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Shrinking the psoriasis assessment gap: Blood derived profiling of proteomic biomarkers predicts clinical outcome to treatment

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Clinical response to a treatment is determined by the bimolecular changes induced soon after treatment-initiation. However, an "assessment gap" exists between the moment the patient's response is biologically determined and when a response can actually be measured clinically. Patients' biochemical profiles are a major determinant of clinical outcome for a given treatment. It is therefore feasible that molecular-level patient information could be used to minimize the assessment gap. Psoriasis is an excellent disease to test the prospect of predicting treatment outcome from molecular data. This is due to clinically accessible biopsy samples and availability of high-quality molecular data for psoriasis patients. In our recently published study we demonstrated that statistical classifiers, built using transcriptomic data derived from baseline-week4 psoriasis patient skin biopsies, were able to accurately predict PASI75 response to a broad range of psoriasis treatments. To build on this research we aim to train similar classifiers using baseline and week-4 inflammatory and cardiovascular-disease biomarker proteomic profiles, derived from the blood of psoriasis patients. PASI75 response predictions were made for patients treated with the JAK inhibitor tofacitinib (Xeljanz) achieving max AUROC ~80%, and the TNF inhibitor etanercept (Enbrel) with max AUROC ~75%. These results support previous findings that pre-and post-treatment high-throughput data can be used to make accurate predictions of treatment response in psoriasis patients, including using blood-derived molecular profiles. This finding could pave the way to a simple blood test for predicting treatment response that would be less invasive than using skin-biopsy data.

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