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Non-targeted metabolomics approach for dissecting the alt-phenotype in *Saccharomyces cerevisiae*

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Statement of the Problem: Metabolomics is an important emerging tool for understudying the molecular underpinnings and developing new medicines for complex diseases. For example, most cancers require to avoid the telomere replicative attrition to maintain an unnatural lifespan. Therefore, drugs that target the telomere maintenance mechanism (TMM) are highly attractive as a therapy. The TMM relies either on the telomerase enzyme, or the telomerase-independent alternative lengthening of telomeres (ALT) pathway to maintain the telomere length. Because, in tumors both phenotypes can co-exist, it is necessary to target both TMM mechanisms simultaneously. Unfortunately, the key molecular changes that make ALT phenotype viable are not completely understood.

Methodology & Theoretical Orientation: The model organism *Saccharomyces cerevisiae* has been a model organism for cancer research for many years. Furthermore, the development of the ALT phenotype is one example where yeast can be directly compared to cancer cells. Given the strong connection between the cancer phenotype and metabolism; here, we profiled the metabolome of yeast strains that have lost telomerase expression using mass spectrometry. To dissect unwanted technical variation from biologically relevant variation between ALT and control states, we used a two-step normalization strategy, i.e., first, an empirical Bayesian framework; and next, we corrected for second order technical effects.

Conclusion & Significance: Our results show that ALT-positive yeast strains present two different types of metabolic responses to the genetically-induced telomerase dysfunction: (i) systemic and (ii) specific. The key-difference between these responses are that the systemic response lasts even after the yeast strains have been genetically rescued, while the specific response does not. Interestingly, these metabolic changes can be associated with generic stress responses (e.g., DNA damage) as well as specific responses like accelerated aging of early telomerase-inactivation.

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