

Cutting Edge: Bacterial Modulation of Epithelial Signaling via Changes in Neddylation of Cullin-1

This information is current as of October 21, 2019.

Lauren S. Collier-Hyams, Valerie Sloane, Brigid C. Batten and Andrew S. Neish

J Immunol 2005; 175:4194-4198; ;
doi: 10.4049/jimmunol.175.7.4194
<http://www.jimmunol.org/content/175/7/4194>

References This article **cites 33 articles**, 24 of which you can access for free at:
<http://www.jimmunol.org/content/175/7/4194.full#ref-list-1>

Why *The JI*? [Submit online.](#)

- **Rapid Reviews! 30 days*** from submission to initial decision
- **No Triage!** Every submission reviewed by practicing scientists
- **Fast Publication!** 4 weeks from acceptance to publication

**average*

Subscription Information about subscribing to *The Journal of Immunology* is online at:
<http://jimmunol.org/subscription>

Permissions Submit copyright permission requests at:
<http://www.aai.org/About/Publications/JI/copyright.html>

Email Alerts Receive free email-alerts when new articles cite this article. Sign up at:
<http://jimmunol.org/alerts>

Cutting Edge: Bacterial Modulation of Epithelial Signaling via Changes in Neddylation of Cullin-1¹

Lauren S. Collier-Hyams, Valerie Sloane, Brigid C. Batten, and Andrew S. Neish²

The human enteric flora plays a significant role in intestinal health and disease. Certain enteric bacteria can inhibit the NF- κ B pathway by blockade of I κ B- α ubiquitination. I κ B- α ubiquitination is catalyzed by the E3-SCF ^{β TrCP} ubiquitin ligase, which is itself regulated via covalent modification of the cullin-1 subunit by the ubiquitin-like protein NEDD8. Neddylation is a biochemical event associated with diverse cellular processes related to cell signaling, however, physiological regulation of cullin neddylation has not been described in mammalian systems. We report that interaction of nonpathogenic bacteria with epithelial cells resulted in a rapid loss of neddylated Cul-1 and consequent repression of the NF- κ B pathway. This observation may explain the ability of intestinal bacterial communities to influence diverse eukaryotic processes in general and inflammatory tolerance of the mammalian intestinal epithelia specifically. The Journal of Immunology, 2005, 175: 4194–4198.

Virtually unique among mammalian cell types, the intestinal epithelia coexists in intimate contact with a normal flora of $\sim 10^{12}$ prokaryotic organisms without activation of proinflammatory responses that would typically be evoked in other tissues. We have observed that colonization of human model epithelium in vitro with certain strains of nonpathogenic bacteria could abrogate the host cell responses to subsequent proinflammatory challenges by blockade of the key proinflammatory/antiapoptotic NF- κ B pathway (1). This effect was mediated by the inhibition of I κ B- α ubiquitination (but not phosphorylation), thus preventing regulated I κ B- α degradation, NF- κ B nuclear translocation, and the subsequent transcriptional activation of proinflammatory/antiapoptotic genes. Additionally, we observed that these bacterial interactions inhibited ubiquitination of β -catenin, suggesting a common mechanism of action.

Substrate phospho-I κ B- α and phospho- β -catenin are normally ubiquitinated by a specific ubiquitin ligase complex designated E3-SCF ^{β -TrCP} (2, 3). This and other E3-SCF com-

plexes are themselves regulated by transient covalent modifications. The ubiquitin homologue NEDD8 must be conjugated to the cullin subunit of the E3-SCF complex on Lys⁷²⁰ for optimal ubiquitin ligase activity (4–7). Furthermore, NEDD8 modification of cullin-1 (Cul-1)³ has been demonstrated to be necessary for the ubiquitination of I κ B- α and p100/p105 and the subsequent activation of NF- κ B in mammalian cells (8–12), for ubiquitination of Dorsal, a *Drosophila* homologue (13), as well as for a myriad of signaling events in organisms as disparate as yeast and plants (*Arabidopsis*).

NEDD8 is a small protein of 81 aa that shares 80% homology (60% identity) with ubiquitin (6). “Neddylation” of substrate proteins proceeds by a successive series of enzymes structurally related to the ubiquitination enzymes, including an ATP-dependent charging enzyme (E1) and enzymes with transferase/ligase activities (E2/E3) (14). Unlike ubiquitination, however, substrates for neddylation are restricted to proteins of the cullin class (4, 7, 15). Cullins are components of E3-SCF complexes, an observation supportive of the generally accepted hypothesis that Cul-1 neddylation evolved as a regulatory modification specific to the ubiquitination machinery, and thus represents a control point in many signaling pathways and cellular processes governed by regulated protein degradation. However, to date, physiologic regulation of Cul-1 neddylation has not been described in a mammalian system, though it is well described in plant signaling pathways (16).

