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Conclusion

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According to the endosymbiotic theory at least two organelles of present eukaryotes, namely mitochondria and chloroplasts, originate from the symbiosis of a protoeukaryote with gram-negative prokaryotes. This theory is supported by the presence of a double membrane, DNA, a protein synthesizing machinery and functionally related proteins in the corresponding membranes of mitochondria and chloroplasts as well as in gram-negative prokaryotes. However, since the early days of this symbiosis a lot of time has passed, and many changes must have occurred which confuse today's picture. For instance, many originally mitochondrial genes must have moved to the nucleus, since today more than 90% of all mitochondrial proteins are encoded by nuclear DNA. Similarly, proteins which may have a common origin, like the porins of the outer membrane, might have diverged according to the needs of their host organism. For most bacteria it must have been useful to have small, cation-selective pores with an exclusion limit of 600–800 D, whereas the pores of mitochondria and chloroplasts were selected to be larger (exclusion limit around 6000 D and 7000–13,000 D, respectively [1]) and anion selective. Both kinds of channels are voltage-gated (VDAC) and consist of multiple membrane-spanning β-sheets [2].

Features which clearly distinguish between the mitochondrial and bacterial porins that the present review focusses on are the absence of sequence homology and the differences in their tertiary structure (trimers for bacterial [10] and monomers or dimers for mitochondrial porins [6]). Why the different requirements? Bacterial porins control the passage of various ions and hydrophilic solutes up to the size of ATP. Their expression is dependent on the osmolarity of the surrounding media [1]. In contrast, mitochondria have pores with an exclusion limit ten times as large, and the necessity for this is not fully understood. The absence of porin from yeast mitochondria only causes transient respiratory problems in a few yeast strains, suggesting the presence of alternative pores [5]. Since the alternative pores found in porinless mutants have an exclusion limit of about 600 D, the most important mitochondrial substrates which cross the outer membrane must either be rather small or pass through specialized channels rather than unspecific pores. Since the respiratory problems of porinless yeast mutants seem to be caused by a reduction in the levels of mitochondrial cytochromes, an involvement of porin in the biogenesis of these proteins has to be considered. Thus the rate-limiting step could be the import into mitochondria of either the apocytochromes themselves, or of the precursors of heme which later associates with them inside the mitochondria. In fact, cytochrome *c* binds to mitochondrial porin in vitro [6]. Whether this interaction is also meaningful in vivo and has biological significance like the binding of hexokinase to porin [3] will become clear once the outer membrane receptor(s) for mitochondrial protein import has(have) been identified.

Other differences between bacterial and mitochondrial porins are due to the reverse orientation of the mitochondrial and the bacterial membranes: bacterial porins are

exported into the outer membrane, thereby crossing the inner membrane. This requires a cleaved signal sequence and additional sorting signals in the mature part of the protein [7]. In contrast, mitochondrial porins are directly imported into the outer mitochondrial membrane; their insertion does not require cleavage of the NH_2-terminal signal sequence, but recent experiments suggest the involvement of carboxy-terminal sequences [5]. Interestingly, bacterial porins are thought to reach the outer membrane via periplasmic intermediates [7], whereas mitochondrial proteins destined to cross both membranes have been shown to go through 'contact-sites' of the outer and inner membrane [5,9].

How could one explain all the differences between bacterial and mitochondrial porins on the basis of the endosymbiotic theory? If the theory were right, there should be a common ancestor for eukaryotic and prokaryotic porins. The existence of such an ancestor would become more likely with the finding of a 'missing link', a protein sharing some of the features of both types of porins. The putative new pore discovered in porinless yeast mitochondria could be such a protein; with its cation selectivity and small exclusion limit it resembles bacterial porins, but it is localized in mitochondria [5].

Toxic pore proteins represent a completely different type of channel; both eukaryotic killer-toxin [4] and bacterial colicins [8] are secreted proteins which are made as larger precursors. Their unrelated cleavage and assembly pattern makes a common origin extremely unlikely. It is therefore interesting how both prokaryotes and lower eukaryotes invented the same trick to kill unpleasant neighbors by destroying their membrane potential. Unfortunately our knowledge about the structure and function of the yeast killer toxin is not large enough to allow a mechanistic comparison with bacterial colicins. The beautiful model presented by Pattus et al. [8] for the insertion of colicin A into its target membrane allows for the first time insight into the conformational change involved in channel opening after contact of the protein with the membrane. Similar work is needed also for eukaryotic and prokaryotic porins as well as yeast killer toxin before we will be able to fully understand and compare their mechanism of action.

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Research Articles

A new dopaminergic terminal plexus in the ventral horn of the rat spinal cord. Immunohistochemical studies at the light and electron microscopic levels

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Summary. It has been thought that the ventral motor column in the rat spinal cord is virtually free of dopaminergic fibers. However, a new dopaminergic terminal plexus was visualized at all spinal levels in the ventral horn using electron as well as light microscopic immunohistochemistry.
Key words. Anti-dopamine serum; rat; spinal cord; ventral horn; electron microscopy.

The existence of dopaminergic neurons in the vertebrate spinal cord was suggested first by biochemical studies [1,2]. These neurons had been demonstrated morphologically, using histofluorescence and tyrosine hydroxylase-immunohistochemical techniques. In these studies, DAergic innervation was found in a part of the spinal cord, but it was difficult to distinguish the dopamine from the approximately 10-fold more dense noradrenaline (NA) neu-