

• 肺动脉高压专题研究 •

# 泛素-蛋白酶体系统在肺动脉高压中的研究进展

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**【摘要】** 泛素化是真核细胞中最重要的蛋白质翻译后修饰形式之一, 可参与调节细胞的各种生理过程, 包括细胞周期进程、细胞分化、细胞凋亡以及先天性和适应性免疫反应。目前越来越多的靶向泛素-蛋白酶体系统 (UPS) 的药物被开发出来。有证据表明, 肺动脉高压 (PH) 发病过程中存在UPS功能紊乱, 但其机制尚不明确, 也无相关药物应用于临床。本文回顾了UPS的结构和功能, 并对PH中功能异常的UPS相关蛋白及其作用机制进行综述, 以为临床精准诊断及靶向治疗方案的制定提供新思路。

**【关键词】** 肺动脉高压; 泛素-蛋白酶体系统; 泛素蛋白连接酶类; 泛素连接酶E3; 去泛素化酶; 综述

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**Research Progress of Ubiquitin-proteasome System in Pulmonary Hypertension** DING Chaowei, GUO Chang, YUAN Yadong

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**【Abstract】** Ubiquitination, one of the most important types of post-translational protein modifications in eukaryotic cells, has played a role in regulating various physiological processes including cell cycle progression, cell differentiation, cell apoptosis, and innate and adaptive immune responses. At present, more and more drugs targeting ubiquitin proteasome system (UPS) have been developed. There is evidence that UPS dysfunction exists in the pathogenesis of pathogenesis of pulmonary hypertension (PH), but its mechanisms was still unclear, and no related-drugs were applied in clinic. This paper reviews the the structure and function of UPS, and summarizes the functional abnormalities of UPS related protein in PH and their mechanism of action, so as to provide new ideas for accurate clinical diagnosis and the formulation of targeted therapy.

**【Key words】** Pulmonary hypertension; Ubiquitination-proteasome system; Ubiquitin-protein ligases; Ubiquitin ligase E3; Deubiquitinating enzyme; Review

肺动脉高压 (pulmonary hypertension, PH) 的病理机制目前普遍认为是肺动脉收缩压持续性增高和广泛的肺血管重塑。近年来, 随着对PH的深入研究, 发现PH的病理生理与癌症有诸多相似之处, 如细胞过度增殖、凋亡耐受、逃避生长抑制、过度迁移及内皮-间充质转化等<sup>[1]</sup>。蛋白质泛素化是最普遍的蛋白质翻译后的修饰形式, 随着分子生物学的发展, 蛋白质泛素化在肿瘤靶向治疗领域研究日益深入, 越来越多的证据表明, 靶向调节泛素-蛋白酶体系统 (ubiquitination-proteasome system, UPS) 相关蛋白活性是一种有前景的研究方向<sup>[2]</sup>。因此, 通过调节在PH肺血管重塑、右心室重塑过程中发挥作用

的UPS相关蛋白, 有望成为PH治疗的新方向。本文主要综述了UPS的结构和功能、UPS相关蛋白与PH的关系。

## 1 UPS的结构和功能

真核生物细胞内蛋白质降解主要通过2条途径, 一条由自噬-溶酶体途径介导, 受多种应激条件激活, 如饥饿、低氧、氧化应激、蛋白质聚集等, 主要对长寿蛋白质、不溶蛋白质聚集体进行降解; 另一条由依赖ATP的UPS介导, 是体内蛋白质代谢最重要的过程之一<sup>[3]</sup>。泛素蛋白由76个氨基酸组成, 被泛素激活酶E1以ATP依赖的方式激活并连接到泛素连接酶E2上, 然后由泛素连接酶E3介导其转移至靶蛋白的赖氨酸残基上, 使目的蛋白被蛋白酶体识别、降解或发生功能改变<sup>[4]</sup>。当底物蛋白只有一个赖氨酸残基被泛素蛋白修饰时称为单泛素化, 当多个赖氨酸残基被泛素蛋白修饰时则称为多泛素化。新的泛素蛋白与前一个泛素蛋白羧基末端连接形成泛素链条时, 称为多聚泛素化。泛素链根据连接位点可分

