

HERC5, a HECT E3 ubiquitin ligase tightly regulated in LPS activated endothelial cells

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Summary

By differential screening we isolated genes upregulated in inflammatory cytokine-stimulated human skin microvascular endothelial cells. One of these cDNAs encoded RCC1 (regulator of chromosome condensation 1)-like repeats and a HECT (homologous to E6-AP C-terminus) domain, representing a member of the HECT (HECT and RCC1 domain protein) family of ubiquitin ligases. The mRNA level of this member, *HERC5*, is specifically upregulated in endothelial cells by the pro-inflammatory cytokines tumor necrosis factor α and interleukin 1β , and by lipopolysaccharide (LPS), but is hardly expressed in other cells of the vascular wall such as primary smooth muscle cells and fibroblasts. Regulation of *HERC5* gene expression suggests a critical role for the transcription factor NF- κ B. In contrast to mRNA expression *HERC5* protein is subject of enhanced degradation upon LPS stimulation of endothelial cells. The time course of LPS-induced changes in *HERC5* protein and

mRNA levels suggests that the initial drop in *HERC5* protein is balanced by increased protein synthesis due to upregulation of *HERC5* mRNA. This leads to recovery of *HERC5* protein levels within 12 hours of LPS stimulation and points at a tight control of *HERC5* protein. To analyze functional activity of this putative member of the ubiquitin-conjugating pathway we performed in vitro assays with different ubiquitin-conjugating enzymes. We found that *HERC5* possesses ubiquitin ligase activity and requires the presence of the ubiquitin-conjugating enzyme UbcH5a for its activity. These data show for the first time that a functionally active HECT ubiquitin ligase exhibits a tightly controlled cytosolic level under inflammatory conditions in endothelial cells.

Key words: Endothelial cells, LPS, Inflammation, NF- κ B, Ubiquitin ligase

Introduction

A healthy organism reacts with help of the immune system and a process termed inflammation against microbial infection in order to restore the integrity of the affected tissue. Inflammation is either resolved or can progress towards a chronic state favoring pathologies such as atherosclerosis and rheumatoid arthritis, or even malignancies (Coussens and Werb, 2002; Nathan, 2002). Bacterial endotoxin itself and/or cytokines released from immune cells recruited to the site of injury trigger activation of endothelial cells (ECs) (Bierhaus et al., 2000). Subsequently, altered gene expression of chemokines, cytokines, proinflammatory enzymes, cell surface receptors, adhesion molecules, and components of the complement and coagulation cascades leads to recruitment and activation of immune cells (Bierhaus et al., 2000).

ECs are activated by pro-inflammatory cytokines, including tumor necrosis factor α (TNF α) and interleukin- 1β (IL- 1β), and by bacterial lipopolysaccharide (LPS) through Toll-like receptors (Akira et al., 2001; Suzuki et al., 2001; Zhang and Ghosh, 2000) signaling predominantly through the NF- κ B transduction pathway (Li and Verma, 2002; Yamamoto and Gaynor, 2001). Activation of this pathway is achieved by

phosphorylation of inhibitor of NF- κ B (I κ B) by the I κ B kinase (IKK) complex (Ghosh and Karin, 2002; Ghosh et al., 1998). Phosphorylated I κ B is ubiquitinated by the SCF ^{β TrCP} complex to target it for degradation by the 26S proteasome (Brown et al., 1995; Chen et al., 1995). Subsequently, the released transcription factor NF- κ B translocates into the nucleus, binds to κ B consensus sites and induces gene expression together with other transcription factors also activated by inflammatory stimuli (De Martin et al., 2000).

In addition to transcriptional regulation, protein degradation seems to play a crucial role in the induction and modulation of the inflammatory response. The ubiquitin proteasome system is the major pathway for specific intracellular protein degradation and plays a crucial role in many cellular processes (Weissman, 2001). Proteins modified by polyubiquitination are targeted for proteasomal degradation (Thrower et al., 2000). Monoubiquitination serves other functions such as membrane transport or transcriptional regulation (Hicke, 2001). Ubiquitination of proteins involves a hierarchical enzymatic cascade consisting of a ubiquitin-activating enzyme (E1), ubiquitin-conjugating enzymes (E2) and, in most cases, ubiquitin ligases (E3) (Hershko et al., 2000; Pickart, 2001;

Weissman, 2001). Although only one E1 enzyme is functionally active and the number of E2 enzymes is limited, the number of E3 enzymes is abundant, thereby allowing for substrate specificity. Ubiquitin ligases can be identified by the presence of either a HECT (homologous to E6-associated protein C-terminus) domain (Huibregtse et al., 1995), a RING (really interesting new gene) domain (Lorick et al., 1999) or a U-box (Aravind and Koonin, 2000). So far, only RING ubiquitin ligases involved in inflammation have been identified (Deng et al., 2000; Ohta et al., 1999; Suzuki et al., 2001; Yang et al., 2000).

