Completed genomes give insight in the evolution of short-chain and medium-chain dehydrogenases/reductases

Bengt Persson, Jan-Olov Höög & Hans Jörnvall

Department of Medical Biochemistry and Biophysics
Karolinska Institutet
S-171 77 Stockholm, SWEDEN
E-mail: bpn@mbb.ki.se

The protein families SDR and MDR (short-chain and medium-chain dehydrogenases, respectively) constitute large enzyme families [1,2]. Thanks to the fast progress in sequencing world-wide, the number of members has inreased considerably over the last years. Presently, the MDR family has over 500 members, and the SDR family over 1000 members. The SDR family also contains members with dehydratase, epimerase and isomerase activity. Thus, the SDR family represents three of the six Enzyme Commission main classes.

Database searches have been performed in order to define members of the SDR and MDR families. Multiple sequence alignments have been used to study evolutionary relationships of the SDR and MDR forms. With these methods, patterns are defined and sub-families delineated.

In *E. coli* alone, there are no less than 17 MDR forms, identified as open reading frames, considerably extending previously known MDR relationships in prokaryotes and including ethanol-active alcohol dehydrogenase [3]. Complexity is also large, with several enzyme activity types, subgroups and evolutionary patterns. Repeated duplications can be traced for the alcohol dehydrogenases, with independent enzymogenesis of ethanol activity, showing a general importance of this enzyme activity.

Finally, studies on the complete genome sequences add further insight into the evolution of these super-families.

References:

1. Jörnvall, H., Persson, B., Krook, M., Atrian, S., Gonzàlez-Duarte, R., Jeffery, J. & Ghosh, D. (1995) *Biochemistry 34*, 6003–6013.
2. Persson, B., Zigler, J. S., Jr & Jörnvall, H. (1994) *Eur. J. Biochem. 226*, 15–22.
3. Jörnvall, H., Höög, J.-O. & Persson, B. (1999) *FEBS Lett. 445*, 261–264.