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为8种不同的类型: K6、K11、K27、K29、K33、K48、K63或M1。其中最常见的是K48泛素链可被26S蛋白酶体复合物识别, 导致底物蛋白降解。K6泛素链与DNA损伤修复和线粒体自噬相关, K11泛素链与细胞对低氧的适应及细胞周期调控有关, K27泛素链与核转位有关, K29泛素链与Wnt信号传导有关, K33泛素链与AMP依赖的蛋白激酶(AMP-activated protein kinase, AMPK)信号传导有关, K63泛素链与蛋白质运输和先天免疫有关, M1泛素链通过促进核因子 $\kappa$ B(nuclear factor kappa-B, NF- $\kappa$ B)通路激活而在炎症和免疫反应中发挥重要作用<sup>[5]</sup>。底物蛋白与泛素特异性结合的细胞内降解或调控机制主要由泛素连接酶E3决定, 目前已知的泛素连接酶E3主要有3种: RING结构域家族、HECT结构域家族和U-box基因家族。泛素化的过程是可逆的, 去泛素化酶(deubiquitinases, DUBs)与泛素连接酶E3相似, 能选择性地结合底物蛋白, 裂解底物蛋白上的泛素链, 使其免于被蛋白酶体所识别、降解或逆转相应功能改变。泛素连接酶E3和DUBs同底物蛋白相互作用的动态平衡对蛋白质稳态及功能至关重要<sup>[6]</sup>。

## 2 泛素连接酶E3与PH

### 2.1 鼠双微体蛋白2(mouse double minute 2, MDM2)

MDM2属于RING结构域家族, 包含多个结构域, 主要为N端的p53结合区结构域、C端的RING结构域、中心区域的酸性结构域和锌指结构域<sup>[7]</sup>。目前研究相对深入的是MDM2与p53的相互调控机制。首先, 高水平MDM2可诱导p53多聚泛素化, 使其经蛋白酶体途径降解; 其次, 低水平MDM2可诱导p53单泛素化, 促进p53从细胞核迁出, 降低了p53的核转录因子活性; 最后, 除上述泛素化调控外, MDM2与p53之间还存在一个反馈回路: 当p53水平升高时, 刺激MDM2转录, 导致p53的泛素化降解增加。p53通过这种负反馈调节机制, 维持自身在细胞中的正常生理功能<sup>[8]</sup>。研究发现, PH模型动物肺组织中MDM2表达增高而p53水平下降, 而使用MDM2抑制剂——Nutlin-3a可增加慢性缺氧性肺动脉高压(hypoxia-induced pulmonary hypertension, HPH)模型小鼠及SU5416/低氧(Su/Hx)诱导的PH模型小鼠肺组织中p53水平, 并逆转肺血管重塑<sup>[9]</sup>。此外, SHEN等<sup>[10]</sup>研究表明, MDM2还可作为血管紧张素转换酶2(angiotensin converting enzyme 2, ACE2)蛋白的泛素连接酶E3, 在K788处泛素化ACE2蛋白。低氧条件下, HPH及野百合碱诱导PH模型小鼠肺组织中MDM2表达增高, 促进ACE2蛋白的泛素化降解, 从而引起肾素-血管紧张素系统紊乱和肺动脉内皮细胞(pulmonary arterial endothelial cells, PAECs)功能障碍, 进而参与PH的发生及发展, 而MDM2抑制剂——JNJ-165可有效逆转上述致病过程。因此, MDM2可以作为抑制PH进展的一个潜在治疗靶点。