By differential screening of cytokine-stimulated ECs we identified HERC5, a ubiquitin ligase of the HERC family. We demonstrate its enzymatic activity and specific transfer of ubiquitin via UbcH5a. We further show that *HERC5* gene expression is upregulated in activated ECs in an NF- κ B-dependent manner. HERC5 protein, however, is subject to enhanced degradation upon stimulation of ECs.

Materials and Methods

Cloning of *HERC5*

Differential screening of ECs was performed as described (Stehlik et al., 1998a). A partial cDNA clone, #881, encoding a HECT domain was elongated by cDNA library screening. For this purpose, a library was made from pooled mRNA isolated from human skin microvascular ECs (HSMECs) stimulated with either TNF α or LPS for various time points according to a cDNA library construction protocol (Stratagene). For cloning of the 5'-end a G-tailing strategy (Gibco) and SMART technology (Clontech) were applied. All PCR fragments were cloned into pGEM-T easy vectors (Promega), sequenced and analyzed using Sequence Navigator and MacVector software. The cDNA sequence of 3529 bp with an ORF of 1024 aa, initially termed *Croco*, was renamed *HERC5*.

For cloning of the promoter, BAC clones containing the *HERC5* genomic region were obtained. *Bam*HI/*Bgl*II restriction fragments of these BAC clones were subcloned into pBluescript and transformants were screened for *HERC5* exons. Two clones were isolated containing the 5'UTR sequence of *HERC5* and additional upstream sequence (GenBank AY532389). The genomic region upstream of the cDNA start site was analyzed for potential promoter activity and transcription factor binding sites using the following programs: Promoter Scan, Dragon Promoter Finder, TESS (Transcription Element Search Software) and Transfac database.

The *HERC5* cDNA start (clone GenBank AY337518) was defined as +1 and a fragment corresponding to -1569 to +36 was cloned into the luciferase expression vector pUBT-luc and reporter assays were performed as described previously (Hofer-Warbinek et al., 2000) using the Dual-Luciferase Reporter Assay system (Promega).

Cell culture

Primary HSMECs, human umbilical vein ECs (HUVECs), human smooth muscle cells (HSMCs) and skin fibroblasts (FBs) were isolated as described (Wojta et al., 1993; Wojta et al., 1992; Zhang et al., 1996). All cells were grown on gelatin-coated cell culture flasks at 37°C and 5% CO₂. HSMCs and FBs were cultured in M199 supplemented with 10% bovine calf serum (Hyclone), 2.2 mM L-glutamine, 80 units/ml penicillin, 80 μ g/ml streptomycin and 0.2 μ g/ml fungizone (all BioWhittaker). ECs were cultured in M199, 20% serum, 50 μ g/ml endothelial growth factor supplement (Technoclone, Austria), antibiotics and 3 units/ml heparin (Roche). Primary cells were split in a 1:3 ratio and used up to the sixth passage. An EC line, HM2, (R. Hofer-Warbinek, personal communication) was generated by infection with an amphotrophic helper-free recombinant retrovirus

construct, pLXSN16 E6/E7, containing the E6/E7 open reading frame of human papilloma virus 16 (Fontijn et al., 1995) and cultured under selection of 100 μ g/ml G418 (Sigma). Confluent monolayers were left for 48 hours and subsequent experiments were done without changing the cell culture medium. Quiescence and response to activation of ECs was confirmed by determining either IL-8 secretion or E-selectin (ELAM-1) expression. The following agents were added per ml of medium: TNF α 500 units, LPS 600 ng, IL-1 β 300 units, IL-6 200 units, IL-8 10 ng, IL-10 2 ng, EGF 10 ng, VEGF 10 ng, TGF β 2 ng, CHX 10 μ g. LPS and CHX were obtained from Sigma, all other agents were from Genzyme. Adenoviral infection of ECs with either recombinant adenovirus I κ B α or control virus was performed as described previously (de Martin et al., 1997; Wrighton et al., 1996).

