Mini-Review

A Unified Nomenclature for Peroxisome Biogenesis Factors

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For the past 10 years, there has been substantial progress in the field of peroxisome biogenesis. One key to this progress has been the use of genetic approaches in a wide variety of experimental organisms (4, 8, 11, 15, 18, 21, 26, 35, 38, 47, 48). To date, these systems have been used to identify thirteen proteins required for peroxisome biogenesis, three of which have also been shown to be defective in the lethal peroxisome biogenesis disorders. However, the diversity of experimental systems has also led to a profusion of names for peroxisome assembly genes and proteins. These include the acronyms PAS, PAF, PER, PAY, PEB, and PMP and span an even greater array of numbering systems. At the request of the Editors of *The Journal of Cell Biology* and for the benefit of all concerned, we considered several options for gene and protein names, numbering systems, and possible definitions for the types of genes and protein to be included. We propose here a unified protein and gene nomenclature for peroxisome biogenesis factors.

Proteins involved in peroxisome (microbody) biogenesis (inclusive of peroxisomal matrix protein import, membrane biogenesis, peroxisome proliferation, and peroxisome inheritance) will be designated peroxins, with PEX representing the gene acronym. However, even though defects in peroxisomal metabolic enzymes or transcription factors may affect peroxisome proliferation and/or morphology, such proteins shall not be included in this group. The proteins and genes will be numbered by date of published characterization, both for known factors and for those identified in the future. When necessary, species of origin may be specified by one letter abbreviations for genus and species (e.g., *ScPEX1*[1] for the *Saccharomyces cerevisiae PEX1* gene). To minimize ambiguities in naming additional proteins that may be identified in the future, we urge authors before publication to contact an ad hoc nomenclature committee (see below) who will be responsible for numbering new peroxins.

The new nomenclature for peroxisome assembly genes and proteins is outlined in Table I. Questions should be addressed to the first three authors of this letter, who organized the nomenclature revision and who will comprise the nomenclature committee for the next 12 months. We thank *The Journal of Cell Biology* for stimulating the unification of our nomenclature and for providing the opportunity to present our resolution. We hope that these

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1. *Abbreviations used in this paper*: Sc, *Saccharomyces cerevisiae*; Pp, Pichia pastoris; Rn, *Rattus norwegicus*; Hs, *Homo sapiens*; Pa, *Podospora anserina*; Hp, *Hansenula polymorpha*; Yl, *Yarrowia lipolytica*; Cb, *Candida boidinii*; PBD, peroxisome biogenesis disorder.

Table I. Description of Peroxins and PEX Genes

PEX gene	Peroxin characteristics	Former name
PEX 1	117–127 kD AAA ATPase; subcellular distribution is unknown.	*ScPAS1* (12) *PpPAS1* (16)
PEX 2	C_3HC_4 zinc-binding integral peroxisomal membrane protein; 35–52 kD; mutations responsible for complementation group 10 of the PBD.	*RnPAF1* (33) *HsPAF1* (29) *PaCAR1* (2) *PpPER6* (40)
PEX 3	51–52-kD integral peroxisomal membrane protein lacking similarity to other proteins.	*ScPAS3* (17) *HpPER9* (1) *PpPAS2* (43)
PEX 4	21–24-kD peroxisome-associated ubiquitin-conjugating enzyme.	*ScPAS2* (42) *PpPAS4* (3)
PEX 5	PTS1 receptor; 64–69-kD protein containing 8-7 tetratricopeptide repeats; localized to the cytoplasm and peroxisome; mutations responsible for complementation group 2 of the PBD.	*PpPAS8* (24) *ScPAS10* (37) *HsPXR1* (5) *HsPTS1R* (13, 44) *HpPER3* (36) *HpPAH2* (27) *YlPAY32* (31)
PEX 6	Belongs to the AAA family of ATPases; 112–127 kD; localized to cytoplasm and peroxisome; mutations responsible for complementation group 4 of the PBD.	*PpPAS5* (30) *ScPAS8* (39) *YlPAY4* (25) *RnPAF2* (34) *HsPXAAA1* (45)
PEX 7	PTS2 receptor; 42-kD protein containing 6 WD40 repeats localized to the cytoplasm and peroxisome.	*ScPAS7* (23) *ScPEB1* (46)
PEX 8	71–81-kD peroxisome-associated protein containing a PTS1 signal.	*HpPER1* (41) *PpPER3* (20)
PEX 9	42-kD integral peroxisomal membrane protein lacking similarity to other proteins.	*YlPAY2* (6)
PEX 10	C_3HC_4 zinc-binding integral peroxisomal membrane protein; 34–48 kD.	*HpPER8* (32) *PpPAS7* (19)
PEX 11	27–32-kD peroxisome-associated protein involved in peroxisome proliferation.	*ScPMP27* (9, 22) *CbPMP30* (28)
PEX 12	48-kD C_3HC_4 zinc-binding integral peroxisomal membrane protein.	*PpPAS10* (18)
PEX 13	SH3-containing, 40–43-kD integral peroxisomal membrane protein; binds the PTS1 receptor (7, 10, 14).	

changes will make it easier for the general scientific community, as well as ourselves, to follow the interesting and exciting research on peroxisome biogenesis.

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