### 2.2 Cullin 7

Cullin家族共有8个成员, 均属于RING结构域家族, 其中, Cullin 7由1 698个氨基酸组成, 其编码基因位于人类6号染色体短臂(6p21.1), 其作为核心支架蛋白与ROC1、Skp1和Fbxw8一起构成SCF(Skp1-Cullin-F-box)泛素连接酶E3复合物。研究发现, 在泛素化过程中, Cullin 7可与底物蛋白直接结合, 也可通过SCF泛素连接酶E3复合物发挥作用。与Cullin 7相互作用的蛋白主要有: Cyclin D1<sup>[11]</sup>、Mst1<sup>[12]</sup>、

p53<sup>[13]</sup>等。LIU等<sup>[14]</sup>研究发现, 低氧可上调大鼠肺动脉和肺动脉平滑肌细胞(pulmonary vascular smooth muscle cells, PASCs)中Cullin 7的表达, 而抑制Cullin 7表达又能降低p53水平, 缓解低氧诱导的PASCs过度增殖和迁移。目前, Cullin 7对p53水平的调控存在部分争议, 在小鼠胚胎成纤维细胞中敲低Cullin 7后, p53水平并没有升高, 但Cullin 7可在细胞质中直接与p53结合, 可能抑制了p53细胞核内的部分转录因子活性<sup>[13, 15]</sup>。在肺癌、乳腺癌细胞中敲低Cullin 7, 可检测到p53水平升高, 但这均未直接证明Cullin 7通过泛素化促进p53降解, 同样未明确PASCs中Cullin 7与p53相互作用的具体机制<sup>[16-17]</sup>。因此, Cullin 7与p53之间的调控作用及在PH中的作用机制仍需进一步探究。

### 2.3 Parkin

Parkin是由人类基因组编码的600多种泛素连接酶E3之一, 其首次在帕金森病患者中被发现<sup>[18]</sup>。Parkin由465个氨基酸构成, N端具有泛素样结构域, C端为两个RING结构域及之间的IBR(in-between-ring)结构域组成的多环结构域<sup>[19]</sup>。在线粒体质量控制中, Parkin被PINK1募集至受损线粒体并将其膜上的蛋白泛素化, 进而使线粒体被溶酶体降解<sup>[20]</sup>。LI等<sup>[21]</sup>研究发现, 低氧诱导的PH模型小鼠肺组织中PINK1、Parkin水平升高, 进而促进线粒体自噬途径的激活, 而过度的线粒体自噬可导致PASCs增殖加快及凋亡抑制; 此外分别敲低PINK1、Parkin均可逆转低氧诱导的PASCs增殖和凋亡抑制。最新研究发现, 雌性小鼠PAECs中的Parkin水平高于雄性小鼠, 这可能是女性肺血管对损伤的易感性高于男性, 更易发展为PH的原因<sup>[22]</sup>。但该实验仅进行体外细胞实验, 尚缺乏体内肺血管中Parkin在不同性别PH患者中的差异及调控作用的证据。随着未来研究深入, 靶向Parkin调控线粒体自噬水平, 可能会成为PH治疗的新思路, 而探究体内性染色体或性激素与Parkin介导的线粒体自噬之间的关系, 也许会进一步揭开PH性别悖论的面纱。

### 2.4 VHL(von Hippel-Lindau)

VHL首次出现在20世纪90年代初, 用于描述一种遗传性多血管肿瘤疾病——VHL综合征, 其特征是遗传性视网膜、小脑和脊髓血管母细胞瘤、嗜铬细胞瘤和肾透明细胞癌, 该病患者后被证明存在遗传性VHL基因缺陷<sup>[23]</sup>。VHL基因位于人类3号染色体短臂(3p25), 其所编码的蛋白含有213个氨基酸<sup>[24]</sup>, VHL蛋白(von Hippel-Lindau protein, pVHL)单独存在并不具备酶活性, 但其能够与elongins B、elongins C、Cullin2以及Rbx-1形成ECV(elongin B/C-Cullin2-VHL)泛素连接酶E3复合物, 进而靶向识别、诱导底物蛋白降解<sup>[25]</sup>。众所周知, pVHL底物蛋白为缺氧诱导因子 $\alpha$ (hypoxia inducible factor- $\alpha$ , HIF- $\alpha$ ), pVHL的 $\beta$ -结构域通过识别并结合羟基化的HIF- $\alpha$ , 可使HIF- $\alpha$ 被蛋白酶体降解<sup>[26]</sup>。缺氧诱导因子(hypoxia-inducible factor, HIF)是氧稳态的主要调节因子, 存在3种不同亚型: HIF-1、HIF-2和HIF-3, 每种亚型均是由氧敏感的 $\alpha$ 亚基和氧不敏感的 $\beta$ 亚基组成的异二聚体<sup>[27]</sup>。在正常细胞中HIF-1 $\alpha$ 受脯氨酰羟化酶和pVHL途径降解,  $t_{1/2}$ 在5 min左右, 但在低氧PAECs及PASCs中, 脯氨酰羟化酶和pVHL途径受到抑制, HIF-1 $\alpha$ 羟基化减弱, 逃