Materials and Methods

Bacterial strains

Salmonella typhimurium nonpathogenic mutant strains *phoP*⁻ and *fliC*⁻/*fliB*⁻, and *Escherichia coli* human commensal strains were grown in Luria-Bertani broth in a rotary shaker at 37°C for 6–8 h. This culture was diluted 1/1000 in 100 ml of Luria-Bertani broth and grown 16 h at 37°C under microaerophilic conditions as previously described (1). *Lactobacillus rhamnosus GG* was obtained from the American Type Culture Collection (ATCC cat. no. 53103) and grown in *Lactobacillus* selection broth as above for *E. coli*. *Bacteroides thetaiotaomicron* was obtained from the American Type Culture Collection (ATCC cat. no. 29148) and was grown in trypticase-yeast extract-glucose medium for 24 h under anaerobic conditions.

Epithelial Pathobiology Unit, Department of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta GA, 30322

Received for publication May 24, 2005. Accepted for publication August 1, 2005.

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked *advertisement* in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

¹ This work was supported by National Institutes of Health Grants AI49741 (to A.S.N.), DK068105 (to L.S.C.-H.), and DK064399. A.S.N. is a Burroughs Wellcome Fund Investigator in Pathogenesis of Infectious Disease.

² Address correspondence and reprint requests to Dr. Andrew S. Neish, Epithelial Pathobiology Unit, Department of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta GA, 30322. E-mail address: aneish@emory.edu

³ Abbreviations used in this paper: Cul-1, cullin-1; siRNA, small-inhibiting RNA; MOI, multiplicity of infection; HA, hemagglutinin.

Transient transfections and luciferase assays

HeLa or 293T cells were transiently transfected using Lipofectamine 2000 (Invitrogen Life Technologies) or FuGENE 6 (Roche) according to the manufacturer's instructions. For luciferase reporter assays, cells were transfected with pNF- κ B-Luc (Stratagene) and activity was determined using the Dual Luciferase Reporter Assay System (Promega). All transfections were balanced with empty vector to contain 200 ng of DNA.

Small-inhibiting RNA (siRNA)

HeLa cells were transfected at 100 nM with the following siRNA duplexes (Dharmacon): Lamin A/C, UBC12 SMARTpool, NEDD8 SMARTpool, or nontargeting siRNA. Forty-eight or 72 h after transfection, cells were stimulated with TNF- α for 30 min, lysed in denaturing SDS-PAGE buffer, and subjected to Western blot analysis. For reporter assays, 20 ng of pNF- κ B-Luc was cotransfected with 10–50 nM siRNA. A total of 42–72 h after transfection, cells were treated with TNF- α for 6 h and activity was determined as described previously.

Immunoprecipitation

After transfection and expression of epitope-tagged proteins (Flag, hemagglutinin (HA)), cells were washed in HBSS⁺ and scraped from wells or plates in a small volume (<1 ml) of nondenaturing lysis buffer (50 mM Tris, pH 7.4, 150 mM NaCl, 0.1% Nonidet P40 or SDS, 1 mM EGTA, pH 8.0, 250 nM MG-262, Sigma protease inhibitor mixture diluted 1/200, 10 mM NaF, 0.4 mM Na₃VO₄). The lysates were vortexed for 10 min at 4°C and centrifuged at 13,000 \times g for 15 min. The clarified lysates were precleared with IgG Sepharose (Sigma-Aldrich) for 2 h, and then immunoprecipitated for 4 h at 4°C with epitope-tag-Ab-conjugated agarose (anti-HA, Covance; anti-Flag, Sigma-Aldrich). The bound agarose was washed six times in nondenaturing buffer and the immunopurified proteins were eluted with a minimum volume of denaturing SDS-PAGE buffer. For immunoprecipitation of endogenous Cul-1, HeLa cell lysates were prepared as above, incubated with anti-Cul-1 Ab for 1 h, then with protein A-conjugated Sepharose (Sigma-Aldrich) for 1 h, and washed and eluted as described previously.

Western blot analysis

Immunoreactive proteins immobilized on nitrocellulose were detected with Abs to I κ B- α (Santa Cruz Biotechnology), Cul-1 (Zymed Laboratories), Cul-2 (Zymed Laboratories), NEDD8 (Zymed Laboratories), UBC12 (Rockland), HA epitope tag (Covance), or RH epitope tag (RGS-His; Qiagen) using the ECL protocol (Amersham) and a HRP-conjugated donkey anti-rabbit secondary Ab.

