

Targeted UPLC-MS/MS Lipidomics for Biomarker Research of Prostate Cancer (PCa) and Therapy Responses in Human Serum

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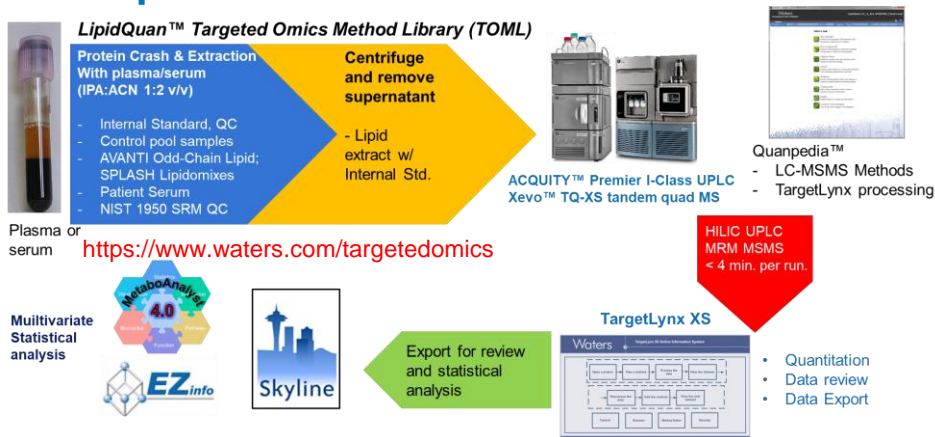
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Introduction

- PCa is 40% of all cancers worldwide,¹ but blood tests for prostate-specific antigens (PSA) are known to be less accurate^{2,3}
- Lipids have been identified as potential PCa biomarkers⁴⁻⁶
- Application of LipidQuan™ targeted lipidomics workflow to detect and quantify key lipids

- Worldwide cancer statistics | <https://www.cancerresearchuk.org>
- Drabovich, A. P., et al. *Mol. Cell. Proteomics* 18, 1807–1823, 2019.
- Lloyd-Price, J., et al. *Nature*, 5697758 569, 655–662, 2019.
- Zhou, X., et al. *PLoS One*, vol. 7, no. 11, 2012.
- Perrotti, F., et al. *Int. J. Mol. Sci.*, vol. 17, no. 12, 2016.
- Isaac, G., et al. Waters Application Note: 720006402EN, 2018.

Experimental Workflow



Results

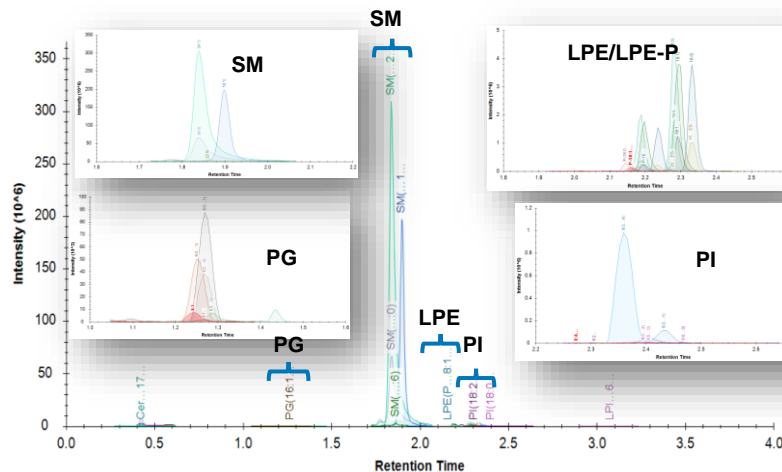


Fig. 2: Example HILIC chromatogram of PCa serum sample (zoomed inserts of key classes)

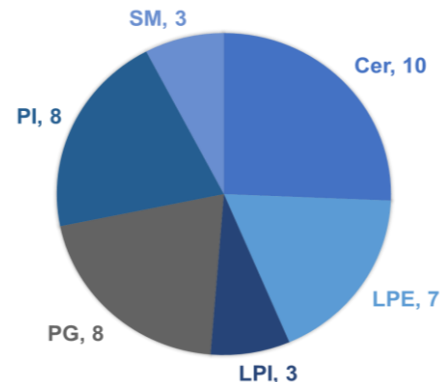


Fig. 1: 39 key lipids monitored using a UPLC MSMS MRM method

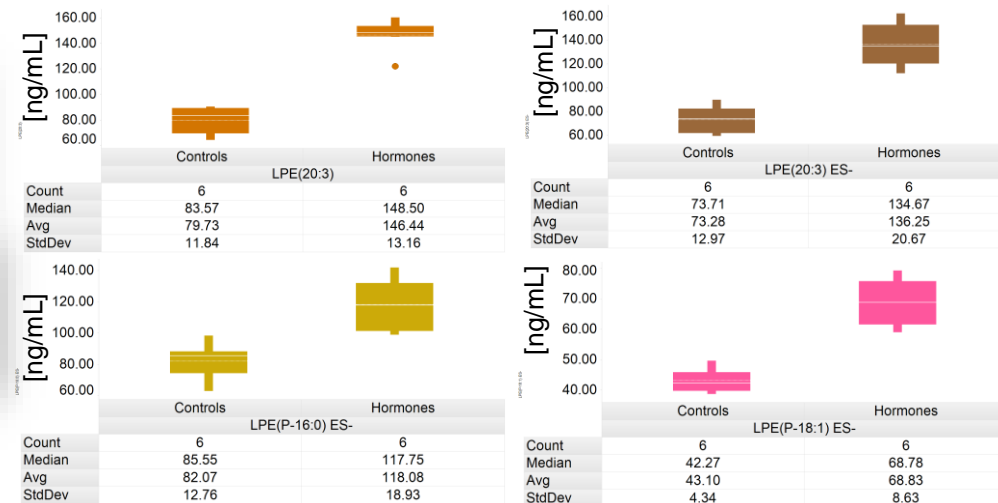


Fig. 3: Quantification of LPE lipids showing upregulation in hormone therapy treated patients (n=6) vs. PCa diagnosed control patients (n=6) in pos. and neg. modes

Conclusions

- A rapid, quantitative lipidomic method (LipidQuan) analyzed serum in a prostate cancer related study.
- The method showed >3-orders of magnitude linearity and sufficient sensitivity to detect lipids at endogenous levels in human serum.
- Lipids eluted according to class via HILIC chromatography, reducing isomeric/isobaric interferences and the number of calibrant and internal standards required for quantification (i.e., cost reductions).
- The methodology quantified key lipid species identified from an integrated lipidomics and proteomics study⁶
- LPEs, Cer, and SM were found to be over expressed in prostate cancer samples compared to control samples