避了pVHL的识别,使其 $t_{1/2}$ 明显延长,进而促进细胞增殖、代谢。研究显示,慢性高海拔暴露、慢性阻塞性肺疾病、肺间质纤维化等相关PH及慢性血栓栓塞性PH患者肺组织中HIF-1 $\alpha$ 水平升高<sup>[28]</sup>。而在动脉性肺动脉高压(pulmonary arterial hypertension, PAH),尤其是特发性动脉性肺动脉高压(idiopathic pulmonary arterial hypertension, IPAH)患者的PASCs中HIF-1 $\alpha$ 水平变化不明确,尚需要更多的数据探讨<sup>[29-30]</sup>。与HIF-1 $\alpha$ 类似,p22phox在细胞中的稳定性同样受到脯氨酰羟化酶和pVHL途径调控。低氧条件下,细胞泛素化能力下降,导致p22phox积累,p22phox为还原型烟酰胺腺嘌呤二核苷酸磷酸(nicotinamide adenine dinucleotide phosphate, NADPH)氧化酶的亚单位,故其异常积累会导致NADPH氧化酶激活,活性氧(reactive oxygen species, ROS)产生增多,进而通过NOX2、NOX4途径进一步上调HIF-1 $\alpha$ 表达<sup>[31]</sup>。pVHL/HIF-2 $\alpha$ 同样可以参与PH的病理改变,与大多数VHL突变不同,VHL R200(598C>T)突变不会导致肿瘤形成,而是与Chuvash红细胞增多症有关,还易合并PH。这可能是由于pVHL与羟化HIF-2 $\alpha$ 亚基结合能力减弱,从而增加了HIF-2 $\alpha$ 水平,导致包括促红细胞生成素(erythropoietin, EPO)、内皮素1、CXCL-12在内的靶基因的表达升高<sup>[32]</sup>,而口服HIF-2 $\alpha$ 抑制剂——MK-6482可成功降低Chuvash红细胞增多症模型小鼠肺动脉压<sup>[33]</sup>。因此,VHL作为一种抑癌基因,是一个很有前景的PH治疗相关靶点。

**2.5 Smad泛素调节因子1 (Smad ubiquitylation regulatory factor-1, SMURF1)** SUMRF1包括N端C2、串联WW和C端HECT结构域<sup>[34]</sup>。在IPAH患者及野百合碱诱导PH模型大鼠肺组织中均可见SMURF1表达增高,并与疾病的严重程度相关<sup>[35-36]</sup>。SMURF1是TGF- $\beta$ 1/骨形态发生蛋白(bone morphogenetic protein, BMP)信号的负调节因子,不仅可与Smad1、Smad5相互作用,还直接参与骨形态发生蛋白受体(bone morphogenetic protein receptor, BMPR)2的泛素-蛋白酶体代谢<sup>[37]</sup>。BMPR的内吞-溶酶体降解有两个独立的途径——基础途径和配体激活途径。通常情况下SMURF1可介导BMPR的基础内吞作用,但当BMPR半胱氨酸残基突变可进一步激活smurf1依赖的内吞作用,导致BMPR泛素化降解增强。突变的BMPR2对BMP信号传导具有负性影响,使得PASCs表型发生改变,这种影响可以通过抑制SMURF1表达得到逆转<sup>[38]</sup>,如miRNA-140-5p、miRNA-424(322)均可靶向抑制SMURF1水平,其中PH患者血液中miRNA-140-5p水平下降,而miRNA-424(322)水平升高<sup>[39]</sup>。BAPTISTA等<sup>[40]</sup>发现,miRNA-424(322)水平与PAH疾病严重程度相关,但高水平miRNA-424(322)与PAH患者更好的预后密切相关。升高的miRNA-424(322)绝大部分由PAECs分泌,其可经循环进入心肌细胞,参与调控SMURF1水平,进而改善患者右心功能。

