

Variable gene expression and parasite load predict treatment outcome in cutaneous leishmaniasis

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Sci Transl Med 11, eaax4204.
DOI: 10.1126/scitranslmed.aax4204

Calling healing lesions

Cutaneous leishmaniasis results in skin sores that can be difficult to treat, resulting in further complications. Amorim *et al.* performed dual RNA sequencing of host and parasite gene expression in pretreatment lesional skin biopsies from two cohorts of patients infected with *Leishmania braziliensis*. A prognostic signature comprising expression of three cytolytic genes plus pathogen load predicted treatment response in both cohorts and could potentially be used to triage patients who are unlikely to respond to conventional treatment as candidates for alternate therapies. This study also provides evidence that inflammasome-mediated IL-1 β production influences treatment outcome in patients, strengthening the argument that therapies targeting these components could treat cutaneous leishmaniasis.

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