

The Lactase Story: From Physiopathology to Biochemistry, Molecular and Cell Biology—and Back?

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It is unusual that one can recount first-hand the early beginnings and developments of a section of biochemistry, physiology, physiopathology, cell biology, and molecular biology. Although neither of us devoted all his scientific efforts in the last 30 years to intestinal disaccharidases—indeed each of us looked into and solved a number of problems in other areas also—we find it gratifying to think back to the very early 1960s, when our interest in these enzymes was triggered by a patient in Fanconi's Childrens' Hospital at the University of Zürich, who had sucrose-isomaltose malabsorption (1). This condition, which was soon found to be transmitted genetically (2), led to the search by one of us (SA) for *human* normal small intestinal pieces, which were meant to serve as controls, since Arne Dahlqvist has mapped the disaccharidases in the hog (3).

One of us (GS) has recounted elsewhere (4) how serendipity in the course of this search revealed in 1962 the existence of a hitherto unknown condition, adult-type lactose intolerance (adult-type hypolactasia) (5). The report was very soon confirmed (6) and followed by an immense literature (reviewed in refs. 7–12). Adult-type hypolactasia was found to be the most common genetic condition in humans, affecting one third to one half of mankind, mostly those populations without dairy culture. It is discussed in the article by Auricchio and Semenza in this volume (13).

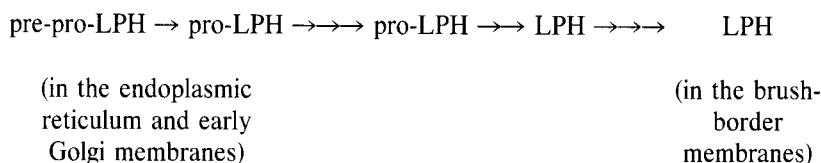
The developments in basic science in this area have been covered throughout the years by a number of reviews (4,12,14–18). Suffice to say that the first, biochemical phase led to the isolation and characterization of intestinal lactase (19–22), which, like the other glycosidases of the brush border, is an intrinsic membrane protein; that is, it can be solubilized only by partial proteolysis (19) or by treatment with detergents (21).

Homogeneous lactase was soon found to be endowed with two catalytic sites, one splitting lactose, cellobiose, and similar β -glycosides (19–21) and the other splitting aryl- and alkyl- β -glycosides, including phlorizin (21,23,24). The natural substrates of the latter site are glycosylceramides (25). In SDS-PAGE, homogeneous lactase-

phlorizin-hydrolase complex (or lactase-glycosylceramidase or β -glycosidase complex) yielded a single, sharp band of approximately 160 kDa. For many years, it was unclear whether the two active sites of this complex are located on a single polypeptide chain, such as in prosucrase-isomaltase (26), or in two different but similar polypeptides, such as in the final sucrase-isomaltase complex (27,28).

At about the same time as the early biochemical phase, the early biological phase was begun. The pioneer work of Kretchmer, Auricchio, and their associates showed that most of the lactase activity develops fairly late in pregnancy, stays at a high plateau from shortly before birth till the time of weaning, and then, within a week or so, declines to the very low levels of adulthood (29–31). The situation in humans is more complex (13). Interestingly, phlorizin-hydrolase, the other activity of the β -glycosidase complex, also declines after birth (24). The two activities, as also other observations showed, must be subject to the same biological control.

When organ cultures of small intestine became possible, the Danish group (32, 33), later confirmed by those in Berne (34) and in Boston (35), demonstrated that the lactase-phlorizin-hydrolase complex (LPH) is synthesized as a single-chain 220 kDa precursor, which is split intracellularly into the final 160 kDa complex at a stage when it is nearly completely insensitive to endo-H. A very much simplified scheme of events is, therefore



A couple of years ago, considering the new possibilities that the unprecedented developments in molecular biology now offered, we decided to reenter the field. Time seemed to be ripe for tackling at least the following problems: (a) Are the two active sites in LPH located in one or two polypeptide chains? (b) How is LPH anchored to the brush-border membrane? (c) What are the amino acid sequences of LPH and of pro-LPH, and what relationships are there between the two? (d) At what level is the decline of LPH at weaning controlled?

