Comparison of Fatty Acid Composition of Cell Homogenates and Isolated Chloroplasts in *Acetabularia crenulata* (Lamouroux)

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Algal preparations from *Acetabularia crenulata* were analyzed for their fatty acid composition to establish the suitability of this alga as a model to study fatty acid oxidation and oxylipin biosynthesis. The work was based on two goals. The first goal of this study was to determine the contribution of fatty acids from contaminating bacteria and how this influenced the total fatty acid composition of cell homogenates of *A. crenulata* collected in the wild as compared to specimens cultured in sterile conditions. The major fatty acids detected for both specimens were palmitic (C16:0), palmitoleic (C16:1*n*-7), oleic (C18:1*n*-9), linoleic (C18:2*n*-6), linolenic (C18:3*n*-3), and octadecatetraenoic acid (C18:4*n*-3). Significant amounts of odd-chain fatty acids common to bacteria were not detected in either sample. Furthermore, branched-chain fatty acids, typical bacterial biomarkers, were not detected in either sample. Data suggest that bacteria do not greatly contribute to the total fatty acid pool of *A. crenulata*.

The second goal was to compare the fatty acid composition of cell homogenates with that of isolated chloroplasts. Comparatively speaking palmitoleic and octadecatetraenoic acid were found at significantly lower concentrations in the chloroplast whereas oleic and linolenic acid were found at significantly higher amounts in this organelle. Furthermore, the amount of hexadecatrienoic acid (C16:3), a fatty acid commonly esterified to monogalactosyldiacylglycerol (MGDG; lipid present at high concentrations inside the chloroplasts of algae), was present at very low concentrations in these plastids (0.7%). Typically green algal follow the "prokaryotic pathway" for MGDG biosynthesis where C18:3 is esterified at the s*n*-1 position of the glycerol backbone and C18:3 or C16:3 at the s*n*-2 position, making C16:3 a major fatty acid inside chloroplasts. Interestingly, our results suggest that chloroplasts of *A. crenulata* appear to follow the "eukaryotic pathway" for MGDG biosynthesis where C18:3 is both at the s*n*-1 and s*n*-2 position of MGDG. Taking into account the exceptions noted, the fatty acid composition for *A. crenulata* is similar to that reported for most chlorophytes.

Key words: Acetabularia crenulata, Fatty Acids, MGDG