**2.6 SIAH (seven in absentia homologue)** SIAH是一类高度保守的RING结构域家族,是哺乳动物体内泛素系统重要的组成部分,人类编码其中3个基因,即SIAH1、SIAH2、SIAH3。其中SIAH1、SIAH2参与细胞的多种代谢活动,包括低氧反应、免疫防御、DNA损伤修复等<sup>[41]</sup>。符代炎等<sup>[42]</sup>发现,

HPH患者肺小动脉壁中SIAH1水平升高,其可能是通过靶向脯氨酰羟化酶1、脯氨酰羟化酶3及HIF抑制因子,间接抑制HIF- $\alpha$ 的泛素化降解,进而参与PH的发展<sup>[43]</sup>。SIAH2同样在HPH模型大鼠及野百合碱诱导PH模型大鼠肺组织中表达升高,其可能通过降低脯氨酰羟化酶3的稳定性,抑制HIF- $\alpha$ 的羟化,参与HIF通路的调节<sup>[44]</sup>。此外,WANG等<sup>[45]</sup>还发现,SIAH2可通过靶向Hippo信号通路中LATS2,破坏其稳定性,诱导Yes相关蛋白(Yes associated protein, YAP)的生成,而YAP作为Hippo信号通路的关键转录激活因子,可介导多种细胞增殖及抗凋亡相关基因的表达。YAP也可与HIF-1 $\alpha$ 直接形成复合物,增加HIF-1 $\alpha$ 的稳定性,进一步激活HIF通路。SIAH2抑制剂——维生素K<sub>3</sub>可改善野百合碱诱导PH模型大鼠肺血管重塑,延缓PH的进展<sup>[46]</sup>。

**2.7 其他 LI等**<sup>[47]</sup>发现,HECT结构域家族UBR5能靶向ATMIN蛋白,间接调节ATM磷酸化,在PAH患者PAECs中,过氧化物酶体增殖物激活受体 $\gamma$ (peroxisome proliferator activated receptor  $\gamma$ , PPAR  $\gamma$ )与UBR5相互作用减弱,导致ATMIN蛋白表达升高、ATM信号传导受损和持续性DNA损伤。而PPAR  $\gamma$ 激动剂——噻唑烷二酮类药物,如罗格列酮可能通过PPAR  $\gamma$ /ATM信号通路减轻PAECs线粒体损伤,增强细胞的DNA修复功能<sup>[48]</sup>。

$\beta$ -转导重复相容蛋白( $\beta$ -transduction repeat-containing protein,  $\beta$ -TrCP)最重要的作用之一是作为YAP的泛素连接酶E3。研究发现,PASCs中 $\beta$ -TrCP受S1P/STAT3/miR-135b的抑制,导致PASCs中YAP泛素化降解减少,Hippo信号通路激活,增加Notch3表达,最终促进了PASCs的增殖<sup>[49]</sup>。

环指蛋白213(ring finger protein 213, RNF213)属于RING结构域家族,由5207个氨基酸组成,其突变与东亚患者烟雾病密切相关。在其他血管疾病中也能观察到RNA213突变,如主动脉夹层<sup>[50]</sup>、颅内动脉瘤<sup>[51]</sup>、冠状动脉疾病<sup>[52]</sup>等。RNF213 p.Arg4810Lys突变可能引起IPAH,与BMPR2突变的IPAH患者类似,均对目前主流血管扩张剂的治疗反应差,且RNF213突变患者较BMPR2突变患者预后更差<sup>[53]</sup>。因相关病例及研究不足,尚不明确RNF213突变与几种血管疾病之间的关系及相关的分子机制,还需要进一步研究阐明<sup>[54]</sup>。

