

mutation when *in cis*. The proband's sister III-2 has normal red-blood-cell (RBC) GALT activity, but her GALT genome includes three mutations. She is homozygous for N314D, and the paternally derived allele also contains the E203K mutation. Since E203K alone reduces GALT activity by 50% (Elsas et al. 1995) and the N314D homozygote has 50% reduction in activity, our interpretation of her normal RBC GALT activity in the presence of these three mutations is that the oppositely charged amino acid substitutions stabilize the dimeric active enzyme and enable catalysis of uridyl transfer. I-1 and II-1 have "near-normal" activity as well, despite one normal allele and the presence of the E203K-N314D codon changes *in cis* on the other allele, which should produce >50% reduction in GALT activity. We are eager to test these hypotheses in controlled experiments using expression systems as described by Fridovich-Keil et al. (1995). We thank Dr. Reichardt for his continued interest in our work and hope that this answers his questions.

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Reply to Reichardt

To the Editor:

In his letter Dr. Reichardt raises a number of issues concerning two articles recently published in the *Journal* (Elsas et al. 1995; Fridovich-Keil et al. 1995). I have addressed each of the issues relating to Fridovich-Keil et al., below:

1. Dr. Reichardt suggests that we have misattributed to him the "assumption" that nonconserved residues (within the galactose-1-phosphate uridylyl transferase [GALT] sequence) are likely to be "unimportant" for function. In fact, our article described this idea as a "commonly invoked assumption" (Fridovich-Keil et al. 1995, p. 645). With regard to the R148W substitution, the Reichardt et al. article (1992a, p. 599) states that "the mutated arginine is not conserved. . . . However, this mutation results in an unstable polypeptide and, therefore, the mutated arginine 148 is probably not enzymatically important." We certainly apologize for any misunderstandings resulting from our interpretation, or possible misinterpretation of these words.

2. Dr. Reichardt's second point is that Fridovich-Keil et al. (1995) "disregard" his mammalian expression data "when they are at odds with" our yeast system. We have at no point disregarded his data, and in fact went out of our way to cite his work and to offer logical explanations that might account for the differences observed using the two systems. We agree with Dr. Reichardt that the most important comparisons, however, are not between the two model systems (COS cells vs. yeast), but between each of these systems and patient cells. For both of the mutations described in Fridovich-Keil et al. (1995) that have also been modeled in the COS cell system, Q188R and S135L, the activity data derived from the yeast system more closely parallel what is seen in patient cells than do the COS cell data. To summarize, Q188R-GALT expressed in yeast encodes null activity (Fridovich-Keil and Jinks-Robertson 1993), and S135L-GALT encodes ~5% wild-type GALT activity (Fridovich-Keil et al. 1995). According to Dr.

Reichardt's COS cell system, Q188R-GALT retains ~10% residual activity (Reichardt et al. 1991), and S135L-GALT is "a polymorphism because it encodes normal GALT specific activity" (Reichardt et al. 1992*b*, p. 5432). Hemolysates from seven Q188R homozygotes (Elsas et al. 1994) and lymphoblast extracts from three unrelated Q188R homozygotes (Fridovich-Keil and Jinks-Robertson 1993) have all demonstrated a complete absence of GALT activity, and both hemolysates and lymphoblast extracts from patients (or carriers) with the S135L mutation have demonstrated extremely low, if any, GALT activity attributable to the S135L allele (Fridovich-Keil et al. 1995).

With regard to Dr. Reichardt's concern over the current lack of published data illustrating detection of human GALT protein (not just activity) in yeast; these data were alluded to in an abstract published in the *Journal* in 1994 (Fridovich-Keil et al. 1994), and some of these data are also included in a manuscript currently under review (J. L. Fridovich-Keil, B. B. Quimby, L. Wells, L. A. Mazur, and J. P. Elsevier, unpublished data).

3. Dr. Reichardt is correct that "no reports on expression of the common N314D mutation in yeast have been published." These data are, however, included in the manuscript under review. Dr. Elsas referred to these data when he stated that "N314D in yeast encodes near normal activity" (see letter above). Similarly, Reichardt and Woo (1991, p. 2636) have reported from their COS cell work that "the aspartate-314 polymorphism actually increases the specific activity of the GALT enzyme."

I would like to stress, however, that regardless of how many times the yeast system may "give the right answer" in terms of modeling human biochemical phenotypes, it, as with any other model system, including one that uses mammalian cells, is still a model, and must always be interpreted with caution as such.

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Defining "Proband"

To the Editor:

Bennett et al. (1995) presented recommendations of the Pedigree Standardization Task Force of the National Society of Genetic Counselors. As the authors clearly state, the importance of standardized nomenclature is without question for reducing the chances of incorrect interpretation of patient and family information and for facilitating communication between researchers and clinicians involved in genetic family studies.

Most of the recommendations are appropriate and allow recording of the complex situations that can result from today's reproductive and diagnostic technologies. However, there is a problem with the definition presented for "proband" (Bennett et al. 1995, fig. 1, p. 746), i.e., the "first affected family member coming to medical attention".

This definition illustrates the dichotomy that seems to have developed in the use of the term "proband" by clinicians versus researchers. The Bennett et al. (1995) definition is the one that clinicians seem to have evolved