

the duplicated sequence is perhaps non-functional in LADH, it has evolved a regulatory function in GDH and GPDH.

The different register shifts shown in figs. 1 and 2 may be an indication that the observed homologies have arisen by chance or through convergent evolution. On the other hand they may reflect repeated partial gene duplication in the evolution of these proteins. Homologous regions of DNA in the gene, once established, would facilitate the recurrence of such duplications. In this connection it may be noted that:

- i) sequences 111... and 209... are homologous
- ii) each of these sequences is homologous with a sequence nearer the carboxyl end, the register shift being in one case 44, and, in the other, 45, residues.
- iii) homology 2D, which again involves residues 111—124, requires a register shift of 88, exactly twice 44.
- iv) homology 2E, between 2 sequences near the carboxyl terminal, again requires a register shift of 44 residues.

These relationships may reflect random coincidence. Nevertheless it seems clear that the available dehydrogenase sequences should be subjected to a close and systematic scrutiny by the methods developed by Fitch [13]. Such a study should provide good

evidence for or against the hypothesis of repeated duplication and is now in progress.

References

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