Clearly, sequencing a polypeptide chain of some 220 kDa, that is, of around 2,000 amino acids (e.g., pro-LPH), would not be a trivial task, even using modern cDNA technology. We had to secure the collaboration of a first-class molecular biologist, and we were lucky in finding one in Dr. N. Mantei. He, together with some very enthusiastic and capable students and biochemists, could accomplish the heroic feat of sequencing the 1,927 and 1,926 amino acids-long pre-pro-LPH of humans and rabbits (36), respectively. The wealth of biochemical knowledge deduced from this major work was, however, commensurate to it.

First, the N-terminal amino acid of final LPH was identified with pos. 867 (in rabbit) pre-pro-LPH, and all the peptides derived from final LPH as isolated from the brush borders could be unequivocally localized, without exception, in the polypeptide chain of pre-pro-LPH after this position (Fig. 1). Clearly, final LPH derives

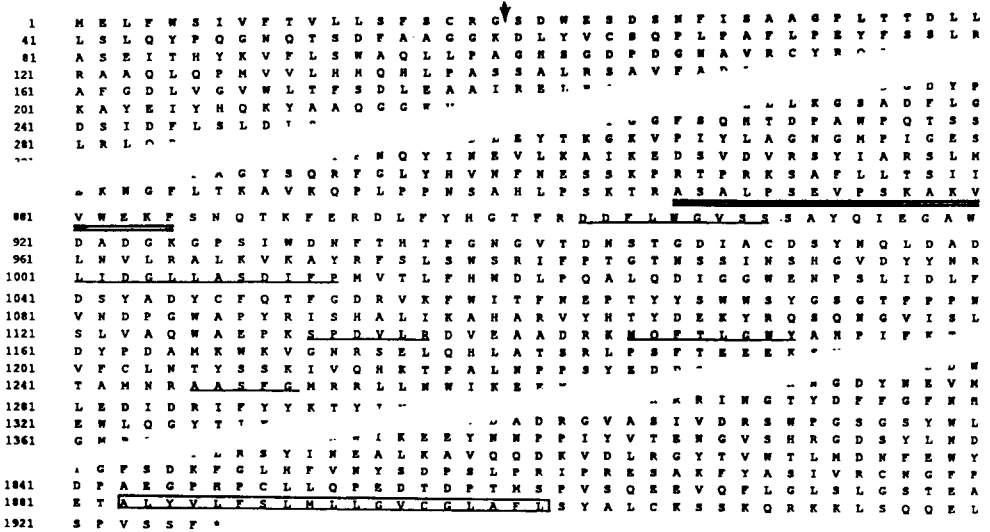


FIG. 1. Parts of the amino acid sequence of rabbit pre-pro-lactase-phlorizin-hydrolase. ↓, putative cleavage site. Doubly underlined sequence, the N-terminal sequence of the final lactase-phlorizin-hydrolase, as isolated from the brush-border membrane. Singly underlined sequences, tryptic peptides obtained from isolated lactase-phlorizin-hydrolase. All peptides from isolated lactase-phlorizin-hydrolase could be localized unambiguously in the cDNA-deduced sequence of pre-pro-lactase-phlorizin-hydrolase from pos. 867 onward. The hydrophobic segment in the C-terminal region is boxed (from res. 1,883 to res. 1,901). Data adapted from Mantei N, *et al.* (36).

solely from the C-terminal portion of pre-pro-LPH after pos. 867. It follows that LPH is composed of a single type of polypeptide, which must, therefore, carry both active sites. This observation by itself answered in a straightforward manner the question of why lactase activity and phlorizin hydrolase activity are subject to the same biological control—because they belong to the same translational unit, and, indeed, they are located in the same polypeptide. The N-terminal portion of pre-pro-LPH prior to pos. 867 does not appear in the brush-border membrane. Its cellular location, its possible enzymatic activity, and its physiological role still are unknown.

Final LPH shows only one hydrophobic sequence of sufficient length, some 20 amino acids, to act as the membrane anchor (Fig. 2). This is clearly the *permanent* anchor and is not exchanged for a phosphatidyl inositol anchor (36), as is the case for several other brush-border proteins. This C-terminal location of the anchor is very uncommon, if not unique, among intrinsic brush-border membrane proteins.

The sequence of pre-pro-LPH begins with a typical signal for which Heijne's algorithm gives a very high splitting score between pos. 19 and 20. Between this position and the beginning of the hydrophobic anchor at the C-terminal (or rather the beginning of the putative stalk), the sequence shows a fourfold inner homology (Fig. 3), which is strongly indicative of two cycles of gene duplication. Of the four homologous regions, only two occur in final LPH. Each of these four encompasses a segment that clearly is a part of a catalytic site.