与肌肉消耗相关的泛素连接酶E3(MuRF1、MuRF2、atrogin-1)在常见慢性心肺疾病的骨骼肌中呈过表达<sup>[55-57]</sup>。敲除MuRF1、MuRF2基因可有效保护野百合碱诱导PH模型小鼠的外周骨骼肌,但存在的问题是MuRF1/MuRF2双敲除小鼠表现出严重的心脏肥大,左心室射血分数明显降低和心力衰竭<sup>[58]</sup>。而OAKLEY等<sup>[59]</sup>研究显示,MuRF1基因敲除小鼠低氧处理3周后,其右心对低氧的耐受性增加,且促进骨骼肌血液灌注。PAFFETT等<sup>[60]</sup>发现,atrogin-1在野百合碱诱导PH模型大鼠心肌、PASCs中表达降低,这降低了肌纤维蛋白的泛素化降解。因此,在对PH模型动物肌原纤维蛋白代谢相关的MuRF1、MuRF2、atrogin-1进行调控时,要进一步把握骨骼肌与心、肺系统中肌纤维蛋白代谢的平衡。

Hsc70相互作用蛋白(carboxyl terminus of Hsc70-interacting protein, CHIP)属于U-box基因家族,通过与伴侣

蛋白Hsp70和Hsp90相互作用及靶向多种伴侣蛋白底物,进而调节细胞生长、分化、凋亡等<sup>[61]</sup>。DONG等<sup>[62]</sup>发现,在HPH模型大鼠PASCs中CHIP表达升高,而使用siRNA敲低CHIP后,通过抑制钙库操纵性钙离子内流及细胞内钙浓度( $[Ca^{2+}]_i$ ),逆转了低氧诱导的PASCs过度增殖。

TRIM32是三结构域蛋白(tripartite motif protein, TRIM)家族成员之一,可通过靶向识别c-Myc<sup>[63]</sup>、Abi2<sup>[64]</sup>和p53<sup>[65]</sup>等蛋白而参与细胞生命活动。近期研究显示,TRIM32在PAH患者血浆及低氧处理的PASCs中表达降低,而TRIM32过表达可能抑制细胞PI3K/Akt信号通路活性及PASCs增殖,进而提高细胞凋亡率<sup>[66]</sup>。但未明确TRIM32在PASCs中的具体作用靶点及确切机制,仍需更多的相关研究解释TRIM32在PAH中的相关调控作用。

Cullin 2属于Cullin家族,近期一项研究通过对GSE113439数据集进行差异基因分析,发现Cullin 2在PAH患者肺组织中表达上调,而抑制其在PAECs中的表达,可有效减轻低氧诱导的细胞增殖、迁移<sup>[67]</sup>。该研究主要集中于对相关差异基因的富集分析,尚不明确Cullin 2在PAECs及PH中的具体作用位点及调控机制。

### 3 DUBs与PH

3.1 家族性圆柱瘤基因(cylindromatosis, CYLD) CYLD最初是在家族性圆柱瘤病中发现的突变基因<sup>[68]</sup>。ZHOU等<sup>[69]</sup>研究显示,先天性心脏病相关性肺动脉高压(congenital heart disease-pulmonary arterial hypertension, CHD-PAH)患者和野百合碱+主动脉腔静脉分流诱导的PH模型大鼠肺动脉中CYLD表达增加,而抑制CYLD表达可以减轻模型大鼠肺动脉压及肺血管重塑。上调CYLD表达可通过调节p38和ERK激活而调控PASCs表型转化,进而导致PASCs过度增殖,肺血管重塑。

