BSP2023

Hybridization between human and livestock schistosomes – Ancient or ongoing?

Roy "Neal" Nelson Platt II: Host-Pathogen Interactions Program, Texas Biomedical Research Institute, San Antonio, TX, USA

Abstract: Hybridization between human and animal parasites can transfer biomedically important traits between species and negatively impact human health. The human parasitic blood fluke, *Schistosoma haematobium* can hybridize with the livestock parasite *S. bovis* as evidenced by laboratory crossing experiments in rodent hosts and introgressed mitochondrial and nuclear markers in parasite samples from the field. These results have been widely interpreted to suggest that hybridization between these species occurs frequently. However, work from several, independent groups using exome sequence, single nucleotide polymorphism, or microsatellite markers suggest that hybridization events were ancient, rather than `ongoing, and have led to the adaptive introgression of *S. bovis* alleles into the *S. haematobium* population. Here, we expand on this work by analyzing 34.6 million genome-wide, single nucleotide variants in 167 *S. bovis* and *S. haematobium* samples collected from 18 countries across Africa and aided with a chromosomal-scale genome assembly. We found strong differentiation between *S. haematobium* and *S. bovis* populations and no evidence for recent or ongoing hybridization in these samples. Our results confirm the presence of an ancient introgression event(s) that occurred 421 – 22,108 (median=2,738) generations ago and was restricted to west African populations. Three introgressed *S. bovis* genome regions containing 52 genes on Chr. 4 and 6 are at, or near (>95% allele frequency), fixation in west African *S. haematobium* populations. Further, we identified some regions of the *S. haematobium* genome that are depleted of *S. bovis* alleles indicating selection against introgression. These results demonstrate (i) that strong reproductive barriers maintain species integrity between *S. haematobium* and *S. bovis* in wild populations (ii) that ancient hybridization has led to adaptive introgression between these two species and (iii) suggests caution when interpreting patterns of parasite epidemiology using limited numbers of genetic markers.