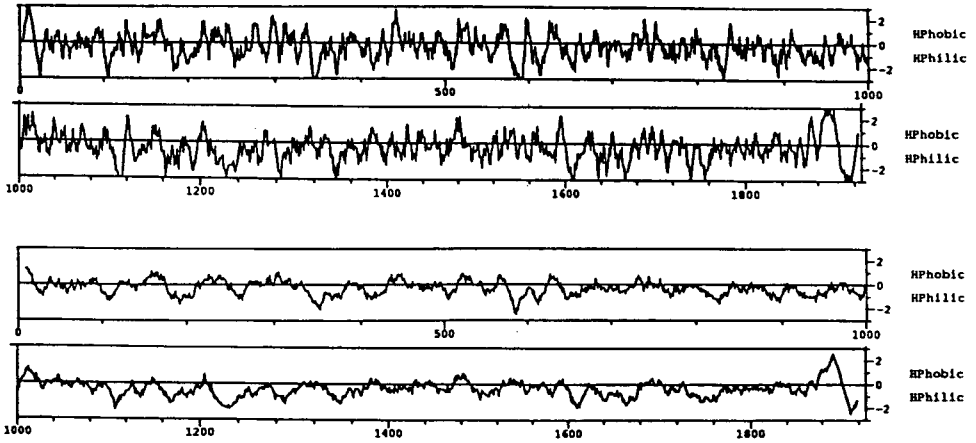


FIG. 2. Kyte-Doolittle plots of human pre-pro-lactase-phlorizin-hydrolase. Windows: 7 residues (top) or 19 (bottom). The top panel clearly shows the hydrophobic sequence within the (cleavable) signal, and the much longer one in the C-terminal region, which serves as anchor. The bottom panel shows clearly the latter only.

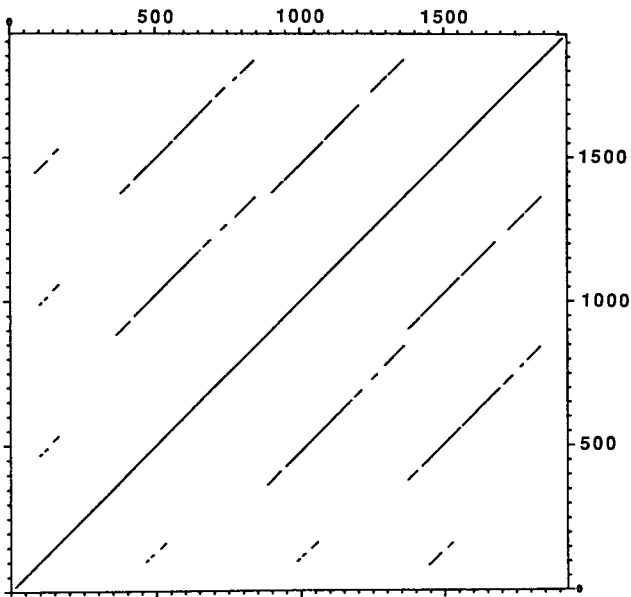


FIG. 3. Dot plot of pre-pro-LPH versus pre-pro-LPH.

