Genomic impact of mass dru administration on human infective *Schistosoma mansoni*

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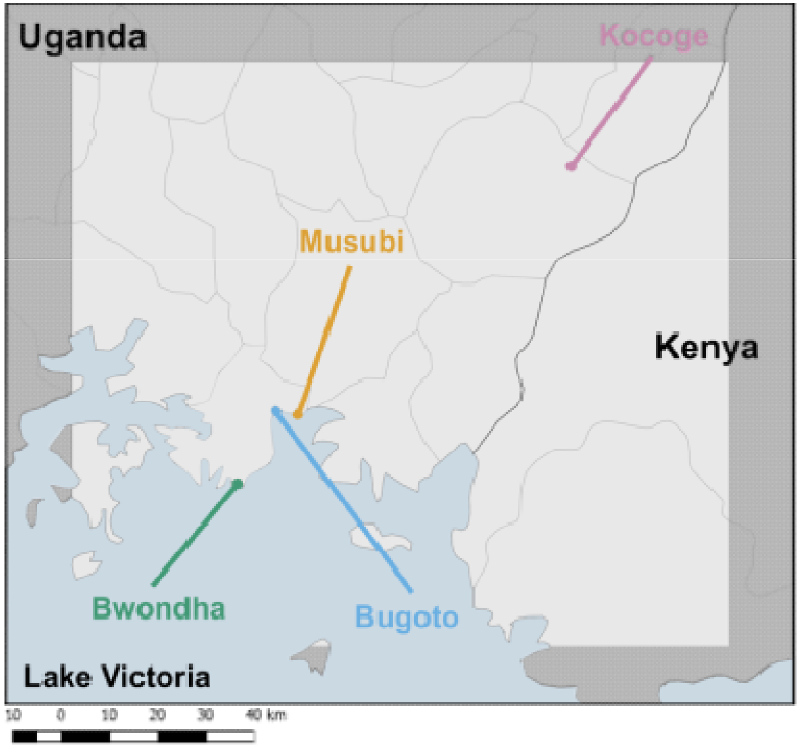
LCNTDR anniversary event - Beyond 2020: Resea
innovations for a new agenda

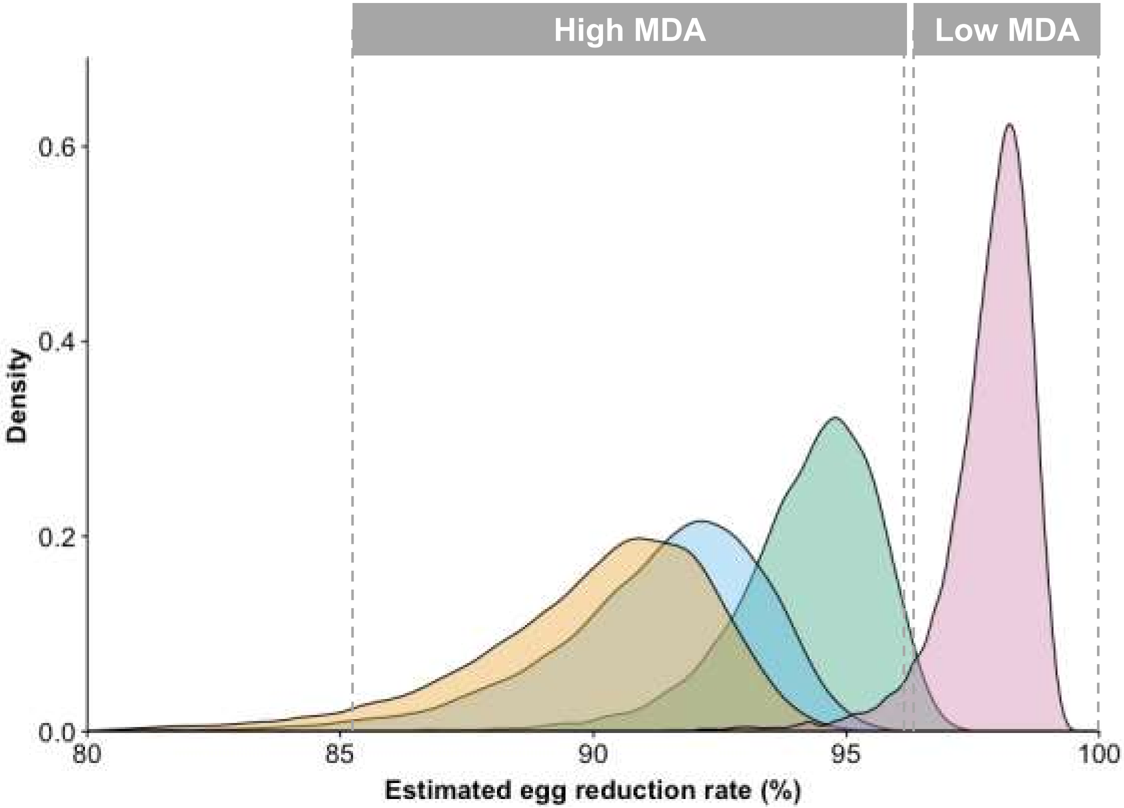
RVC Royal Veterinary College University of London

