How much variation in drug response is found in schistosome populations?

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Schistosmes are outbred, sexually reproducing parasites and extensive genomic and phenotypic variation is found within natural and laboratory populations.

We have previously demonstrated that there is standing variation for oxamniquine resistance in *S. mansoni* populations that resulted in treatment failure in Brazil and East Africa. As new anti-schistosomal drugs are developed, it is important to determine levels of pre-existing phenotypic variation in response to these compounds.

We hypothesize that there will be extensive phenotypic and genetic variation for drug response within schistosome populations. Using a combination of high throughput phenotyping assays, based either on single worm metabolism (Lactate assay) or a newly developed movement assay (SWAMP - Single Worm Analysis Movement Pipeline), we are quantifying phenotypic variation in drug response to nine drugs in our genetically diverse laboratory schistosome populations. The presence of natural genetic variation in drug response within schistosome populations allows use of whole genome association methods to determine the genomic region(s) involved, and ultimately to decipher the mechanism(s) of action of these drugs.