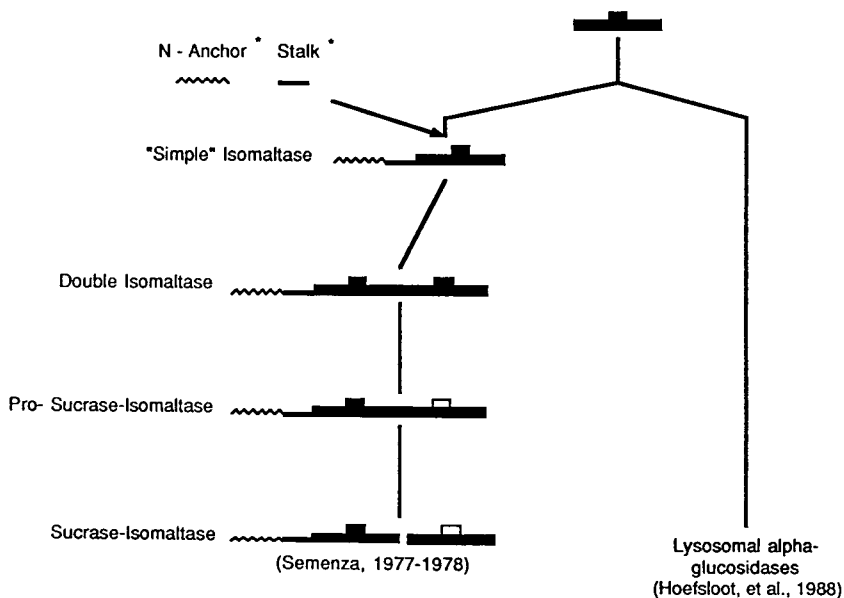


FIG. 4. Phylogenetic pedigree of sucrase-isomaltase as of 1988. The N-anchors and the stalks are homologous to those in maltase-glucoamylase, endopeptidase 24.11 (both brush-border enzymes) and those in the asialoglycoprotein receptors (of the basolateral membrane). From Semenza G (18).

As mentioned previously, little is known about the role of the pro portion (i.e., of homologous regions I and II). However, it is clear that the same translational unit leads to two proteins at different cellular locations, one (LPH) in the brush-border membrane, the other (the pro portion of the precursor) in a cytosolic organelle.

This situation should be compared with the evolutionary pedigree of the sucrase-isomaltase complex and of the related lysosomal α -glucosidase. In this system, an archetypal α -glucosidase gene duplicated into the gene eventually leading to the lysosomal enzyme (37), on the one hand, and to another α -glucosidase (the isomaltase), which, on receiving the exon of the N-terminal anchoring led to an ancient brush border isomaltase. Partial duplication followed by mutation(s) led eventually to prosucrase-isomaltase (Fig. 4) (17,18). In the β -galactosidase system, the exons coding for the brush-border enzyme and those coding for the glycosidase of a different cellular location are still associated in a single translational unit.

Otherwise, brush-border α -glucosidases and brush-border β -glycosidases show very little resemblance in that their mode of anchoring is different, their sequences show no homology, their biological control mechanisms are quite different, and their genes are located in different chromosomes (38,39). The patterns of spontaneous development of lactase and sucrase are quite different. In baby rabbits, lactase appears before birth, reaches a maximum in the early days of life, and declines at the time of weaning (40-46). Sucrase, again in rabbits (but not in humans) appears after birth (at weaning, in fact) and remains high in adulthood (Fig. 5) (31). The events

THE LACTASE STORY

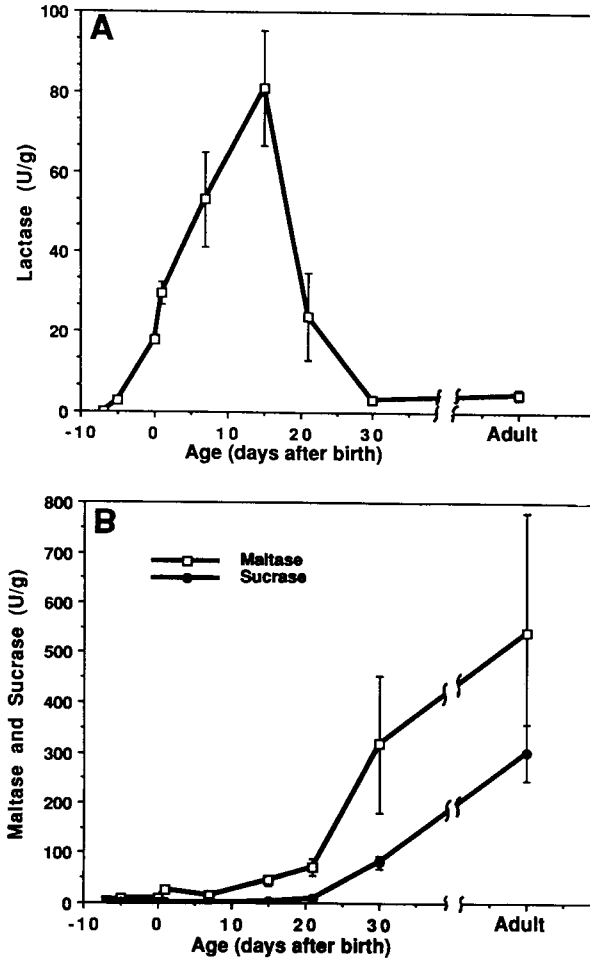


FIG. 5. Jejunal disaccharidase activities (U/g protein) in rabbits at different ages of prenatal and postnatal life. **A.** Lactase activity. **B.** Sucrase and maltase activities. From Sebastio G, *et al.* (31).

involved in the decline of lactase in most mammals at the time of weaning, which are most likely to be similar to or identical with those leading to the adult-type of lactose intolerance in humans, are quite complex and interesting.

