

Integrative transcriptome analysis of psoriasis disease and treatment datasets for developing therapeutic intervention strategies

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Psoriasis is a chronic inflammatory skin disease with autoimmune origin and complex pathological features. The goal of our study is to develop strategies for therapeutic intervention by exploring underlying molecular mechanisms of psoriasis, and the subsequent alterations following therapeutic interventions through an integrative transcriptomics analysis. To this effect, we conducted a meta-analysis on ten genome-wide transcriptomics studies consisting of over 700 human skin biopsies from normal and psoriatic skins including non-lesional, lesional, and treated, as well as samples from *in vitro* human epidermal keratinocyte model. We identified a meta-set of 595 genes with high concordance across disease sets and selected an 87-gene disease signature for psoriasis. We present potential therapeutic intervention strategies, based on functional enrichment analysis of disease- and therapeutically intervened data. Additionally, we share our strategies on identifying new drug targets and drug repurposing opportunities for psoriasis. To the best of our knowledge, this is the first comprehensive analysis integrating both disease and treated datasets from psoriasis at such a scale. We anticipate that approaches similar to the one that we outline here, would help elucidate underlying mechanisms and help in developing therapeutic intervention strategies for psoriasis.

Biography

Angela Qu has Master degree in Biomedical Informatics from Columbia University. She has completed her Ph.D. in Bioinformatics/Biomedical Engineering from University of Cincinnati and postdoctoral studies from Columbia Genome Center. She is currently a Senior Scientific Investigator in Quantitative Science Division at GlaxoSmithKline. She has published over 20 papers in peer-reviewed journals and book chapters in areas of systems biology, bioinformatics, and drug discovery and development.

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