LONDON CENTRE FOR NEGLECTED TROPICAL DISEASE RESEARCH

wellcome sang institute

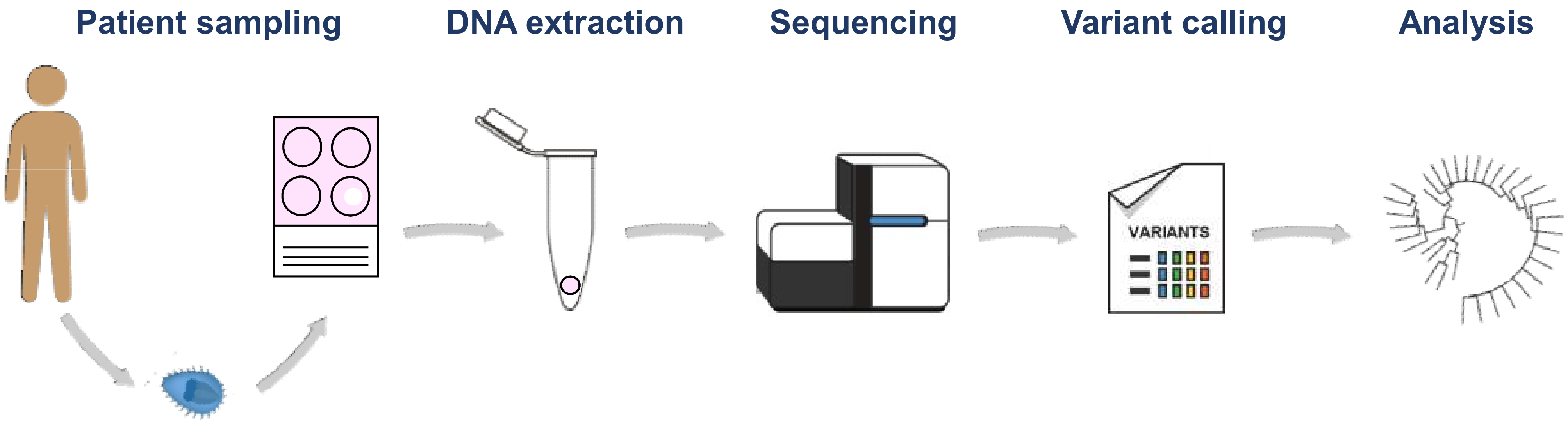
Reduced praziquantel efficacy is associated with multiple rounds of mass-drug administration





, 2016. *Clinical infectious diseases*, 63(9), pp.1151–1159.

Can whole-genome sequencing provide insights?



