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# Novel insights into mitochondrial phospholipid homeostasis in a disease-relevant yeast model

The proper function of mitochondria critically depends on their membrane lipid composition. To ensure lipid homeostasis, de novo synthesis, intracellular and intraorganellar transport, remodeling, and degradation of lipids must be tightly regulated.

Several studies have emphasised the importance of the mitochondrial signature phospholipid, cardiolipin (CL) for the organelle function. The acquisition of mature CL species is catalyzed by the phospholipid acyltransferase, *Tafazzin*. The importance of CL remodeling is underscored by the fact that mutations in *Tafazzin* lead to a life-threatening genetic disorder, Barth syndrome (BTHS). Currently, the biochemical processes underlying this clinical disorder remain unclear. Deletion of the yeast homologue Taz1 results in similar phenotypes to those observed in patients suffering from BTHS, making this organism an optimal model system to study the pathomechanism of the disease. To shed light on the pathomechanism of BTHS, I searched for yeast multi-copy suppressors of the *taz1Δ* growth defect and identified the branched-chain amino acid transaminases (BCATs) *BAT1* and *BAT2* as such suppressors. Similarly, overexpression of the mitochondrial isoform BCAT2 in mammalian cells lacking *TAZ* improves their growth. Accordingly, supplying both yeast and mammalian cells lacking Tafazzin function with certain amino acids restored their growth behavior. Although elevated levels of Bat1 or Bat2 did not restore all the mitochondrial defects of BTHS, it could correct the higher respiration rate observed in *taz1Δ* cells. These findings outline that the metabolism of amino acids can influence the BTHS phenotype and has an important and disease relevant role in cells lacking *Tafazzin* function.

(For more info: Antunes et. al, doi: 10.1007/s00109-018-1728-4)