RNA isolation, northern blot analysis and RT-PCR

For RNA isolation, cells were washed, lysed directly in TRIzol reagent (Life Technologies) and total RNA was precipitated according to the manufacturer's protocol. For Northern blotting, 10 μ g of total RNA each were separated on agarose/formaldehyde gels, transferred to GeneScreen Plus membranes (Du Pont) and hybridized with 10⁶ cpm/ml of [α -³²P]dATP-labeled cDNA probes (Brostjan et al., 1997). The following HERC5 probes were used: bp 2890-3530 and bp 1-411. Blots were reprobated with both I κ B α and IL-8 probes. Equal loading of RNA was confirmed by rehybridization with a GAPDH probe. Signals were analyzed with a PhosphorImager using ImageQuant software (Molecular Dynamics). The multiple tissue blot was hybridized according to the manufacturer's protocol (Clontech). Quantitative real-time RT-PCR was performed essentially as described previously (Kadl et al., 2002). Extracted RNA (High Pure RNA Isolation, Roche) was reverse transcribed using Superscript II (Invitrogen) and hexamer primers. Tissue RNA was obtained from Clontech. β 2-microglobulin (β 2M) primer pair: 5'-gatgagtatcctg-cctgtg-3' and 5'-caatccaatgcccctct-3'; HERC5 primer pair: 5'-gggatgaaagtctgaggag-3' and 5'-cattttctgaagcgtccaca-3'. Primers were obtained from Invitrogen and RT-PCR efficiency was 1.82 for the β 2M primer pair, and 2.17 for the HERC5 primer pair, respectively.

Antibody production and testing

The plasmid pQE32-HERC5-CT encoding the C-terminus of HERC5 (aa 659-1024) was used to express 6 \times His-tagged HERC5-CT protein in *E. coli* M15 and the recombinant protein was purified according to standard protocols (Qiagen). Immunization of rabbits was carried out according to standard immunization protocols. For testing of immune sera in immunoprecipitation, proteins were synthesized in a TNT-coupled transcription/translation system (Promega) in the presence of L-[³⁵S]methionine. 50 μ l aliquots were diluted with lysis buffer (1% Nonidet P-40, 50 mM Tris/HCl, pH 7.5, 150 mM NaCl, 5 mM MgCl₂) and pre-cleared with protein A-Sepharose (Pharmacia). Samples were split and precipitated with 2 μ l of either pre-immune or immune serum. After washing, samples were separated by SDS/PAGE. Fixed and dried gels were exposed and analyzed by autoradiography. Positive reacting serum was termed anti-HERC5 antiserum and used for further experiments.

Cell labeling, immunoprecipitation and pulse-chase

Quiescent ECs (5 \times 10⁶ cells per sample) were metabolically labeled with 20 μ Ci/ml L-[³⁵S]methionine or Promix (Amersham) in deficient RPMI 1640 medium (Gibco) supplemented as described above, but serum was dialysed against PBS. The presence of LPS in the labeling medium is indicated. For protein half-life measurements, metabolically labeled cells were washed and incubated in the presence of a 100-fold excess of unlabeled methionine/cysteine (chase) for the indicated times in the absence or presence of LPS. Protein extracts

were prepared on ice in 1% Nonidet P-40, 50 mM Tris/HCl pH 7.5, 150 mM NaCl, 5 mM MgCl₂, 20 µg/ml phenylmethylsulfonyl fluoride (PMSF) and protease inhibitor cocktail (Roche). Samples normalized to equal amounts of trichloroacetic acid-precipitable radioactivity were precipitated with 20 µl of anti-HERC5 antiserum and protein A-Sepharose (Pharmacia) according to standard protocols. After washing three times with buffer B (10 mM Tris/HCl pH 7.5, 150 mM NaCl, 0.2% Nonidet P-40 and 2 mM EDTA), twice with buffer C (buffer B but 500 mM NaCl) and once with 10 mM Tris/HCl pH 7.5, samples were separated by SDS-PAGE and gels were analyzed using a PhosphorImager and ImageQuant software for quantification (both Molecular Dynamics).

E2 preparation and testing

Genes encoding the E2 enzymes were subcloned into bacterial expression vectors and fused to either a His-tag (H3, H5b, H5c, H8) or a GST-tag (H5a, H6, H7). pT7-7-H10 was expressed as described (Townsend et al., 1997). Expression conditions were optimized and bacterial lysates were prepared. Therefore, 50 ml of bacterial culture overexpressing a particular E2 enzyme were lysed in 1 ml of lysis buffer (50 mM Tris/HCl pH 7.5, 1% Triton X-100, 20 µg/ml PMSF) and sonicated. Supernatants were tested for thioester bond formation essentially as described (Jensen et al., 1995), but using GST-ubiquitin in the assay and subsequent detection by anti-GST antibody (Zymed) and a HRP-labeled secondary antibody (Amersham). Active enzyme preparations were used for further experiments.

Thioester bond formation assay

A fragment encoding aa 613-1024 of HERC5 was cloned into a pcDNAFlag vector (constructed by cloning an oligo encoding a Flag epitope into the *Hind*III-*Bam*HI site of pcDNAHisA) and the C994A mutation was introduced by PCR (Ho et al., 1989). The thioester assay was performed as described (Huibregtse et al., 1995). Where indicated, 2-4 µl of bacterially expressed E2 enzymes were added and samples were incubated for 20 minutes. GST-ubiquitin was expressed in *E. coli* DH5α and purified as described (Scheffner et al., 1993).