It has been suggested that the decline of lactase at the time of weaning takes place by at least two mechanisms acting in sequence (47): first, the accelerated movement of enterocytes along the villous surface makes them shed off before they fully express lactase. Subsequently, lactase synthesis declines, or its processing is disturbed, or its degradation is accelerated.

Our data (31) on the levels of lactase mRNA in rats and rabbits give interesting

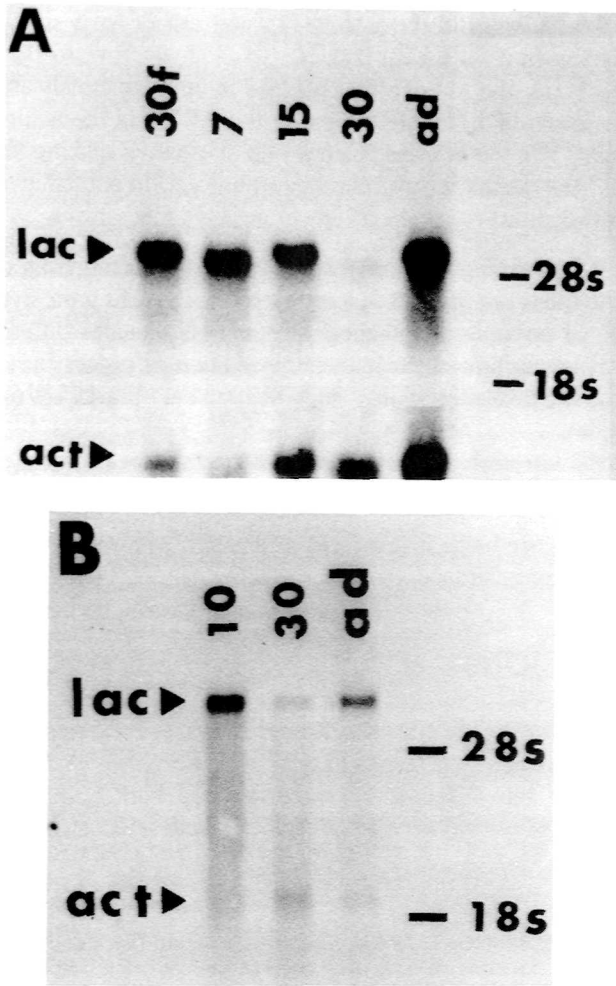


FIG. 6. Northern blot of (A) rabbit and (B) rat intestinal poly(A)⁺ RNAs from animal of various ages. The upper bands correspond to lactase mRNA, with an approximate size of 7 kb. The lower bands correspond to β -actin. The migration of 18S and 28S RNA is indicated. From Sebastio G, *et al.* (31).

clues (Fig. 6). Northern blots clearly show that lactase mRNA is high at birth in rabbits and remains at high levels till the verge of weaning. At the end of weaning, that is, at 30 days of extrauterine life, the lactase mRNA is at low levels. This observation is compatible with a transcriptional control and also with the suggested mechanism of the accelerated cell kinetics (48,49).

However, and perhaps even more interesting, the levels of LPH-mRNA in the

adult animal are high again, although their lactase activity is very low. This we have shown for the rat and the rabbit (47), and others have simultaneously and independently shown it for the rat (50).

Clearly, therefore, the low levels of lactase in adult mammals are *not* due to a decline in the levels of LPH-mRNA, but is the mRNA in the adult identical with that in the baby? Are we perhaps dealing with alternative splicing, frame shifts, or other changes? We cannot answer these questions yet. In particular, we cannot yet distinguish between the two main groups of possible mechanisms.

1. Adult lactase may differ in some subtle but decisive details from the baby counterpart, with the result that it is susceptible to intracellular proteolytic degradation (this group of possible hypothetical mechanisms includes differences in chromosomal genes, differences in either transcription or processing of the mRNA, differences in posttranslational modification of pro-LPH or LPH, e.g., glycosylation).
2. In adult small intestine, there may exist a processing or degrading machinery for lactase that does not exist or operate in the baby small intestine.

These questions are being investigated at present, with respect to adult mammal and human lactose intolerance.

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