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| Title: | Glutathione Degradation |
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| Abstract: | Significance: Glutathione degradation has for long been thought to occur only on noncytosolic pools. This is because there has been only one enzyme known to degrade glutathione (γ-glutamyl transpeptidase) and this localizes to either the plasma membrane (mammals, bacteria) or the vacuolar membrane (yeast, plants) and acts on extracellular or vacuolar pools. The last few years have seen the discovery of several new enzymes of glutathione degradation that function in the cytosol, throwing new light on glutathione degradation. Recent Advances: The new enzymes that have been identified in the last few years that can initiate glutathione degradation include the Dug enzyme found in yeast and fungi, the ChaC1 enzyme found among higher eukaryotes, the ChaC2 enzyme found from bacteria to man, and the RipAY enzyme found in some bacteria. These enzymes play roles ranging from housekeeping functions to stress responses and are involved in processes such as embryonic neural development and pathogenesis. Critical issues: In addition to delineating the pathways of glutathione degradation in detail, a critical issue is to find how these new enzymes impact cellular physiology and homeostasis. Future directions: Glutathione degradation plays a far greater role in cellular physiology than previously envisaged. The differential regulation and differential specificities of various enzymes, each acting on distinct pools, can lead to different consequences to the cell. It is likely that the coming years will see these downstream effects being unraveled in greater detail and will lead to a better understanding and appreciation of glutathione degradation. Antioxid. Redox Signal. 27, 1200-1216. |
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