Statistics

Results, when applicable, are given as means±s.d. and significance was assigned to *P*-values of <0.05 (paired or unpaired *t*-test and one-way analysis of variance followed by Dunnett's test as post-test, respectively). Regression analysis was performed using non-linear regression curve fit. All statistic analyses were done using the GraphPad Prism3 Program.

Results

Identification and cloning of HERC5

Differential screening of a cDNA library to identify genes expressed in LPS- and TNFα-activated ECs, but not in quiescent ECs, resulted in several cDNA clones. Among those, a sequence encoding a HECT domain protein was identified owing to its homology to the C-terminus of E6-associated protein (E6-AP). The originally identified clone was elongated to 3529 bp by cDNA library screening and specific 5'-RACE PCR methods. An open reading frame encoding 1024 amino acids (aa) was determined containing a RCC1-like domain (RLD) at the N-terminus, separated from the HECT domain by a region of 275 aa without homology to any known protein domain (Fig. 1A). Members of the HECT family containing an RLD are designated HERC (HECT and RCC1 domain proteins). The clone identified by us, initially termed Croco

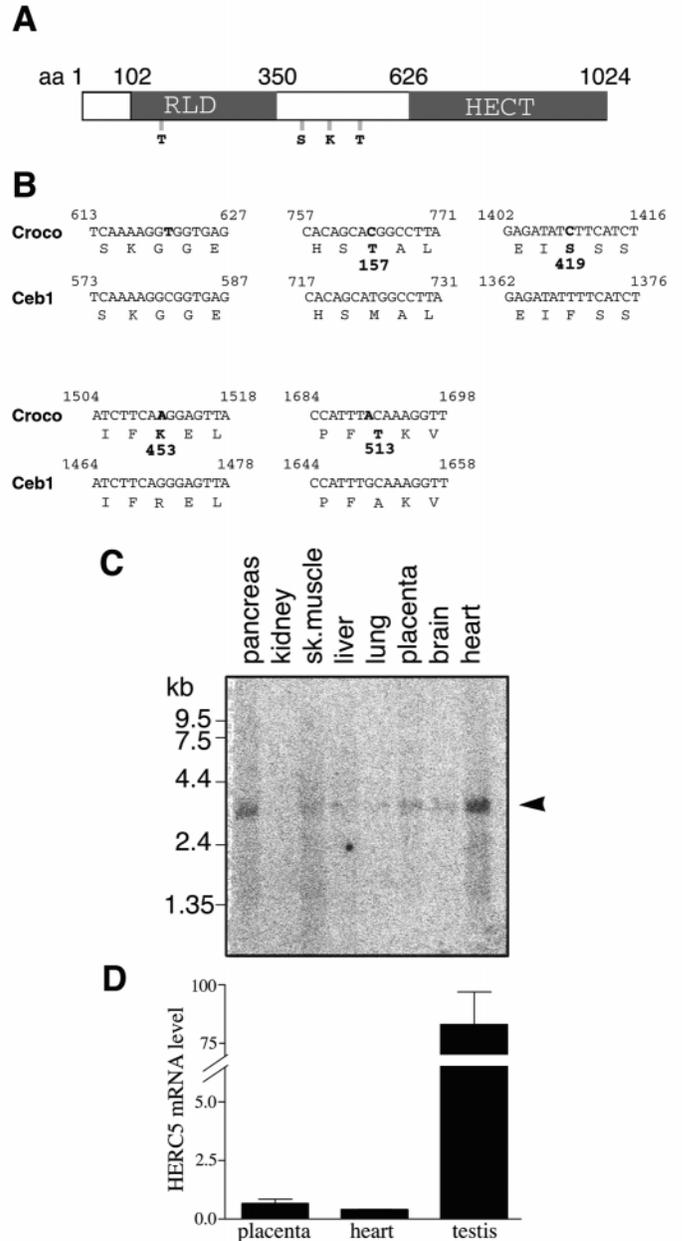


Fig. 1. Structure and expression of HERC5. (A) Schematic domain structure of HERC5. Amino acids in Croco different from those in Ceb1 are shown as grey bars. aa, amino acid; HECT, homologous to E6-AP C-terminus; RLD, RCC1-like domain. (B) Comparison of *Croco* and *Ceb1*. Differences in the cDNA and protein sequences are indicated in bold. Amino acids are given in the single-letter code and positions of amino acids are indicated below. GenBank accession numbers: *Ceb1*, AB027289; *Croco*, AY337518. (C) *HERC5* mRNA expression in human tissues. A commercially available multiple tissue blot containing poly(A)⁺ RNA derived from different human tissues was probed for *HERC5* transcripts. sk. muscle, skeletal muscle. (D) Quantification of *HERC5* mRNA in selected tissues. Quantitative real-time RT-PCR was performed to quantify *HERC5* expression in heart, placenta and testis normalized to β₂-microglobulin expression.