Results and Discussion

A tempting explanation for the observation of bacterially mediated inhibition of I κ B- α ubiquitination is that these bacteria attenuate activity of the E3-SCF ^{β -T₁CP} ubiquitin ligase. Given the established role of Cul-1 neddylation on SCF activity, we sought to determine whether prokaryotic

eukaryotic interactions could influence this particular post-translational modification. We colonized polarized T84 epithelial cells with various commensal and nonpathogenic bacteria over a time course, prepared lysates, and immunoblotted for Cul-1 and NEDD8. Characteristically, Cul-1 appears as a doublet of 85 and 90 kDa, with the higher molecular mass species presumably representing neddylated Cul-1 (Ref. 17 and Fig. 1, A and B). NEDD8 appears as a free monomer at 8 kDa and associated with cullins around 90 kDa. Both high molecular mass Cul-1 and NEDD8 were virtually abolished in colonized cells (Fig. 1A). High throughput analysis of proteins associated with active (phospho-) I κ B- α has demonstrated that SCF complexes contain Cul-1 or the related family member Cul-2 (18). Consistently, loss of high molecular mass Cul-2 was observed under the same conditions as that for Cul-1 (Fig. 1C). Expression of other cullin family members was not observed in our epithelial cell lines (data not shown).

To verify that the high molecular mass (90 kDa) Cul-1 detected in immunoblots represented the NEDD8-modified form, NEDD8 immunoreactivity was shown in immunoprecipitations of endogenous Cul-1 in uninfected epithelial cells (Fig. 1B). Furthermore, an epitope-tagged HA-Cul-1 plasmid was transfected into epithelial cells that were subsequently colonized with bacteria. Lysates were immunoprecipitated with anti-HA agarose and immunoblotted with anti-HA and anti-NEDD8 Abs. Immunoprecipitated HA-Cul-1 showed total loss of high molecular mass Cul-1 in the bacterially colonized cells. Interestingly, increased high molecular mass Cul-1 was detected in TNF-treated cells relative to control, and in both cases NEDD8 immunoreactivity could be detected in the HA-Cul-1 precipitated extracts (Fig. 1D). A wide variety of bacteria were able to mediate loss of Cul-1 neddylation with similar kinetics and multiplicity of infection (MOI) requirements. These bacteria include human intestinal commensal bacteria *E. coli*, *L. rhamnosus GG*, and *B. thetaiotaomicron*, as well as mutant strains of *S. typhimurium* rendered nonpathogenic, such as the regulatory mutant *phoP*⁻ and the flagellin-deficient mutant *fljC*⁻ *fljB*⁻ (Fig. 1E). Collectively, these experiments demonstrate that colonization of epithelial cells by various bacterial strains causes a rapid loss of neddylated Cul-1.

