Shahbazi et al., 2013). MCA3D mouse keratinocytes (a gift from Amparo Cano, Biomedical Research Institute, Madrid, Spain) (Navarro et al., 1991) were cultured in Ham F12 with 10% FBS.

p53 knockout mouse keratinocytes were generated by infecting mouse keratinocytes (Drosten et al., 2014) with lentCas9-Blast (gift from Feng Shang, The Rockefeller University, New York, NY) (Perez-Moreno et al., 2008). Mouse keratinocytes were plated onto 10 µg/ml fibronectin-coated glass-bottom culture dishes (Matsunami). Live-imaging microscopy was performed in a Leica TCS-SP5 confocal microscope with the LAS-AF software.

For immunohistochemistry, formalin-fixed and paraffin-embedded skin sections were deparaffinized following standard protocols. For peptide competition assays, staining was performed in the presence of 10 µg GST (control) and 10 µg GST–Clasp2 (human; nucleotides 3074–3976 of the KIAA0627 cDNA as previously described) (Shahbazi et al., 2013). Live-cell microscopy
Mouse keratinocytes were plated onto 10 µg/ml fibronectin-coated glass-bottom culture dishes (Matsunami). Time-lapse experiments were performed in a Leica workstation AF6000 with controlled temperature and CO2 levels. Bright-field and Fucci-expressing mouse keratinocyte images were captured every 5 min. Images of H2B–GFP-expressing mouse keratinocytes were captured every 3 min.

Cell cycle, proliferation and apoptosis analyses
Cell cycle analysis of live cells that had been stained with 10 mg/ml propidium iodide were conducted using a LSR FORTESSA flow cytometer (Becton Dickinson) and the FlowJo software.

Cell cycle synchronization experiments, performed by blocking mouse keratinocytes at the G1/S boundary with a double thymidine block, and cell cycle profiles were analyzed at different time points after release from block.

To analyze cell cycle phases, mouse keratinocytes were infected with lentiviruses expressing the Fucci sensors (Sakave-Sawano et al., 2008). For H2B–EGFP expression, mouse keratinocytes were transiently transfecnd with a KER14–H2B–EGFP vector (gift from Elaine Fuchs, The Rockefeller University, New York, NY) (Perez-Moreno et al., 2008). For cell proliferation analysis, equal numbers of mouse keratinocytes were plated in triplicate. To analyze apoptosis, TUNEL-positive cells were detected using the In Situ Cell Death Detection Kit (Roche, Mannheim, Germany). For colony formation assays, cells were plated on fibronectin (Merck, New Jersey), fixed 1 week after plating and stained with Rhodamine B.

RNA isolation and RT-PCR
Total RNA was isolated using TRIzol (Invitrogen). cDNA synthesis was performed using Ready-to-Go You-Prime It First-Strand beads and random primers (GE Healthcare). RT-PCR reactions were performed using specific primers (Table S2), and expression levels were normalized to those of genes encoding actin or GAPDH.

Immunofluorescence and immunohistochemistry
Optimal cutting temperature (OCT) compound-embedded frozen tissue sections or cells plated in coverslips were fixed in −20°C methanol for 3 min, blocked in blocking buffer (Shahbazi et al., 2013) and incubated with primary (Table S3) and secondary antibodies. Images were acquired in a Leica TCS-SP5 confocal microscope with the LAS-AF software.

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Live-imaging microscopy
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For cell cycle arrest, mouse keratinocytes were treated with 30 µM nocodazole (M1404, Sigma) or with 1 µM taxol for 24 h. AurKα activity was inhibited with 10 µM MLN 8237 in DMSO (S1133, Selleckchem, Houston, TX).

Primary human keratinocytes (American Type Culture Collection, PCS-200-010) were cultured in CntF7 (CELLnTEC, Bern, Switzerland). Clasp2 expression was downregulated using four specific siRNAs (IDs SASI_Hs01_00146296-97, Sigma) and Lipofectamine RNAiMAX (ThermoFisher). p53KD human keratinocytes were generated through lentiviral infection with a pLKO1 shRNAp53 plasmid with 6 µg/ml polybrene.

Ca2+ switch experiments were conducted by switching cells from LC to normal Ca2+ (1.8 mM) medium. All cells were routinely tested for mycoplasma contamination.
Immunoblot

Cells were lysed in RIPA buffer and SDS-PAGE was performed using standard procedures.

Fluorescence in situ hybridization

Probes RP23-324C12 and RP24-285E22 BACs (11q11.1 band) and RP23-228E2 and RP24-386B9 BACs (2q13 band) (Human BAC Clone Library, Children’s Hospital Oakland Research Institute, Oakland, CA) were labelled by using a nick-translation assay with TexasRed and FITC, respectively. FISH was performed on paraffin tissue sections using the FISHility FISH Accessory Kit (DAKO), denaturing samples at 66°C for 10 min, hybridizing probes at 45°C for 120 min, and washing samples with 2× saline-sodium citrate (SSC) buffer and 1× Tween-20 at 63°C before mounting.

Quantification and statistical analysis

Image analyses were performed using ImageJ and Imaris software (Bitplane Scientific Software, Zurich, Switzerland). For statistical analysis of quantitative data, the data normality was evaluated with a Kolmogorov-Smirnov test. Data that presented a Gaussian distribution was analyzed using two-tailed Student’s t-test or ANOVA. Otherwise Mann–Whitney and Kruskal–Wallis tests were used. Qualitative data were analyzed with a Chi-squared test. Statistical analyses were performed using GraphPad Software. All data are representative of at least two independent experiments performed in triplicate.

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Competing interests

The authors declare no competing or financial interests.

Author contributions

M.N.S. and D.P.-J. designed, performed and analyzed experiments. F.A. assisted with the experiments. M.D. provided reagents and intellectual input. M.P.-M. designed and supervised experiments. M.N.S. and M.P.-M. wrote the manuscript.

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Supplementary information

Supplementary information available online at http://jcs.biologists.org/lookup doi:10.1242/jcs.194787 supplemental

References


