May 20th, 12:30 PM

Utilization of Molecular Inversion Probes in Malaria Sequencing

Ozkan Aydemir  
*University of Massachusetts Medical School*

Alice Tran  
*University of Massachusetts Medical School*

Yasin Kaymaz  
*University of Massachusetts Medical School*

*See next page for additional authors*

Follow this and additional works at: [https://escholarship.umassmed.edu/cts_retreat](https://escholarship.umassmed.edu/cts_retreat)

Part of the Bioinformatics Commons, Computational Biology Commons, Genetics Commons, Genomics Commons, Molecular Genetics Commons, Parasitic Diseases Commons, and the Translational Medical Research Commons

Aydemir, Ozkan; Tran, Alice; Kaymaz, Yasin; Hathaway, Nicholas J.; and Bailey, Jeffrey A., "Utilization of Molecular Inversion Probes in Malaria Sequencing" (2014). UMass Center for Clinical and Translational Science Research Retreat. 9.  
[https://escholarship.umassmed.edu/cts_retreat/2014/posters/9](https://escholarship.umassmed.edu/cts_retreat/2014/posters/9)
Presenter Information
Ozkan Aydemir, Alice Tran, Yasin Kaymaz, Nicholas J. Hathaway, and Jeffrey A. Bailey

Comments
Abstract of poster presented at the 2014 UMass Center for Clinical and Translational Science Research Retreat, held on May 20, 2014 at the University of Massachusetts Medical School, Worcester, Mass.

Creative Commons License
This work is licensed under a Creative Commons Attribution-Noncommercial-Share Alike 3.0 License.

This is available at eScholarship@UMMS: https://escholarship.umassmed.edu/cts_retreat/2014/posters/9
Utilization of Molecular Inversion Probes in Malaria Sequencing

Özkan Aydemir (1), Alice Tran (1), Yasin Kaymaz (1), Nicholas J. Hathaway (1), Jeffrey A. Bailey (1,2)
University of Massachusetts Medical School, (1) Program in Bioinformatics and Integrative Biology and (2) Division of Transfusion Medicine
Contact: jeffrey.bailey@umassmed.edu

Abstract
While massively parallel sequencing of whole genomes shed light on many previously puzzling genetic questions, the high costs associated with this approach makes its use impractical when large cohorts need to be sequenced at high coverage. Available capture technologies reduces the sequencing costs by enriching template material for the regions of interest. However, these technologies are also prohibitively costly at high sample numbers. Capture methods utilizing molecular inversion probes (MIPs) offer a flexible alternative to enrich template material that multiplex well for thousands of samples and require minimal resources.

Here, for our work in malaria, we extend the utility of MIPs, improving the capture length and efficiency. We have also dramatically decreased the capture time from 24-48 h to 1 h. Combined, these improvements allow the potential for rapid and reliable application of MIP captures in research and, importantly, clinical settings.