Patient sampling

DNA extraction

Sequencing

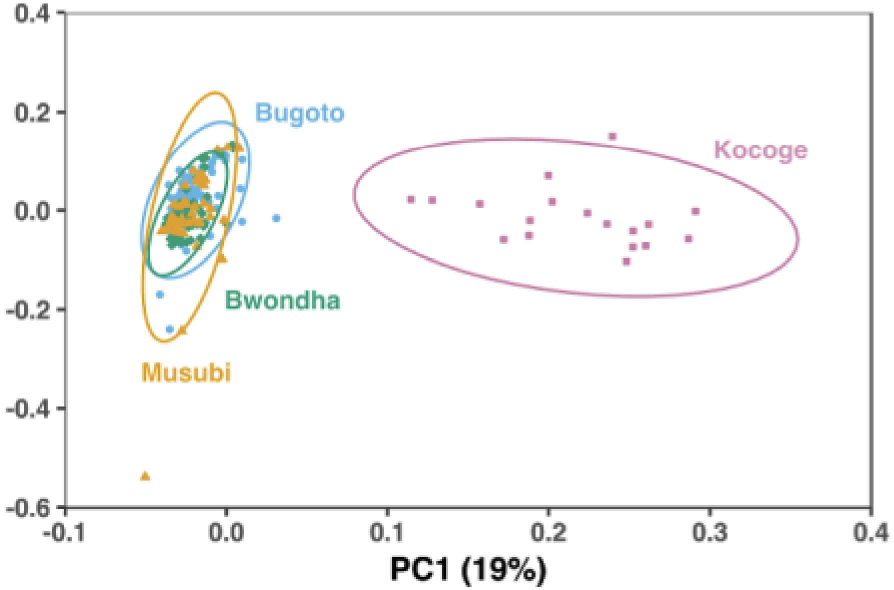
Variant calling

Analysis

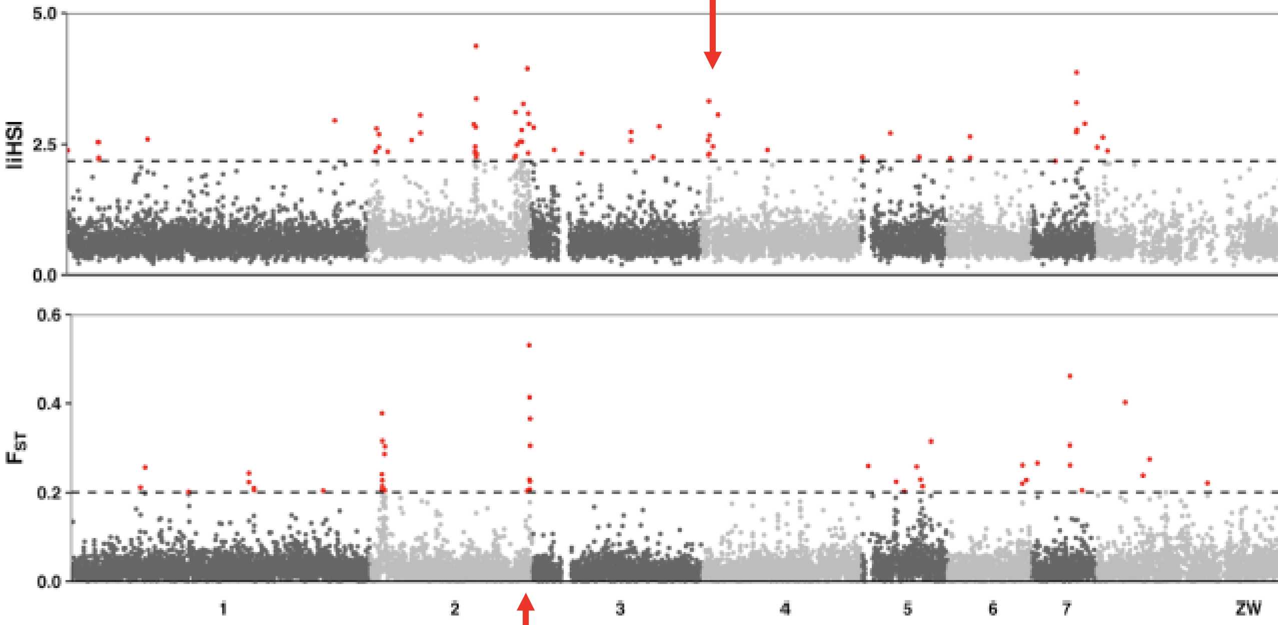
n: Genome Research Limited, 2019
Broad Institute, 2019