(GenBank accession number AY337518), is very similar to the cyclin E binding protein 1 (*Ceb1*) (Mitsui et al., 1999) and was

classified as *HERC5* according to human genome approved nomenclature. The two sequences differ by a one base pair deletion in the 5'-UTR, by an additional 40 bp at the 5'-UTR of *Croco*, and five point mutations resulting in exchange of four amino acids. As shown in Fig. 1B, aa M157, F419, R453 and A513 of *Ceb1* are changed to T, S, K and T, respectively, in *Croco*.

Tissue- and cell-specific expression of *HERC5*

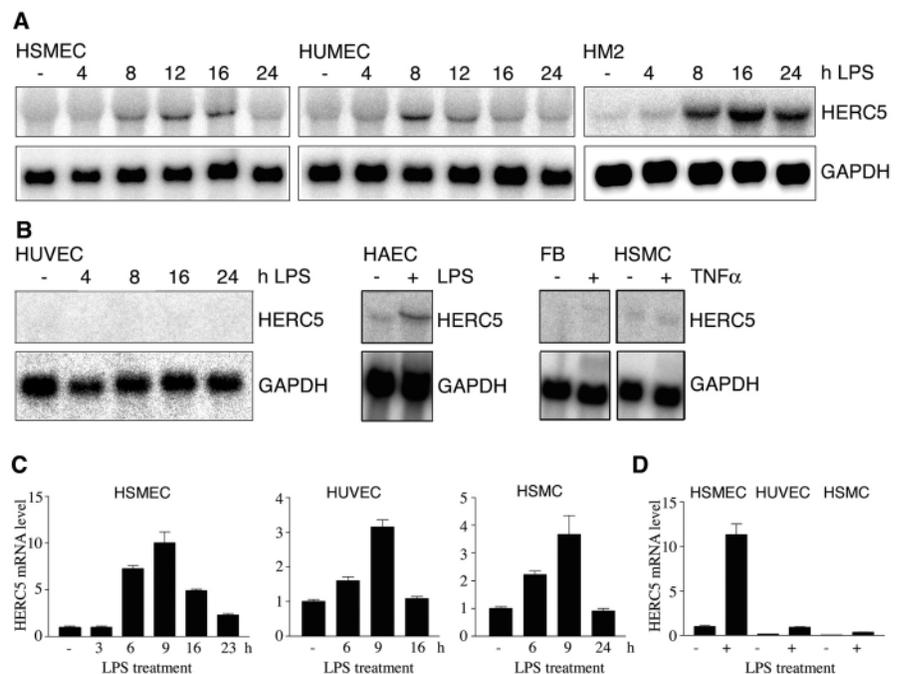
By hybridization of a multiple tissue blot with a *HERC5*-specific probe we detected *HERC5* mRNA transcripts of approximately 3.7 kb in heart and pancreas. Weak signals are detectable in placenta and skeletal muscle (Fig. 1C). High *Ceb1* expression was reported for testis tissue (Mitsui et al., 1999), therefore we compared *HERC5* mRNA levels in placenta and heart to testis by quantitative real-time RT-PCR. *HERC5* mRNA level in testis was about 100 times higher than in placenta and heart tissue when normalized to β_2 -microglobulin expression (Fig. 1D). We were interested in *HERC5* expression in ECs and detected *HERC5* transcripts in LPS-activated primary human skin microvascular ECs (HSMCECs), human uterus microvascular ECs (HUMECs) and the HSMCEC-derived cell line HM2. This cell line reflects endothelial cells in terms of inducible expression of adhesion molecules, LDL-uptake, and tube formation (R. Hofer-Warbinek, personal communication). As shown in Fig. 2A,B, *HERC5* mRNA is hardly detectable in quiescent cells by northern blot analysis, whereas upon LPS stimulation signals are detectable between 6 and 16 hours. Activation of microvascular ECs by TNF α revealed both a similar time course and a similar extent of *HERC5* mRNA expression (data not shown). Apart from microvascular ECs we also analyzed ECs derived from large vessels. By northern blot analysis we detected *HERC5* mRNA expression in primary human aortic ECs (HAECs) upon treatment with LPS for 6 hours, but not in primary human umbilical vein ECs (HUVECs) upon LPS or

TNF α stimulation up to 24 hours (Fig. 2B and data not shown). No signals were detected in other cell types present in the vascular wall, such as skin fibroblasts (FBs) or human smooth muscle cells (HSMCs) after TNF α stimulation for up to 24 hours (Fig. 2B and data not shown). Additionally, *HERC5* expression in vascular cells was analyzed by quantitative real-time RT-PCR and normalized to β_2 -microglobulin expression. The upregulation of *HERC5* mRNA level is approximately tenfold in HSMCECs (Fig. 2C) and, owing to better sensitivity of this method, inducibility of *HERC5* mRNA in both HUVECs and HSMCs upon LPS stimulation was detectable (for 9 hours $P < 0.01$, $n = 4$). As shown in Fig. 2D, both basal and induced levels of *HERC5* mRNA in HUVECs and HSMCs are significantly lower than in HSMCECs. In contrast to primary cells, *HERC5* mRNA levels were not inducible upon TNF α treatment in selected cell lines of either epithelial, haematopoietic, lymphatic or melanocytic origins (data not shown).

