

SPLICED LEADER PULL OUT FOR TRYPANOSOMATID GENOMICS

The power of whole-genome sequencing for epidemiology remains throttled by parasite sample quality and quantity.

Parasite cells are inherently tethered to vector/host tissue, typically swamped by orders of magnitude in contaminating material that challenges direct extraction and cedes too little sample to sequence. Follow-up cell culture often proves ineffective, many costly *ex vivo* systems raising more bias and frustration than parasite.

To bypass this laboratory bottleneck in the landscape genomics of Chagas disease, we are developing a magnetic-capture-hybridization protocol to recover genome-wide information on *Trypanosoma cruzi* directly from its arthropod vector. We target an idiosyncrasy of trypanosomatid gene expression, the 39-nucleotide “spliced leader” sequence that primes each RNA message for translation, to bait the transcriptome all at once for RNAseq without prior parasite extraction or culture.

Employing a variety of sample types, we examine our method's performance (sensitivity, reproducibility, bias, etc.) and its ultimate reach...

RAD-like reduced representation for landscape genomics – or more?

PROTOCOL DIAGRAM AND RESULTS TO FOLLOW....

(EXPERIMENTS IN PROGRESS)