A tissue-specific approach to the analysis of metabolic changes in Caenorhabditis elegans

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Author(s) Hench, Jürgen; Brati? Hench, Ivana; Pujol, Claire; Ipsen, Sabine; Brodesser, Susanne; Mourier, Arnaud; Tolnay, Markus; Frank, Stephan; Trifunovi?, Aleksandra
Author(s) at UniBasel Frank, Stephan ; Tolnay, Markus ;
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The majority of metabolic principles are evolutionarily conserved from nematodes to humans. Caenorhabditis elegans has widely accelerated the discovery of new genes important to maintain organismic metabolic homeostasis. Various methods exist to assess the metabolic state in worms, yet they often require large animal numbers and tend to be performed as bulk analyses of whole worm homogenates, thereby largely precluding a detailed studies of metabolic changes in specific worm tissues. Here, we have adapted well-established histochemical methods for the use on C. elegans fresh frozen sections and demonstrate their validity for analyses of morphological and metabolic changes on tissue level in wild type and various mutant strains. We show how the worm presents on hematoxylin and eosin (H&E) stained sections and demonstrate their usefulness in monitoring and the identification of morphological abnormalities. In addition, we demonstrate how Oil-Red-O staining on frozen worm cross-sections permits quantification of lipid storage, avoiding the artifact-prone fixation and permeabilization procedures of traditional whole-mount protocols. We also adjusted standard enzymatic stains for respiratory chain subunits (NADH, SDH, and COX) to monitor metabolic states of various C. elegans tissues. In summary, the protocols presented here provide technical guidance to obtain robust, reproducible and quantifiable tissue-specific data on worm morphology as well as carbohydrate, lipid and mitochondrial energy metabolism that cannot be obtained through traditional biochemical bulk analyses of worm homogenates. Furthermore, analysis of worm cross-sections overcomes the common problem with quantification in three-dimensional whole-mount specimens.
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