Differential protein expression during growth on model and commercial mixtures of naphthenic acids in Pseudomonas fluorescens Pf-5

Boyd McKew[1], Richard Johnson[1], Lindsey Clothier[2], Karl Skeels[1], Matthew Ross[3], Metodi Metodiev[1], Max Frenzel[4], Lisa Gieg[5], Jonathan Martin[6], Michael Hough[1], and Corinne Whitby[1]

[1]University of Essex
[2]Nautilus Environmental
[3]MacEwan University
[4]Oil Plus Ltd
[5]University of Calgary
[6]Stockholm University

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Abstract

Naphthenic acids (NAs) are carboxylic acids with the formula (CnH2n+ZO2) and are the toxic, persistent constituents of oil sands process-affected waters (OSPW), produced during oil sands extraction. Currently, the proteins and mechanisms involved in NA biodegradation are unknown. Using LC-MS/MS shotgun proteomics, we identified proteins overexpressed during the growth of Pseudomonas fluorescens Pf5 on a model NA (4-n-butylphenyl)-4-butanoic acid (n-BPBA) and commercial NA mixture (Acros). By day 11, >95% of n-BPBA was degraded. With Acros, a 17% reduction in intensity occurred with 10-18 carbon compounds of the Z family -2 to -14 (major NA species in this mixture). A total of 554 proteins (n-BPBA) and 631 proteins (Acros) were overexpressed during growth on NAs; including several transporters (e.g. ABC transporters), suggesting a cellular protective response from NA toxicity. Several proteins associated with fatty acid, lipid and amino acid metabolism were also overexpressed; including acyl-CoA dehydrogenase and acyl-CoA thioesterase II, which catalyze part of the fatty acid beta-oxidation pathway. Indeed, multiple enzymes involved in the fatty acid oxidation pathway were upregulated. Given the presumed structural similarity between alkyl-carboxylic acid side chains and fatty acids, we postulate that P. fluorescens Pf-5 was using existing fatty acid catabolic pathways (among others) during NA degradation.

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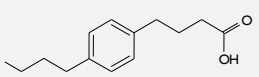
A



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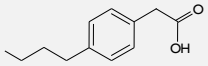
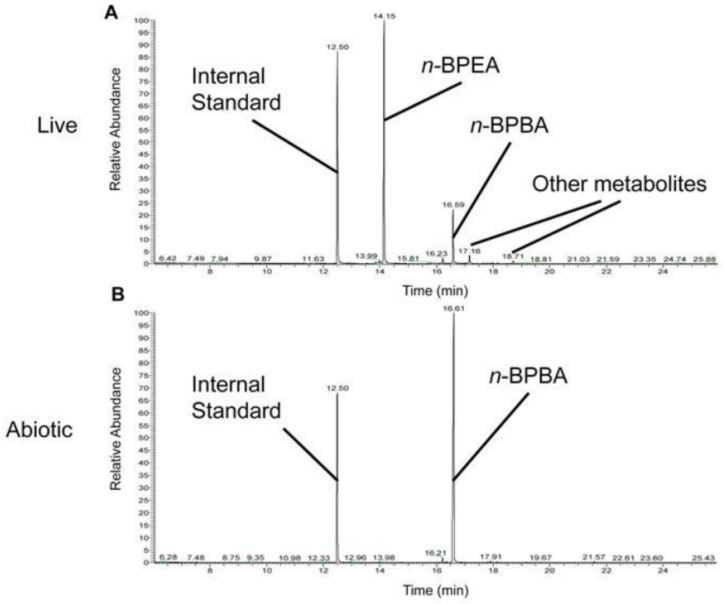


Fig 1



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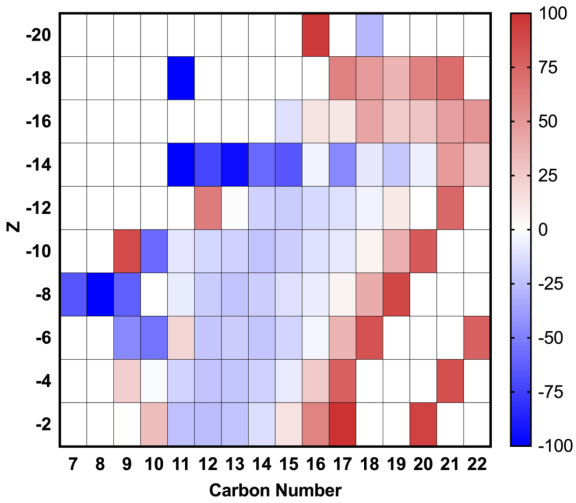

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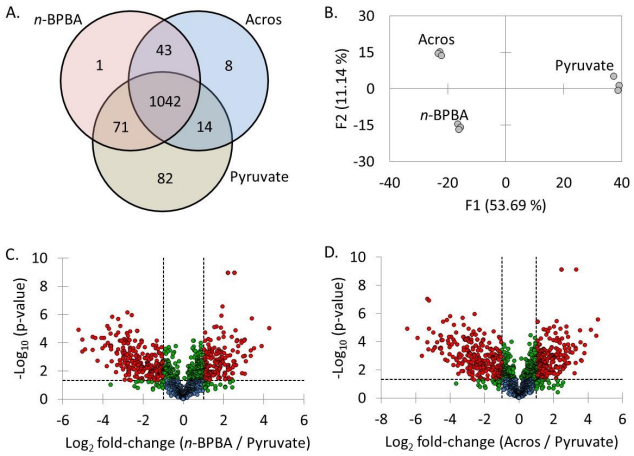