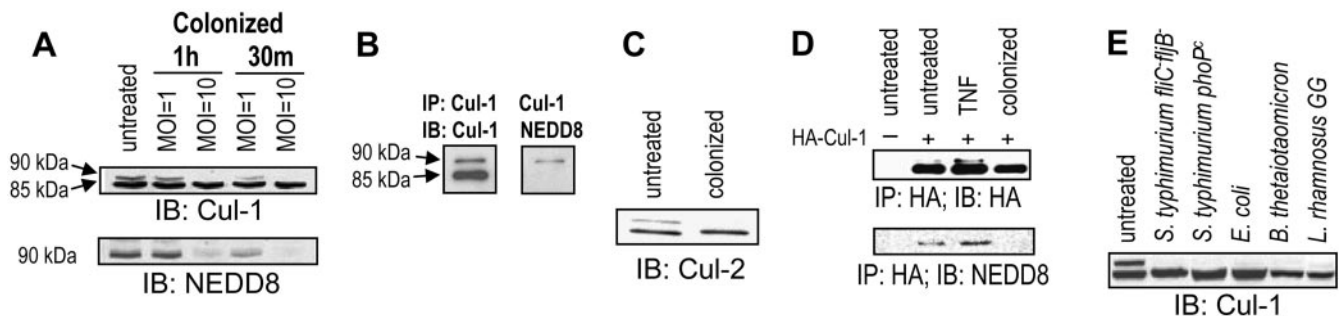


FIGURE 1. Bacterial coculture with epithelial cells results in rapid loss of neddyated Cul-1. Epithelial cells were colonized with nonpathogenic and commensal bacteria at a MOI of 10 for 1 h unless otherwise stated. *A*, Immunoblots with anti-Cul-1 and anti-NEDD8 Abs. Whole-cell extracts from model T84 epithelia colonized by nonpathogenic *S. typhimurium* for 30 min and 1 h at a MOI of 1 and 10 showing 85-kDa Cul-1 and 90-kDa NEDD8-conjugated Cul-1. *B*, Immunoprecipitation of endogenous Cul-1 showing the high molecular mass (90 kDa) band represents neddyated Cul-1. *C*, Immunoblot of whole-cell Cul-2 levels in HeLa cells untreated or colonized by commensal *B. thetaiotaomicron*. *D*, Immunoprecipitation of HA-Cul-1 with anti-HA agarose and immunoblots with anti-HA and anti-NEDD8 Abs of lysates from transfected HeLa cells untreated, challenged with TNF- α for 30 min, or colonized by nonpathogenic *S. typhimurium* for 1 h. *E*, Immunoblot of whole-cell Cul-1 levels in HeLa or T84 cells colonized by the indicated bacteria for 1 h.

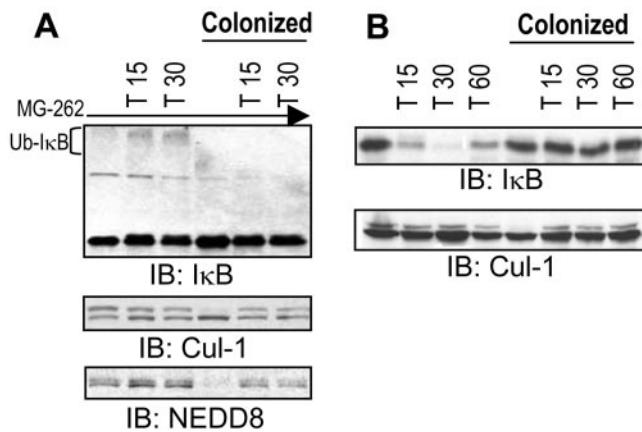


FIGURE 2. Loss of Cul-1 neddylation results in inhibition of I κ B- α ubiquitination and degradation. *A*, Immunoblots of whole-cell I κ B- α , Cul-1, and NEDD8 levels in 293T cells pretreated with MG-262 (proteasome inhibitor, 250 nM) for 1 h, colonized by nonpathogenic *S. typhimurium* at an MOI of 10 for 30 min where indicated, washed, and subsequently challenged with TNF- α (T; 10 ng/ml) for 15 and 30 min. Ubiquitinated I κ B is marked. *B*, Immunoblots with anti-I κ B- α and anti-Cul-1 Abs of whole-cell extracts from model T84 epithelia untreated or colonized by nonpathogenic *S. typhimurium* for 1 h at an MOI of 10, washed, and subsequently challenged with basolateral TNF- α (T; 10 ng/ml) for 15, 30, or 60 min.

To test whether the bacterially mediated loss of Cul-1 neddylation resulted in inhibition of the NF- κ B pathway, control and bacterially colonized epithelial cells were challenged by a proinflammatory stimulus (TNF- α) and the effects on I κ B- α processing were evaluated. First, epithelial cells were treated with MG-262, an inhibitor of the 26S proteasome—a condition that allows visualization of labile phosphorylated and ubiquitinated I κ B- α adducts. In cells pretreated with MG-262 and challenged with TNF- α , phospho- and ubiquitinated I κ B- α species and neddylated Cul-1 were observed as expected (Fig. 2*A*). Also as expected, Cul-1 neddylation was lost in cells pretreated with MG-262 and colonized with nonpathogenic bacteria in the absence of TNF- α . However, in colonized cells challenged with TNF- α , I κ B- α was phosphorylated but no ubiquitinated I κ B- α was detected. Interestingly, Cul-1 showed rapid reddylation (within 15 min) in the presence of TNF- α .

Second, a similar experiment was performed in the absence of MG-262 to evaluate TNF-induced I κ B- α degradation. Without bacterial colonization, I κ B- α is rapidly degraded in the presence of TNF- α (Fig. 2*B*). However, when colonized epithelia were challenged with TNF- α , even though Cul-1 returned to a neddylated state within 15 min, I κ B- α was not degraded and thus, the NF- κ B pathway remained blocked. This is consistent with the bacterially mediated inhibition of NF- κ B previously described (1). Together, these data show that loss of Cul-1 neddylation correlates with blockade of I κ B- α ubiquitination and degradation.

