

Localization of the human dihydrolipoamide dehydrogenase gene (DLD) to 7q31→q32

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Abstract. The gene for human dihydrolipoamide dehydrogenase (DLD) has been localized to the long arm of chromosome 7, within bands q31→q32, by gel-blot hybridization analysis

with DNA from a panel of somatic cell hybrids containing various portions of human chromosome 7.

Dihydrolipoamide dehydrogenase (commonly known as lipoamide dehydrogenase, or DLD [E.C.1.8.1.4.]) is a 50-kDa subunit protein comprised of at least three distinct mitochondrial multienzyme complexes: the pyruvate dehydrogenase complex, the 2-oxoglutarate dehydrogenase complex, and the branched chain α -keto and dehydrogenase complex (Sakurai et al., 1970). Functionally, this enzyme acts to transfer a pair of electrons from reduced lipoyl groups to NAD within each of these complexes, thus releasing oxidized lipoate to participate in reductive acylation. It may also participate in another multienzyme complex that is responsible for glycine cleavage (Kochi et al., 1986; Carothers et al., 1987). A rare inborn error of metabolism in man characterized by reduced lipoamide dehydrogenase activity and concomitant reduction of all α -keto acid dehydrogenase complex activities has been described in a small number of patients (Robinson, 1989). Isolation and sequencing have been reported for cDNAs encoding the entire protein sequence of human (Otulakowski and Robinson, 1987; Pons et al., 1988) and porcine (Otulakowski and Robinson, 1987) lipoamide dehydrogenase and the human gene assigned to chromosome 7 (Otulakowski et al., 1988; Olson et al., 1990).

Using a panel of rodent \times human somatic cell hybrids containing various portions of chromosome 7, we have refined the chromosome localization of the human DLD gene to 7q31→q32.

The somatic cell hybrids used in the hybridization analysis have been described previously (Zengerling et al., 1987; Rommens et al., 1988). The amount of human chromosome 7 present in each of these hybrids is shown in Fig. 1. High-molecular-weight DNA (5–10 μ g) was isolated from hybrid cell lines, digested with *Eco*RI, separated by electrophoresis on a 0.8% agarose gel, and transferred to nylon membranes (Zeta-probe, Bio-Rad). A 1.1-kb fragment from the cDNA clone LD4a (Otulakowski and Robinson, 1987) labeled with [α -³²P]dCTP by the random priming method (Feinberg and Vogelstein, 1983), was used as the probe in the hybridization analysis. Filters were prehybridized and hybridized in CGH solution (0.5 M sodium phosphate buffer [pH 7.2], 1 mM EDTA, 7% SDS) at 65 °C (Church and Gilbert, 1984). Following hybridization, the blots were washed three times consecutively in 2 \times SSC, 1 \times SSC, and 0.1 \times SSC (all with 0.1% SDS) for 20 min each at 65 °C (SSC = 150 mM NaCl, 15 mM sodium citrate). The filters were exposed to Kodak XAR-5 film with intensifying screens for 1–6 days at –70 °C.

An example of the hybridization results is shown in Fig. 2, and the data are summarized in Fig. 1. As shown in Fig. 2, the DLD cDNA probe detected a single 4.0-kb band in all of the hybrids containing human DNA from the 7q31→q32 region but not in hybrids that did not contain this region. The 4.0-kb human-specific band was easily distinguished from cross-hybridizing sequences (presumably the corresponding genes) of the mouse and hamster DNAs. The regional localization information for DLD was derived mainly from the hybridization result with the human \times mouse hybrid GM1059Rag5, which contained a single human chromosome 7 with an interstitial deletion (7pter→q22::q32→qter), and with 2068Rag22-2, which contained a single translocated chromosome (7qter→q22::) (Rommens et al., 1988). The result clearly showed that the DLD sequence was present in 2068Rag22-2 but absent in GM1059Rag5, indicating that the DLD gene maps within 7q31→q32.

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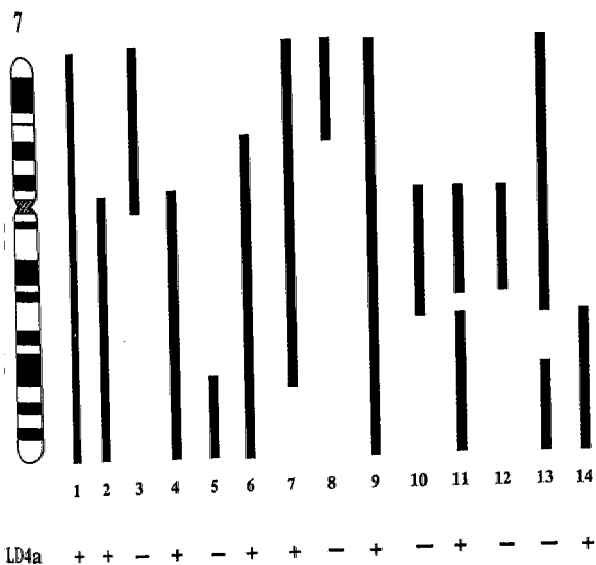


Fig. 1. Somatic cell hybrid lines and summary of hybridization data. The top panel shows the human X rodent somatic cell hybrid panel used in this study and the portion of human chromosome 7 contained in each of them. The presence (+) or absence (-) of the DLD gene in each of these cell lines was determined by gel-blot hybridization analysis with the cDNA probe. Examples of the hybridization results are presented in Fig. 2, but not all the results are shown.

A detailed long-range restriction map has been constructed for a 4.5×10^6 bp region encompassing the gene for cystic fibrosis (CF) (Drumm et al., 1988; Poustka et al., 1988; Rommens et al., 1989). Preliminary data (not shown) suggest that DLD is not in close proximity of the met protooncogene (MET), CF, and D7S8, which, together, span approximately 1.5×10^6 bp. Over 60 unique chromosome 7-specific DNA fragments have been localized to the 7q31 → q32 interval with use of the somatic cell

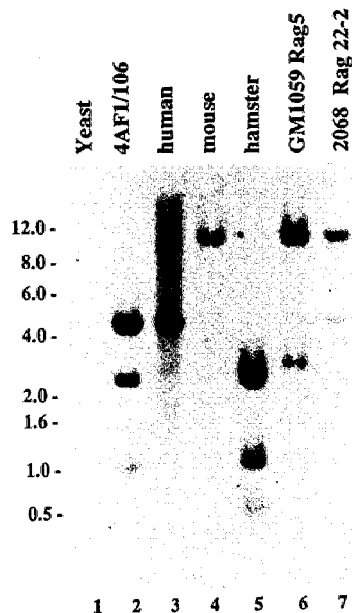


Fig. 2. Examples of gel-blot hybridization. The autoradiograph shows the result of hybridization of the LD4a cDNA to two of the somatic cell hybrids, GM1059Rag5 and 2068Rag22-2. Total human, mouse, and hamster DNAs are included as controls. The arrow indicates the 4.0-kb human-specific sequence present in lanes 2, 3, and 7.

hybrids described here (Rommens et al., 1988). The localization of the DLD gene to this interval, which is estimated to be approximately 30×10^6 bp in size, adds yet another DNA segment for use in the construction of a long-range physical map of 7q31 → q32, now underway.

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