Regulation of *HERC5* mRNA expression

Having identified *HERC5* as an LPS-inducible gene in ECs, we tested whether cytokines targeting ECs would induce *HERC5* mRNA expression. Only the inflammatory stimuli LPS, TNF α , and IL-1 β caused pronounced upregulation of *HERC5* mRNA levels in microvascular ECs after 8 hours of treatment (Fig. 3A). To analyze whether de novo protein synthesis is required for *HERC5* mRNA regulation, we used cycloheximide (CHX). As shown in Fig. 3A, no upregulation of *HERC5* mRNA was seen in the presence of CHX. These data indicate that *HERC5* mRNA upregulation by inflammatory stimuli is dependent on de novo protein synthesis in ECs. The transcription factor NF- κ B is a central mediator of gene regulation in inflammation and is activated by TNF α , IL-1 β and LPS (De Martin et al., 2000). Adenovirus-driven overexpression of I κ B α , the inhibitor of NF- κ B, abolishes NF- κ B-dependent upregulation of inflammatory genes such as IL-1, IL-6, IL-8 and VCAM-1 in

Fig. 2. *HERC5* mRNA expression in vascular cells. (A,B) Total cellular RNA from human ECs of different origin stimulated with either LPS or TNF α for the indicated periods of time was probed for *HERC5* mRNA by northern blotting. HAEC were stimulated for 6 hours, FB and HSMC were stimulated for 9 hours. FB, human skin fibroblasts; HAEC, human aortic endothelial cells; HM2, a microvascular endothelial cell line; HSMC, human smooth muscle cells; HSMCEC, human skin microvascular endothelial cells; HUMEC, human uterus microvascular endothelial cells; HUVEC, human umbilical vein endothelial cells. (C) *HERC5* expression analysis by quantitative real-time RT-PCR. Cells were stimulated as described in A and quantitative real-time RT-PCR was performed. *HERC5* expression levels are normalized to β_2 -microglobulin expression. Changes in *HERC5* mRNA level are significant over time. (D) Comparison of *HERC5* expression levels as determined by quantitative real-time RT-PCR in HSMCECs, HUVECs and HSMCs.



LPS-stimulated ECs (Wrighton et al., 1996). We used this recombinant I κ B α adenovirus to investigate the influence of NF- κ B on *HERC5* gene expression. We found that overexpression of I κ B α strongly reduces *HERC5* mRNA expression in LPS-activated HSMCEs suggesting a crucial role of NF- κ B in *HERC5* gene regulation (Fig. 3B). Similar results were obtained in LPS-stimulated HUMECS when *HERC5* mRNA expression levels were quantified by real-time RT-PCR (Fig. 3C).

To further characterize the NF- κ B dependency of *HERC5* regulation, we cloned the putative *HERC5* promoter region of 1569 bp upstream of the cDNA start site into luciferase expressing reporter constructs. Bioinformatics analysis of this region revealed several sites for inflammation-related DNA-binding proteins, but no NF- κ B consensus site was found. In reporter assays, basal promoter activity was barely detectable in HEK293 cells. In primary ECs neither basal nor inducible