UBC12 is the NEDD8 transferase/ligase enzyme (E2) and, as is typical for enzymes that mediate this function for all ubiquitin-like proteins, uses the Cys¹¹¹ residue in the catalytic site to form a thioester bond with activated NEDD8 before transfer to a cullin substrate and catalysis of an isopeptide bond (14). Wada et al. (17) described a dominant-negative UBC12 (Cys¹¹¹Ser) mutant that acts by allowing formation of an irreversible peptide bond between activated NEDD8 and the hydroxyl group on the substituted Ser¹¹¹ residue, thus sequestering and reducing the free pool of NEDD8. When dominant-negative UBC12 (C111S) and Cul-1 were cotransfected into epithelial cells, loss of neddylated Cul-1 was observed in Cul-1 immunoblots while wild-type UBC12 had no effect (Fig. 3*A*). Presumably, the sequestration of free NEDD8 irreversibly bound on an “active site trap” results in a blockade of new neddylation and allows deneddylase activities such as that by the COP9 signalosome, a multisubunit assembly that bears homology to the 16S “lid” regulatory subunit of the proteasome that is physically associated with SCF complexes, to deconjugate NEDD8 from Cul-1 (19, 20). Consistently, dominant-negative UBC12 (C111S) but not wild-type UBC12 overexpression blocked ubiquitination of overexpressed I κ B- α (Fig. 3*B*) and repressed activation of a TNF- α -induced NF- κ B-dependent reporter construct (Fig. 3*C* and Ref. 21), mechanistically demonstrating that loss of neddylated Cul-1 can inhibit I κ B- α ubiquitination and NF- κ B transactivation in epithelial cells.

To confirm that repression of UBC12 results in loss of Cul-1 neddylation and NF- κ B blockade, siRNA to UBC12 were used and compared against results from NEDD8 siRNA. When

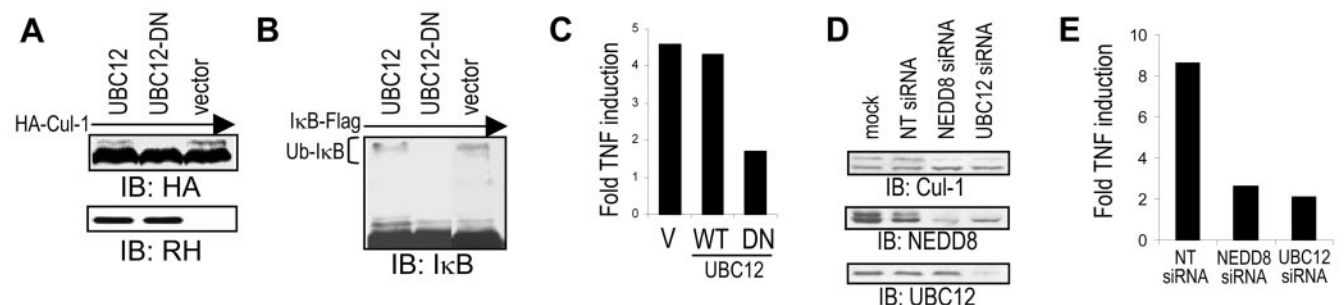


FIGURE 3. Blockade of UBC12 function causes loss of Cul-1 neddylation and results in inhibition of NF- κ B activation. *A*, Immunoblots of whole-cell extracts with anti-HA and anti-RH (RGS-His) Abs from HeLa cells transfected with HA-Cul-1 and RH-UBC12 (wt), RH-UBC12-DN (C111S), or empty vector. *B*, Immunoblots of whole-cell I κ B- α from extracts of HeLa cells transfected with I κ B-Flag and RH-UBC12 (wt), RH-UBC12-DN (C111S), or empty vector, pretreated with MG-262 (250 nM) for 1 h, and challenged with TNF- α (T; 10 ng/ml) for 30 min. Ubiquitinated I κ B species are marked. *C*, Luciferase activity of an NF- κ B-Luc reporter in transfected HeLa cells overexpressing wild-type UBC12 (WT), UBC12-C111S (DN), or vector alone (V), and stimulated by TNF- α . Data are shown as fold TNF induction and are representative of more than three independent experiments. *D*, Immunoblots of whole-cell Cul-1, NEDD8, and UBC12 from extracts of HeLa cells transfected with nontargeting (NT) siRNA, NEDD8 siRNA, or UBC12 siRNA. *E*, Luciferase activity of an NF- κ B-Luc reporter in HeLa cells cotransfected with nontargeting (NT) siRNA, NEDD8 siRNA, or UBC12 siRNA and stimulated by TNF- α . Data are shown as fold TNF induction and are representative of more than three independent experiments.

