using multiple sequencing platforms including Illumina, PacBio and 10X Genomics. These data were assembled to yield genome sizes of ~80Mb in ~1000 to ~5,000 contigs, encoding ~10,000 proteins in each genome. The completeness of these genomes was evaluated using BUSCO, a software that measures the fraction of Single Copy Orthologs expected to be conserved within a taxa. The BUSCO score for both *M. perstans* and *M. ozzardi* is > 85%, similar to the scores of other filaria with complete genome sequences, indicating the high quality of these *Mansonella* genomes. We performed orthology analysis and comparisons to other filarial parasites to identify shared as well as species-specific proteins. The availability of genomes sequences from *M. perstans* and *M. ozzardi* will provide further insight into the evolution and phylogenetic relationships between the *Mansonella* species from different continents. The genomes will also serve as an important resource for further biochemical, molecular and genetic studies, as well facilitate the development of new diagnostic biomarkers and therapeutic tools.

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FILARIAL POPULATION GENOMICS AND ITS ROLE IN ELIMINATION PROGRAMS

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Lymphatic filariasis and onchocerciasis have been targeted for elimination, primarily using mass drug administration at the community level, with global elimination as a public health problem the endpoint for lymphatic filariasis and elimination of transmission in 80% of affected sub-Saharan countries by 2025 as the current onchocerciasis target. Where duration, treatment coverage, and compliance are sufficiently high, it has been demonstrated that elimination is achievable for both parasites within defined geographic areas. However, transmission has re-emerged after apparent elimination in some areas, and in others has continued despite years of drug treatment. a critical question is whether this observed re-emergence and/or persistence of transmission is due to local parasites—i.e., the result of inadequate duration, drug coverage, poor response of the parasite to drugs, or inadequate methods of assessment and/or cutoffs for determining when to stop treatment—or due to parasites introduced to the area via human or vector movement from another endemic area. We review population genomics in *Onchocerca volvulus*, the filarial nematode that causes onchocerciasis, and *Wuchereria bancrofti*, the major pathogen for lymphatic filariasis. We focus in particular on the combination of genetic epidemiology and genome-wide associations to define transmission zones and distinguish between local and introduced parasites as the source of resurgence and to identify genetic markers associated with parasite response to chemotherapy. Our ultimate goal is to assist elimination efforts by developing easy-to-use tools that incorporate genetic information about transmission and drug response for more effective mass drug distribution and surveillance strategies.

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ONCHOCERCA VOLVULUS SECRETOMES: A SOURCE OF POTENTIAL TARGETS FOR DETECTING VIABLE PARASITES

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As efforts shift from control to elimination of *Onchocerca volvulus (Ov)*, additional tools to identify those contributing to ongoing Ov transmission in low transmission settings will be needed to reliably detect viable adult female. Building on our previously identified targets for antigen detection, we did comparative proteomic analyses of the secretomes of adult male (AMES) and adult female (AFES) with previously published somatic proteomes of adult female (OvAF), adult male (OvAM), microfilariae (MF), embryonic stages (EMB), L3 and L4 larval stages. Compared to the AFES (650 proteins), the AMES had 7 times as many proteins (~4600) detected. Principal component analyses indicated a high degree of similarity between the OVAFES with the somatic proteomes of MF and embryonic stages. Multivariate analyses resulted in the identification of clusters of proteins that were commonly detected in the AFES, OvAF, MF and/or EMB. Functional analyses of the proteins suggest that the AMES were enriched for proteins involved in nuclear export, post-translational modifications, and peptidase activity. In contrast AFES was enriched for unspecified secreted class of proteins and those that had endopeptidase inhibitor activity. To evaluate if any of the proteins identified commonly between OvAF-AFES or OvAF-AFES-EMB/MF, could be detected in body fluids of infected individuals, we also performed proteomic profiles of serum, exosomes and urine, and compared these with uninfected control fluids. The intersection of these data show that there only a relatively few proteins commonly found in each of these developmental stages and/or anatomical compartments. Among these, however, are a number of potential targets that can be exploited for biomarker assessment in onchocerciasis.

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THE ANTHELMINTIC PRAZIQUANTEL ACTIVATES A SCHISTOSOME TRANSIENT RECEPTOR POTENTIAL CHANNEL

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Schistosomiasis (Bilharzia) is a parasitic worm infection that infects over 200 million people worldwide. No effective vaccine currently exists and the drug praziquantel (PZQ), discovered around 40 years ago, is the key clinical therapy. The clinical formulation of PZQ is a racemate (±PZQ) composed of the enantiomers (*R*)-PZQ and (*S*)-PZQ. (*R*)-PZQ causes Ca^{2+} influx and spastic paralysis of adult worms, with (*S*)-PZQ acting as a less active distomer. From a treatment perspective, it is problematic that despite decades of clinical use, as well as demonstration of PZQ resistance in both lab and field, the target of PZQ remains unknown. This lack of knowledge has proved a longstanding roadblock in schistosomiasis chemotherapy. Resolution of the target of PZQ action in schistosomes would facilitate discovery of new anthelmintics and novel vulnerabilities of parasitic flatworms to chemotherapy. Here, we demonstrate (*R*)-PZQ activates a Ca^{2+}-permeable schistosome transient receptor potential (TRP) channel in *Schistosoma mansoni*, christened *Sm*.$TRPM_{PZQ}$. *Sm*.$TRPM_{PZQ}$ was activated by ±PZQ with an EC_{50} of 1.08±0.14μM in a Ca^{2+} imaging assay and this activation was stereoselective, with the (*R*)-PZQ evoking Ca^{2+} signals over a considerably lower concentration range (EC_{50} of 597±10nM) than (*S*)-PZQ (EC_{50} of 27.9±3.1μM). At 37°C, (*R*)-PZQ activated *Sm*.$TRPM_{PZQ}$ over an even lower concentration range (EC_{50}=154±33nM, Figure 2E), corresponding to the concentration-dependency of (*R*)-PZQ evoked contractions of schistosome worms *in vitro*. Analysis of *Sm*.$TRPM_{PZQ}$ in transcriptomic datasets evidences expression across various schistosome life cycle stages, and analysis of flatworm genomes revealed expression of $TRPM_{PZQ}$ in both free-living and parasitic flatworms that exhibit sensitivity to PZQ. These data provide the first report of a schistosome target activated by PZQ, are consistent with *Sm*.$TRPM_{PZQ}$ being a target of this clinically important therapeutic

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EVALUATION OF A PROTOTYPE DUAL ANTIGEN RAPID TEST TO DETECT EXPOSURE TO *ONCHOCERCA VOLVULUS*

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Serological tools for onchocerciasis are currently limited to the OV-16 ELISa and rapid diagnostic test, with reported high specificity (>98%) but

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