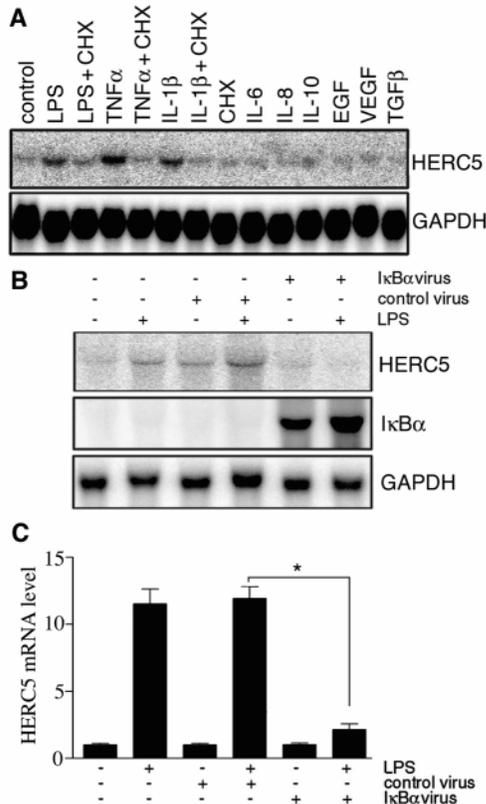


Fig. 3. Regulation of *HERC5* mRNA expression. (A) *HERC5* gene expression in HM2 cells in response to different stimuli after 8 hours of treatment. 10 μ g of total RNA were loaded per lane for analysis. Northern blots were probed for *HERC5* expression and reprobed for *GAPDH* to confirm equal loading of RNA. CHX, cycloheximide; EGF, epidermal growth factor; IL, interleukin; LPS, lipopolysaccharide; TGF β , transforming growth factor β ; TNF α , tumor necrosis factor α , VEGF, vascular endothelial growth factor. (B) Northern blot analysis of rAd.I κ B α -infected cells. HSMCEs were infected with either the rAd.I κ B α or a control adenovirus as indicated above each lane and 48 hours post infection cells were left unstimulated or stimulated with LPS for 6 hours. 10 μ g of total RNA were analyzed for mRNA of *HERC5*, *I κ B α* and *GAPDH* by subsequent hybridizations. (C) HUMECS were treated as described in B but stimulated with LPS for 8 hours; isolated RNA was analyzed by quantitative real-time RT-PCR. * P <0.05.

promoter activity was seen (data not shown). These data indicate that NF- κ B-dependent upregulation of *HERC5* mRNA is probably not mediated via the proximal *HERC5* promoter up to -1569 bp.

Control of *HERC5* protein levels

In order to determine whether *HERC5* mRNA regulation by inflammatory stimuli in ECs is reflected at the protein level, we raised a rabbit polyclonal antiserum against the C-terminal HECT domain of *HERC5*. Immunoprecipitation was performed from cell lysates of metabolically labeled vascular cells to identify endogenous levels of *HERC5* protein. The *HERC5* protein level in quiescent HSMCEs was higher than in HUVECs and HSMCs (Fig. 4A), consistent with the respective mRNA levels (Fig. 2D). In contrast to mRNA upregulation, *HERC5* protein is not increased in HSMCEs and HUMECS upon LPS stimulation for 12-17 hours (Fig. 4B and data not shown). These results prompted us to analyze *HERC5* protein turnover in LPS-treated microvascular ECs. Results from pulse-chase experiments in HSMCEs and HUMECS revealed a half-life of 9 hours in the absence and of 2 hours

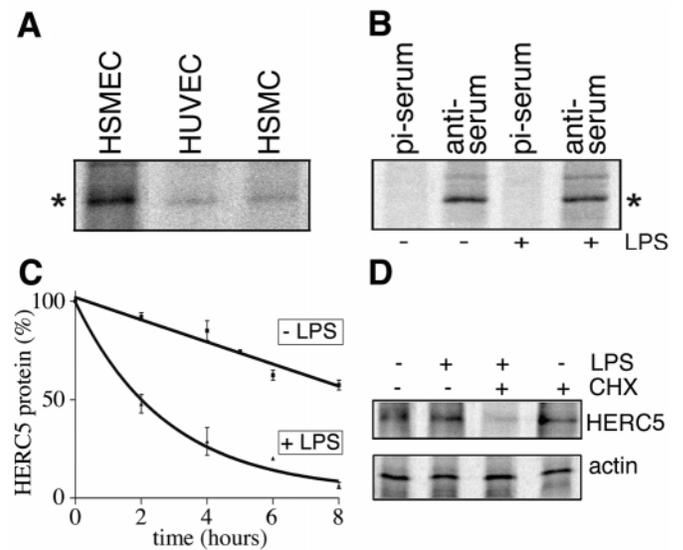


Fig. 4. Expression of *HERC5* protein. (A) *HERC5* protein expression. Immunoprecipitation with anti-*HERC5* serum from HSMCEs, HUVECs and HSMCs metabolically labeled for 16 hours were analyzed by 9% SDS-PAGE. Samples are normalized to cell number. *HERC5* protein is marked by an asterisk. (B) Immunoprecipitation with anti-*HERC5* serum from HSMCEs metabolically labeled for 16 hours in the absence or presence of LPS were resolved by 6.5% SDS-PAGE. Duplicates were immunoprecipitated with pre-immune serum as controls. Integrity of ECs was tested by IL-8 secretion upon proinflammatory cytokine treatment before assaying. Cytosolic cell extracts are normalized to counts. *HERC5* signal is marked by an asterisk. pi-serum, pre-immune serum. (C) Results from pulse-chase experiments in HSMCEs in the absence (■) or presence (▲) of LPS during chase. The calculated regression curves were significantly different to each other (P <0.05). (D) *HERC5* protein was precipitated from cell lysates of HSMCEs metabolically labeled for 20 hours. Where indicated, LPS was added for 8 hours and CHX for 4 hours before cell lysis. As a control, actin was precipitated from the same protein extracts. CHX, cycloheximide.