UBC12 siRNA was transfected into HeLa cells for 48–72 h, a marked reduction in the ratio of endogenous neddylation to unneddylation Cul-1 and of high molecular mass NEDD8 was observed, consistent with the effects of transfected dominant-negative UBC12 on transfected Cul-1 (Fig. 3D). As expected, NEDD8 siRNA also reduced the whole cell pool of neddylation Cul-1 and high molecular mass NEDD8. Finally, cotransfection of the TNF- α -inducible NF- κ B-responsive reporter showed that UBC12 siRNA repressed inducible NF- κ B activity to a similar degree as the dominant-negative protein or NEDD8 siRNA (Fig. 3E).

Currently, the precise role that neddylation of cullins plays in the activation of SCF-mediated ubiquitination is not fully understood at a biochemical level. Most models, which are largely derived from in vitro cell-free experimental systems, suggest that the modification of Cul-1 mediated by the NEDD8 E1 (APP-BP1/UBA3) and E2 (UBC12) results in physical recruitment (22) and/or functional activation of the ubiquitin E2 subunit (15, 23). Alternatively, neddylation may serve in the assembly of a substrate binding subcomplex (β -TrCP/Skp1) with an enzymatically active subcomplex (Cul/E2) (24, 25). We are currently pursuing experiments to explore these possibilities.

Mutations leading to loss of function of Cul-1 neddylation status can have profound functional consequences in a variety of experimental models including yeast (20), *Arabidopsis* (26), *Caenorhabditis elegans* (27), *Drosophila* (13), mice (28), and human cells in vitro (19). However, only limited evidence is available implicating environmental signals in the physiologic regulation of Cul-1 neddylation. For example, yeast Cul was shown to be hyperneddylated in response to UV exposure (29). In *Arabidopsis* studies, wild-type plants showed marked Cul-1 deneddylation when reared in darkness, while mutant plants that fail to respond to light were shown to have an abnormal accumulation of neddylation Cul-1 (16). In this case, deneddylation was achieved by a presumed up-regulation or recruitment of the deneddylation COP9 signalosome. Interestingly, the COP9 signalosome has been shown to coimmunoprecipitate with the barley plant RAR1 signaling intermediate necessary for activation of plant pattern recognition receptors (R-proteins) during the immune response (30), and genetic silencing of COP9 subunits in plants resulted in loss of leucine rich repeat receptor-mediated resistance to tobacco mosaic virus (31), suggesting the provocative notion that NEDD8-dependent protein degradation is involved in plant signaling processes elicited by microbial interactions.

How could bacterial colonization of epithelial (or other eukaryotic) cells mediate loss of Cul-1 neddylation? The environment of the intestinal lumen in immediate contact with the epithelium is largely anaerobic and is suffused with not just a complex ecosystem of living bacteria, but also a miasma of small bacterially produced compounds, and a spectrum of fermentative by-products. Exposure to these bacterial physiochemical stressors may result in compensatory cellular metabolic changes in the epithelium that affect the neddylation machinery, specifically, by limiting activity of UBC12, or augmenting activity of the COP9 signalosome or other deneddylases. A specific example of a metabolic change affecting Cul-1 neddylation was shown in an in vitro system using cytosolic extracts, where ATP depletion with apyrase was shown to efficiently deneddylate

Cul-1, while supplementation of the reaction with ATP augmented neddylation (24).

Bacterially derived compounds themselves may directly affect cellular processes as well. Examples of bacterial byproducts with inhibitory activity on proinflammatory signaling are short chain fatty acids such as butyrate, propionate, and acetate produced from carbohydrate fermentation. These compounds have been used therapeutically (by intraluminal instillation) to dampen intestinal inflammation in inflammatory bowel disease, and have been shown to block NF- κ B activation in vitro (32). Metabolic products/small molecules produced at the eukaryotic/prokaryotic interface may account for the widely known effects of the bacterial flora on normal intestinal function (33), and may influence a range of eukaryotic regulatory processes.

Acknowledgments

We thank Dr. Keith Wilkinson for helpful discussions and Dr. Aaron Ciechanover for the UBC12 plasmids.

Disclosures

The authors have no financial conflict of interest.