3.2 泛素特异性蛋白酶3(ubiquitin-specific protease 3, USP3) USP3是泛素特异性蛋白酶(ubiquitin-specific protease, USP)家族成员之一,含有922个氨基酸,分子量约为59 kDa。与USP3相互作用的蛋白有COL9A3、COL6A5<sup>[70]</sup>、Aurora A<sup>[71]</sup>、KLF5<sup>[72]</sup>等。USP3通过调控这些蛋白的稳定性,延长 $t_{1/2}$ ,从而参与调控多种细胞生物学过程,包括组蛋白修饰、DNA损伤修复及细胞周期调控等。近期研究发现,PAH患者血浆miR-146-5p水平较健康对照人群升高,而USP3 mRNA表达降低,在体外低氧条件下,PAECs过表达miR-146-5p后细胞增殖能力增强,而作为miR-146-5p的靶蛋白,USP3的过表达部分抑制了低氧条件下的PAECs增殖<sup>[73]</sup>。因此,USP3通过介导miR-146-5p对PAECs的增殖促进作用,在维持血管内皮稳态方面发挥着重要作用。

3.3 USP7 USP7最初是从单纯疱疹病毒蛋白ICP0相互作用蛋白中鉴定出的DUB<sup>[74]</sup>,其通过增强细胞内MDM2稳定性,间接调控多种肿瘤细胞的增殖及凋亡,而开发靶向USP7-MDM2-p53网络的小分子物质是一个有前景的抑癌领域<sup>[75]</sup>。ZHU等<sup>[76]</sup>研究发现,在PASCs中,应用siRNA转染抑制USP7表达可逆转血小板衍生生长因子诱导的MDM2上调,进而通过提高p53、FoxO4等下游蛋白表达水平,抑制细胞的过度增殖。

3.4 USP10 USP10属于USP家族,最近的研究显示,USP10

在PAH患者PASCs中表达水平升高,在MST1/2存在的情况下,USP10可稳定BUB3蛋白,进一步激活Akt-mTORC1途径,促进细胞增殖,抑制细胞凋亡<sup>[77]</sup>。岳珍珍等<sup>[78]</sup>研究显示,在HPH模型大鼠中,抑制USP10表达还可能通过调节AMPK信号通路,改善肺血管重塑。

3.5 USP28 USP28同属于USP家族。有研究发现,USP28在低氧PASCs中过表达,使用siRNA敲低USP28基因后可抑制细胞增殖,降低PCNA蛋白表达水平。在PASCs内miR-92b-3p可靶向USP28 mRNA,降低USP28表达水平,抑制低氧诱导的细胞过度增殖<sup>[79]</sup>。

3.6 锌指蛋白A20(zinc finger protein A20) 锌指蛋白A20又称为肿瘤坏死因子 $\alpha$ 诱导蛋白3,其可作用于NF- $\kappa$ B信号通路中I $\kappa$ B激酶(I $\kappa$ B kinase, IKK)复合物上游的关键衔接蛋白,如TRAF2、RIP1等,进而调节NF- $\kappa$ B的活化水平<sup>[80]</sup>。LI等<sup>[81]</sup>研究显示,HPH模型大鼠PAECs在低氧早期锌指蛋白A20表达水平升高,之后其表达水平逐渐下降并低于正常水平,这可能是PAECs早期抵抗损伤的一种自我保护机制。另一项研究显示,过表达锌指蛋白A20可抑制HPH小鼠肺动脉压异常升高、PASCs过度增殖和肺血管重塑<sup>[82]</sup>。

3.7 泛素羧基末端水解酶L1(ubiquitin carboxy terminal hydrolase L1, UCH-L1) UCH-L1是泛素羧基末端水解酶(ubiquitin C-terminal hydrolase, UCH)家族成员之一,目前研究发现,其可通过抑制NF- $\kappa$ B通路,抑制TNF- $\alpha$ 介导的颈动脉血管平滑肌细胞增殖、迁移<sup>[83]</sup>。既往研究发现,野百合碱诱导PH模型大鼠肺组织中UCH-L1表达降低,NF- $\kappa$ B活性增加<sup>[84]</sup>,但尚未明确UCH-L1相关调控在PH中的具体机制。