Population structure and signatures of selection

Population structure



Selection



smdr1 **(Smp_063000)**

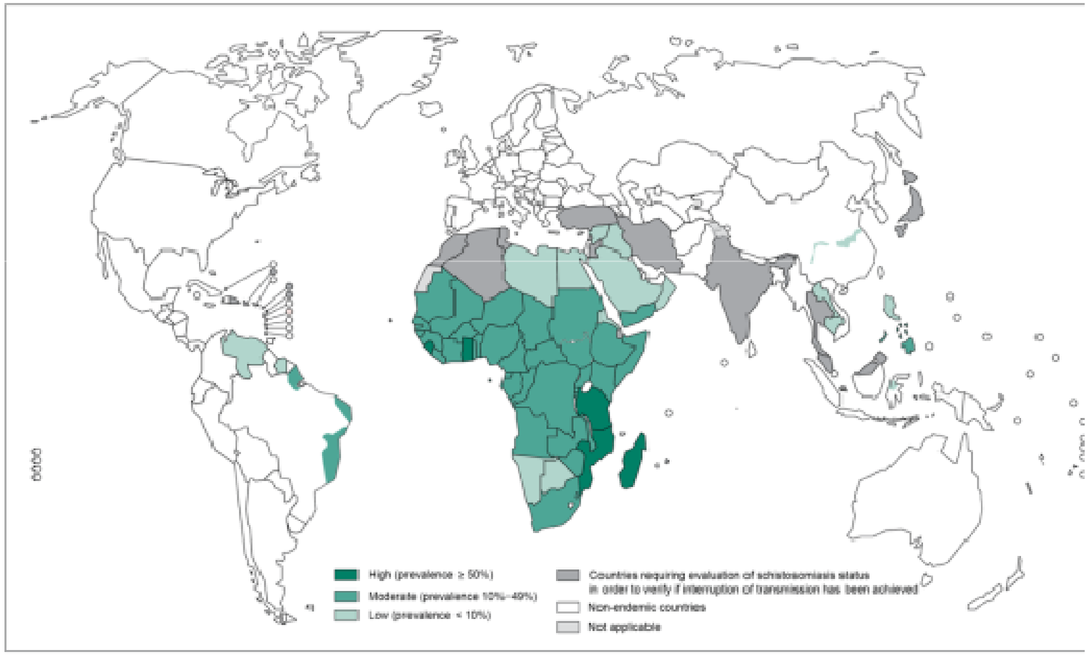
Smp_170450, Smp_336070,
Smp_328710, Smp_094390

Beyond 2020: How can genomics help us understand schistosomiasis?

- **Genomic surveillance**
  - Treatment efficacy and praziquantel resistance
  - Hybridization (Kincaid-Smith et al., 2018; Oey et al., 2019)
  - Diversity of host infrapopulations
  - Global diversity

- **Comparative genomics**
  - Evolution of parasitism (IHGC, 2019)
  - Novel drug and vaccine targets (IHGC, 2019)

Distribution of schistosomiasis, worldwide, 2012



h, et al., 2018. *bioRxiv*.
019. *PLoS Pathogens,* 15 (1): e1007513.
Helminth Genomes Consortium. 2019. *Nature Genetics* 51 (1): 163–74.
Schistosomiasis. World Health Organization, https://www.who.int/schistosomiasis/en/.

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