References

1. Neish, A. S., A. T. Gewirtz, H. Zeng, A. N. Young, M. E. Hobert, V. Karmali, A. S. Rao, and J. L. Madara. 2000. Prokaryotic regulation of epithelial responses by inhibition of I κ B- α ubiquitination. *Science* 289: 1560–1563.
2. Winston, J. T., P. Strack, P. Beer-Romero, C. Y. Chu, S. J. Elledge, and J. W. Harper. 1999. The SCF β -TRCP-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I κ B α and β -catenin and stimulates I κ B α ubiquitination in vitro. *Genes Dev.* 13: 270–283.
3. Spencer, E., J. Jiang, and Z. J. Chen. 1999. Signal-induced ubiquitination of I κ B α by the F-box protein Slimb/ β -TrCP. *Genes Dev.* 13: 284–294.
4. Pan, Z. Q., A. Kentsis, D. C. Dias, K. Yamoah, and K. Wu. 2004. Nedd8 on cullin: building an expressway to protein destruction. *Oncogene* 23: 1985–1997.
5. Liakopoulos, D., G. Doenges, K. Matuschewski, and S. Jentsch. 1998. A novel protein modification pathway related to the ubiquitin system. *EMBO J.* 17: 2208–2214.
6. Kamitani, T., K. Kito, H. P. Nguyen, and E. T. Yeh. 1997. Characterization of NEDD8, a developmentally down-regulated ubiquitin-like protein. *J. Biol. Chem.* 272: 28557–28562.
7. Parry, G., and M. Estelle. 2004. Regulation of cullin-based ubiquitin ligases by the Nedd8/RUB ubiquitin-like proteins. *Semin. Cell Dev. Biol.* 15: 221–229.
8. Ohh, M., W. Y. Kim, J. J. Moslehi, Y. Chen, V. Chau, M. A. Read, and W. G. Kaelin, Jr. 2002. An intact NEDD8 pathway is required for Cullin-dependent ubiquitination in mammalian cells. *EMBO Rep.* 3: 177–182.
9. Read, M. A., J. E. Brownell, T. B. Gladysheva, M. Hottelet, L. A. Parent, M. B. Coggins, J. W. Pierce, V. N. Podust, R. S. Luo, V. Chau, and V. J. Palombella. 2000. Nedd8 modification of cul-1 activates SCF(β -TrCP)-dependent ubiquitination of I κ B α . *Mol. Cell Biol.* 20: 2326–2333.
10. Furukawa, M., Y. Zhang, J. McCarville, T. Ohta, and Y. Xiong. 2000. The CUL1 C-terminal sequence and ROC1 are required for efficient nuclear accumulation, NEDD8 modification, and ubiquitin ligase activity of CUL1. *Mol. Cell Biol.* 20: 8185–8197.
11. Amir, R. E., K. Iwai, and A. Ciechanover. 2002. The NEDD8 pathway is essential for SCF(β -TrCP)-mediated ubiquitination and processing of the NF- κ B precursor p105. *J. Biol. Chem.* 277: 23253–23259.
12. Amir, R. E., H. Haecker, M. Karin, and A. Ciechanover. 2004. Mechanism of processing of the NF- κ B p100 precursor: identification of the specific polyubiquitin chain-anchoring lysine residue and analysis of the role of NEDD8-modification on the SCF(β -TrCP) ubiquitin ligase. *Oncogene* 23: 2540–2547.
13. Ou, C. Y., Y. F. Lin, Y. J. Chen, and C. T. Chien. 2002. Distinct protein degradation mechanisms mediated by Cul1 and Cul3 controlling Ci stability in *Drosophila* eye development. *Genes Dev.* 16: 2403–2414.
14. Gong, L., and E. T. Yeh. 1999. Identification of the activating and conjugating enzymes of the NEDD8 conjugation pathway. *J. Biol. Chem.* 274: 12036–12042.
15. Petroski, M. D., and R. J. Deshaies. 2005. Function and regulation of cullin-RING ubiquitin ligases. *Nat. Rev. Mol. Cell Biol.* 6: 9–20.
16. Wang, X., S. Feng, N. Nakayama, W. L. Crosby, V. Irish, X. W. Deng, and N. Wei. 2003. The COP9 signalosome interacts with SCF UFO and participates in *Arabidopsis* flower development. *Plant Cell* 15: 1071–1082.
17. Wada, H., E. T. Yeh, and T. Kamitani. 2000. A dominant-negative UBC12 mutant sequesters NEDD8 and inhibits NEDD8 conjugation in vivo. *J. Biol. Chem.* 275: 17008–17015.
18. Bouwmeester, T., A. Bauch, H. Ruffner, P. O. Angrand, G. Bergamini, K. Croughton, C. Cruciat, D. Eberhard, J. Gagneur, S. Ghidelli, et al. 2004. A physical and functional map of the human TNF- α /NF- κ B signal transduction pathway. *Nat. Cell Biol.* 6: 97–105.