### 4 其他泛素相关蛋白与PH

泛素-核糖体融合蛋白52(ubiquitin-52 amino acid fusion protein, UBA52)编码一种融合蛋白,该融合蛋白在N端包含泛素,在C端包含核糖体蛋白L40。UBA52缺陷细胞内总泛素水平大致正常,但细胞蛋白质合成大幅下降、细胞周期逐渐停滞<sup>[85]</sup>。最新研究发现,在低氧PASCs中,UBA52表达水平升高,UBA52通过靶向凋亡诱导因子(apoptosis inducing factor, AIF)而加重线粒体功能障碍,增加糖酵解及ROS释放,而抑制UBA52或过表达AIF均可逆转低氧导致的线粒体功能障碍及细胞增殖<sup>[86]</sup>。通过干预UBA52、AIF的表达水平或干预两者相互作用,可能是一种新的PH治疗方式。

### 5 小结与展望

近年来,各种抗肿瘤药物及靶点层出不穷,靶向UPS的小分子物质研究取得了重大进展,除了各种靶向上述对应的泛素连接酶E3或DUBs的小分子物质外,还有多种蛋白酶抑制剂可抑制PAECs、PASCs过度增殖,逆转PH模型动物的肺血管重塑及右心肥厚,如MG-132<sup>[14]</sup>、硼替佐米<sup>[87]</sup>、卡菲佐米<sup>[88]</sup>、Marizomib<sup>[89]</sup>。在临床上,硼替佐米目前主要用于治疗多发骨髓瘤<sup>[90]</sup>,同时,其还可通过影响PPAR $\gamma$ <sup>[91]</sup>、小凹蛋白Caveolin-1<sup>[92]</sup>、Orai-1<sup>[93]</sup>、Mitofusin-2<sup>[89]</sup>等蛋白的表达而纠正PAECs功能紊乱,抑制PASCs增殖,促进细胞凋亡,改善PH模型动物症状。遗憾的是由于硼替佐米心脏毒性等不良反应,不太可能被批准用于PAH的治疗<sup>[94]</sup>。另一种蛋

白酶体抑制剂卡菲佐米具有更小的细胞毒性，可促进血管平滑肌细胞凋亡，与肺血管扩张剂联用可逆转PH动物模型的肺血管重塑<sup>[95]</sup>，是一种潜在的PH治疗药物。

技术逐渐成熟的靶向蛋白降解嵌合体（proteolysis-targeting chimaeras, PROTACs）治疗方式也是通过UPS进行分子治疗，其结构包含结合目标蛋白的配体，可招募泛素连接酶E3的配体及两者之间的连接链，将目标蛋白与泛素连接酶E3拉近，利用细胞内自身蛋白酶体进行靶向降解<sup>[96]</sup>。利用泛素连接酶E3/蛋白酶体的靶向降解功能，不仅具有更高的选择性，还能与许多较难被外源性抑制剂干预的蛋白结合，如STAT3<sup>[97]</sup>、PCAF/GCN5<sup>[98]</sup>等。甚至因其对蛋白抑制机制是利用内源性泛素系统，克服了目前肿瘤细胞的突变耐药问题<sup>[99]</sup>。也许，未来该技术同样可被用于PH的治疗。

近年随着对PH发病机制的研究深入，细胞内各种代谢途径及信号通路的具体机制被逐渐阐明，UPS与PH的关系将会更加清晰，可以预见，将来会有更多的调控UPS的分子靶向药物或PROTACs药物在PH治疗中发挥重要作用。

作者贡献：丁超伟、郭畅、袁雅冬进行文章的构思与设计；丁超伟进行文章可行性分析，撰写论文；丁超伟、郭畅进行文献资料收集和整理；丁超伟、袁雅冬修订论文；袁雅冬负责文章的质量控制及审校，并对文章整体负责、监督管理。

本文无利益冲突。

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