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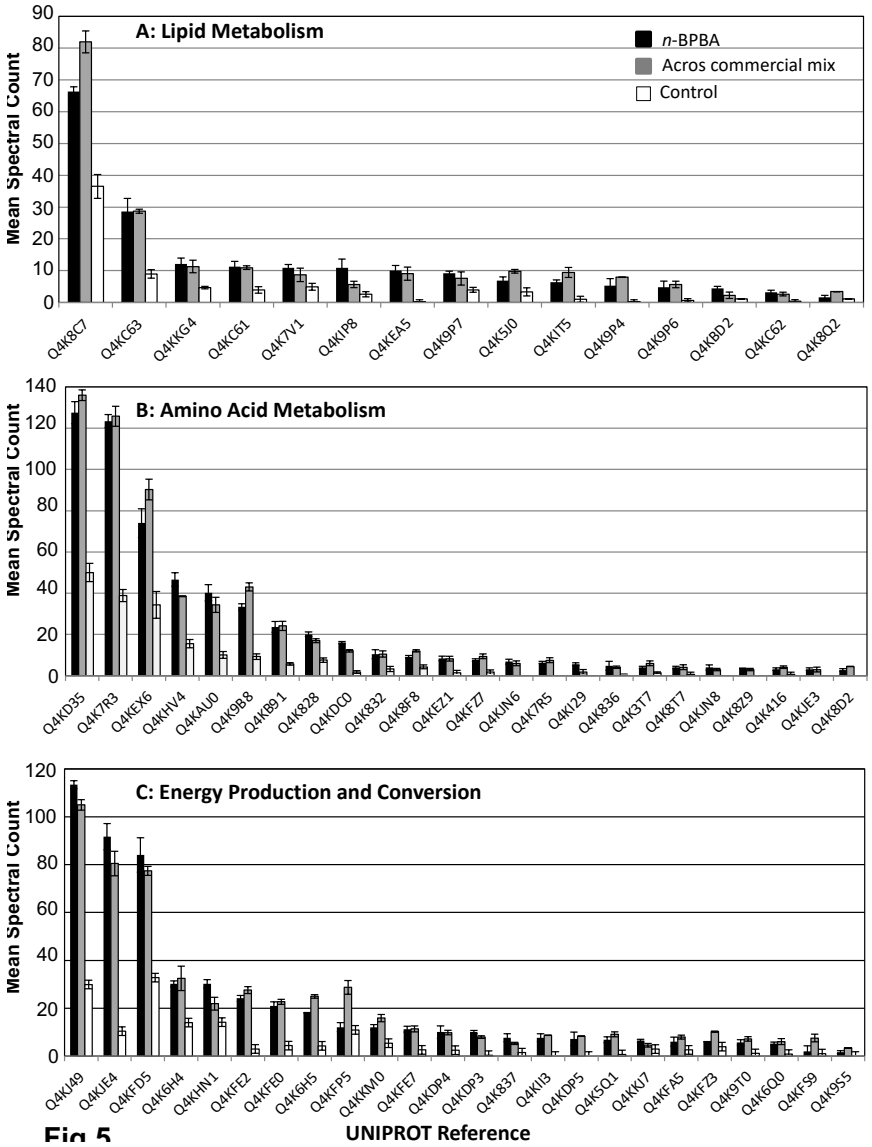

Fig 5

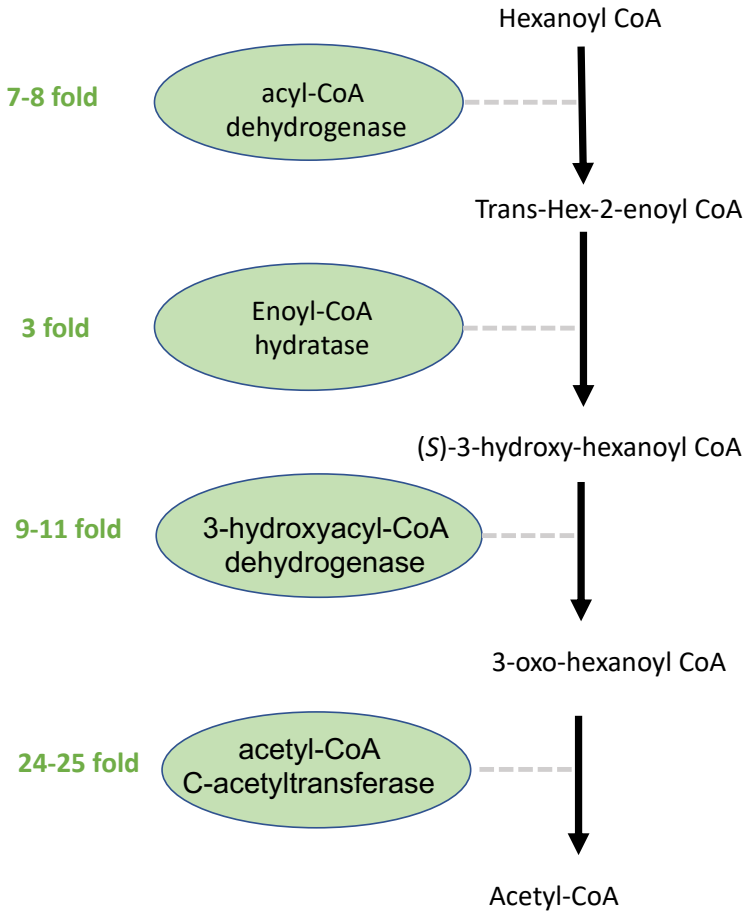

Fig 6