19. Cope, G. A., and R. J. Deshaies. 2003. COP9 signalosome: a multifunctional regulator of SCF and other cullin-based ubiquitin ligases. *Cell* 114: 663–671.
20. Lyapina, S., G. Cope, A. Shevchenko, G. Serino, T. Tsuge, C. Zhou, D. A. Wolf, N. Wei, and R. J. Deshaies. 2001. Promotion of NEDD-CUL1 conjugate cleavage by COP9 signalosome. *Science* 292: 1382–1385.
21. Morris, K. R., R. D. Lutz, H. S. Choi, T. Kamitani, K. Chmura, and E. D. Chan. 2003. Role of the NF- κ B signaling pathway and κ B *cis*-regulatory elements on the IRF-1 and iNOS promoter regions in mycobacterial lipoarabinomannan induction of nitric oxide. *Infect. Immun.* 71: 1442–1452.
22. Kawakami, T., T. Chiba, T. Suzuki, K. Iwai, K. Yamanaka, N. Minato, H. Suzuki, N. Shimbara, Y. Hidaka, F. Osaka, et al. 2001. NEDD8 recruits E2-ubiquitin to SCF E3 ligase. *EMBO J.* 20: 4003–4012.
23. Wu, K., A. Chen, and Z. Q. Pan. 2000. Conjugation of Nedd8 to CUL1 enhances the ability of the ROC1-CUL1 complex to promote ubiquitin polymerization. *J. Biol. Chem.* 275: 32317–32324.
24. Zheng, J., X. Yang, J. M. Harrell, S. Ryzhikov, E. H. Shim, K. Lykke-Andersen, N. Wei, H. Sun, R. Kobayashi, and H. Zhang. 2002. CAND1 binds to unneddylated CUL1 and regulates the formation of SCF ubiquitin E3 ligase complex. *Mol. Cell.* 10: 1519–1526.
25. Liu, J., M. Furukawa, T. Matsumoto, and Y. Xiong. 2002. NEDD8 modification of CUL1 dissociates p120(CAND1), an inhibitor of CUL1-SKP1 binding and SCF ligases. *Mol. Cell.* 10: 1511–1518.
26. Bostick, M., S. R. Lochhead, A. Honda, S. Palmer, and J. Callis. 2004. Related ubiquitin 1 and 2 are redundant and essential and regulate vegetative growth, auxin signaling, and ethylene production in *Arabidopsis*. *Plant Cell* 16: 2418–2432.
27. Kurz, T., L. Pintard, J. H. Willis, D. R. Hamill, P. Gonczy, M. Peter, and B. Bowerman. 2002. Cytoskeletal regulation by the Nedd8 ubiquitin-like protein modification pathway. *Science* 295: 1294–1298.
28. Tateishi, K., M. Omata, K. Tanaka, and T. Chiba. 2001. The NEDD8 system is essential for cell cycle progression and morphogenetic pathway in mice. *J. Cell Biol.* 155: 571–579.
29. Groisman, R., J. Polanowska, I. Kuraoka, J. Sawada, M. Saijo, R. Drapkin, A. F. Kisselev, K. Tanaka, and Y. Nakatani. 2003. The ubiquitin ligase activity in the DDB2 and CSA complexes is differentially regulated by the COP9 signalosome in response to DNA damage. *Cell* 113: 357–367.
30. Azevedo, C., A. Sadanandom, K. Kitagawa, A. Freialdenhoven, K. Shirasu, and P. Schulze-Lefert. 2002. The RAR1 interactor SGT1, an essential component of R gene-triggered disease resistance. *Science* 295: 2073–2076.
31. Liu, Y., M. Schiff, G. Serino, X. W. Deng, and S. P. Dinesh-Kumar. 2002. Role of SCF ubiquitin-ligase and the COP9 signalosome in the N gene-mediated resistance response to Tobacco mosaic virus. *Plant Cell.* 14: 1483–1496.
32. Yin, L., G. Laevsky, and C. Giardina. 2001. Butyrate suppression of colonocyte NF- κ B activation and cellular proteasome activity. *J. Biol. Chem.* 276: 44641–44646.
33. Hooper, L. V., and J. I. Gordon. 2001. Commensal host-bacterial relationships in the gut. *Science* 292: 1115–1118.