ligase activity was hitherto shown only for HERC3 (Cruz et al., 2001; Huijbregtse et al., 1995). The E2 enzymes UbcH5a and UbcH7 have been reported to transfer ubiquitin to HECT domain proteins; in fact, UbcH7 is used by HERC3 (Schwarz et al., 1998). We have identified UbcH5a as the only E2 enzyme capable of transferring ubiquitin to HERC5. With respect to the putative guanine exchange factor (GEF) activity of the RCC1 repeats in HERCs, GEF activity was shown only for HERC1 on ARF1, Rab3A and Rab5, consistent with its vesicular localization (Rosa et al., 1996). For HERC3 such a function was not detectable (Cruz et al., 2001). HERC5 does not localize to cytosolic vesicles (Mitsui et al., 1999) (data not shown) and therefore, a role as GEF for Rab and Rho GTPases is unlikely.

We found that expression of *HERC5* is rather restricted. High expression is only detectable in testis, consistent with the expression of several E2 ubiquitin-conjugating enzymes and other E3 ubiquitin ligases of the HECT family proteins (EDD and E6-AP) in this tissue (Baarends et al., 2000; Wong et al., 2002). During spermatogenesis, the ubiquitin system is required specifically for massive breakdown of proteins (Baarends et al., 2000). In all other tissues, *HERC5* mRNA expression levels are very weak or not detectable. We identified *HERC5* as an inflammatory-stimuli-dependent gene in primary microvascular ECs. Whereas basal expression of *HERC5* was hardly detectable in any of the vascular cells, *HERC5* upregulation followed a specific time course in both TNF α - or LPS-stimulated microvascular ECs, where *HERC5* mRNA levels started to increase after 4 hours and peaked at 9-16 hours. These results characterize *HERC5* as a late inflammatory response gene and are consistent with de novo protein synthesis required for *HERC5* mRNA upregulation. The upregulation was restricted to IL-1 β , TNF α and LPS in ECs, as no regulation was seen by stimulation of ECs with other cytokines such as IL-10, IL-8, IL-6, TGF β , or growth factors such as VEGF and EGF. Cytokines stimulating *HERC5* mRNA expression activate cells via the NF- κ B pathway. In fact, *HERC5* upregulation was also strongly reduced when NF- κ B was inhibited. The NF- κ B effect, however, is likely to be indirect not only because *HERC5* is a late response gene and protein synthesis is required for upregulation of mRNA, but also because no NF- κ B consensus site could be identified yet. The absent promoter activity of reporter constructs in ECs indicates either a role of upstream promoter/enhancer elements or a substantial contribution of mRNA stability to *HERC5* mRNA upregulation. Although no pattern for regulation of mRNA stability was found by bioinformatics analysis (UTRScan), such a possibility cannot be excluded and a regulation of mRNA stability is common in inflammatory gene expression (Kracht and Saklatvala, 2002).

Importantly, the inflammatory-cytokine-induced increase in mRNA levels did not result in increased protein levels. Instead, stimulation of ECs by LPS led to a shorter half-life of *HERC5* protein. Hence, induced mRNA levels are necessary to restore but not to increase *HERC5* protein. Induced mRNA expression levels, but no increase at the protein level is also observed for the RING ubiquitin ligase XIAP in ECs upon treatment with TNF α (Stehlik et al., 1998b). A tight control on protein level was shown for the HECT ubiquitin ligase E6-AP (Nuber et al., 1996). The long half-life of E6-AP is significantly decreased when it is ectopically overexpressed in H1299 cells, because

high levels of E6-AP induce its own degradation. As E3 proteins provide substrate specificity, their tight regulation is necessary to ensure controlled substrate degradation. Although the substrate(s) of *HERC5* are currently unknown, the regulation of *HERC5* upon LPS stimulation suggests a specific role for this E3 enzyme during the inflammatory response of ECs. It is tempting to speculate that in the early phase of inflammation, *HERC5* protein levels are decreased, allowing short-term substrate accumulation. At later time points increased mRNA levels result in recovered protein levels and ensure timely substrate recognition and degradation. Such a mechanism could amplify the initial inflammatory response and, by causing degradation at a later stage could contribute to the resolution of inflammation. In fact, protein degradation has been implied in the process of resolution (Majetschak et al., 2000); however, the mechanism responsible is not known. *HERC5* being an active E3 ubiquitin ligase, with specific transcriptional and post-translational regulation in ECs, might be a good candidate for such a process.

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