Assessing Multiple Micronutrient Deficiencies In Undernourished Populations Through The Plasma Nutriproteome

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Background

- Micronutrient deficiencies remain a complex and "hidden" aspect of malnutrition worldwide.
- Timely and thorough estimation of the prevalence of multiple micronutrient deficiencies is hampered by dependence on complex, time and resource-intensive laboratory indicators of nutritional status.
- We are seeking to establish the validity of a "plasma nutriproteome" that could be used as a basis for developing tests to assess multiple micronutrient deficiencies in populations on a single methodological platform.

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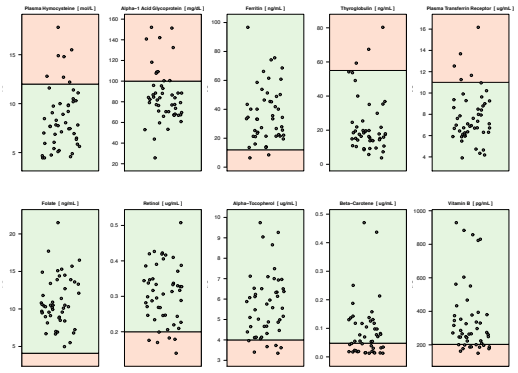
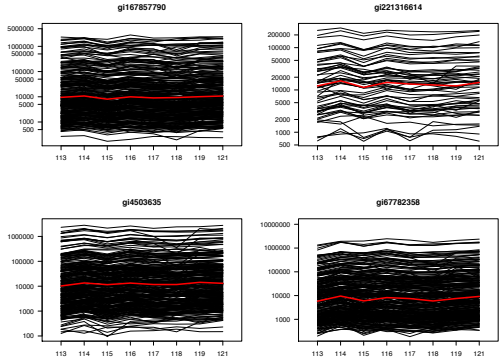
Project overview

- Using 8plex iTRAQ based proteomics, we are identifying plasma proteins that covary with conventional plasma indicators of micronutrient status.
- Plasma samples collected and archived from 1000 Nepalese children, 6-9 years of age, were selected for comprehensive nutritional analyses.
- Pooled plasma proteome analyses have identified 730 unique plasma proteins (FDR of%), 491 of which have been detected to date in individual specimens (n=49 to date, n=500 anticipated by summer 2011).
- Biostatistical methods are developed to quantify the relative protein abundance in the samples, and to detect a protein signature predictive of indicators of micronutrient status.

Micronutrient measurements

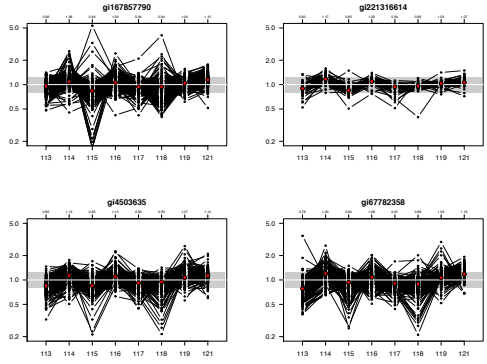


Reporter ion intensities



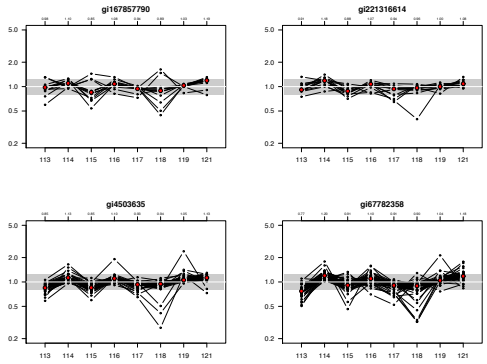
Run with 8 technical replicates of a master pool

Log reporter ion intensities (median polish)



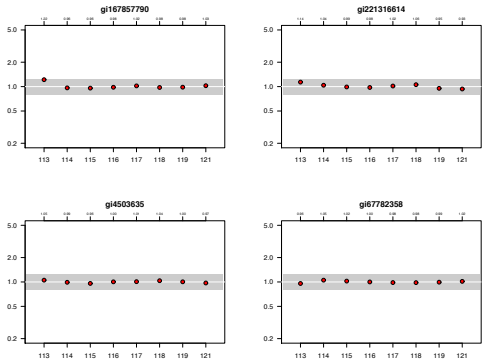
Run with 8 technical replicates of a master pool

Log reporter ion intensities (median polish, by peptide)



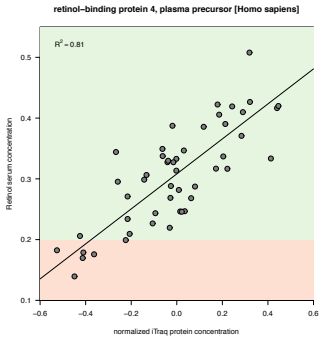
Run with 8 technical replicates of a master pool

Estimated relative protein abundance



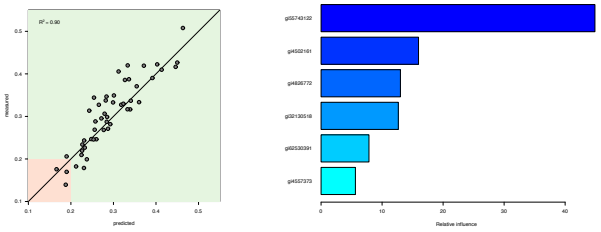
Run with 8 technical replicates of a master pool

Preliminary results



$\longrightarrow$ Some proteins covary with indicators of micronutrient status.

Preliminary results



$\longrightarrow$ Combining measurements from multiple proteins improves the prediction.

Summary

- Based on preliminary analyses with respect to vitamin A (in a small sample), a few plausible proteins explain ∼90% of the variance in plasma retinol, and thus, an interpretable and predictive plasma nutriproteome is likely to exist.
- With assays fully operational, we anticipate a year of discovery, interpretation and reporting as nutritional and proteomics databases continue to grow and are analyzed.
- Analytical tools are developed usind the open source environment R (http://cran.r-project.org/), and will be made publicly available via the Bioconductor respository (http://www.bioconductor.org/).

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