Progress in the control NTDs (human helminth infections) – moving from morbidity control to transmission elimination

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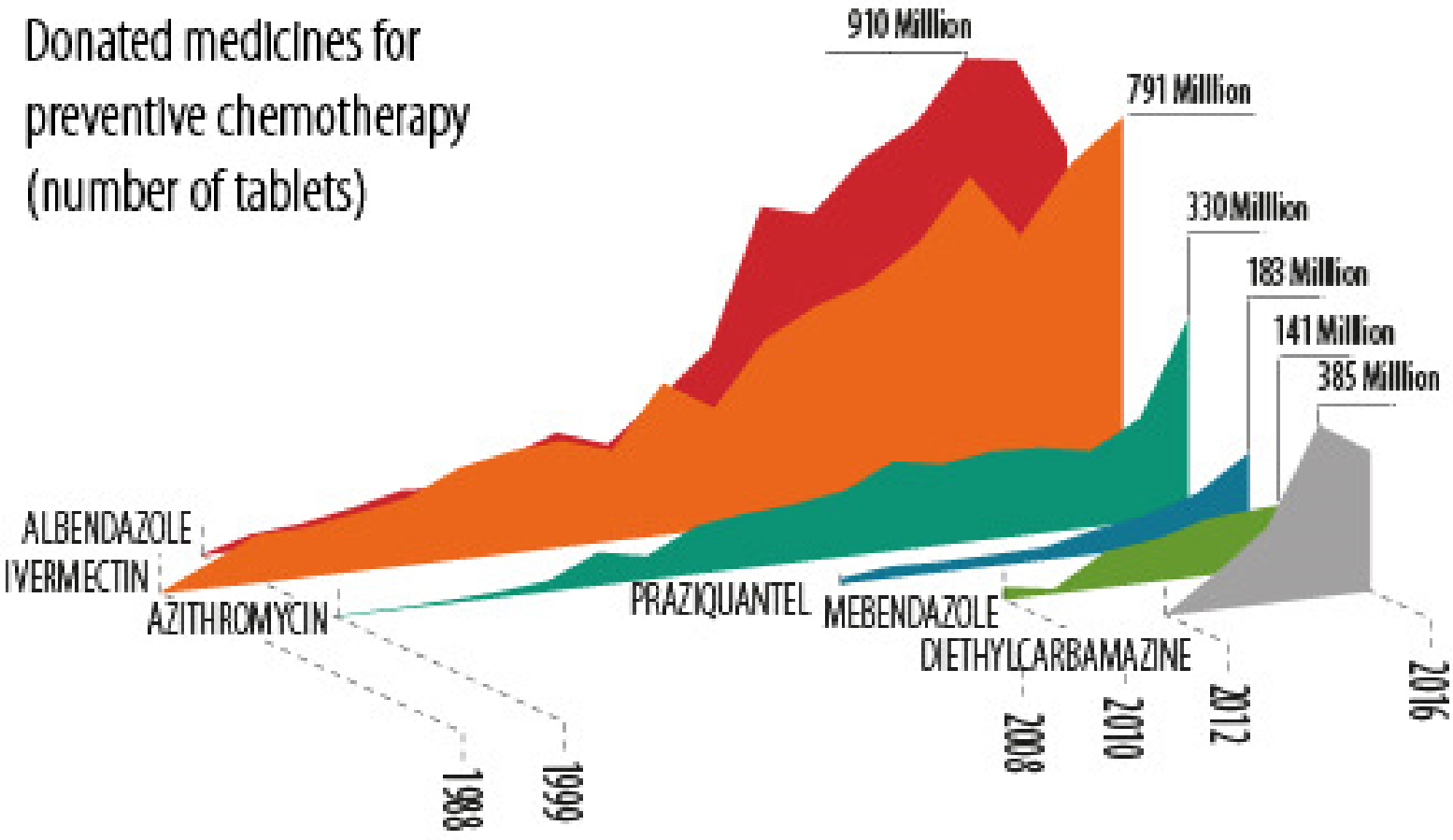
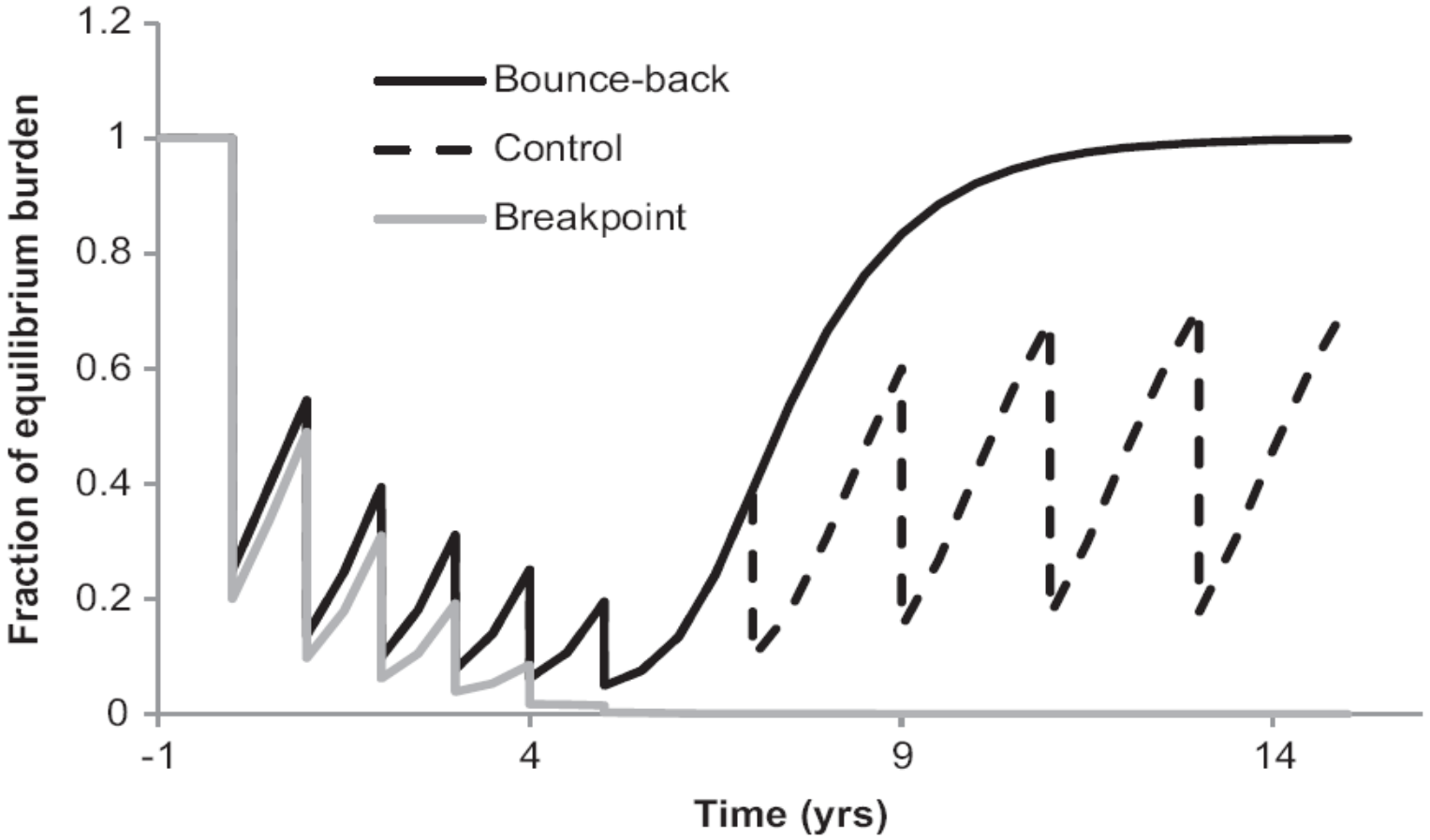
Drug donations - WHO (2017)

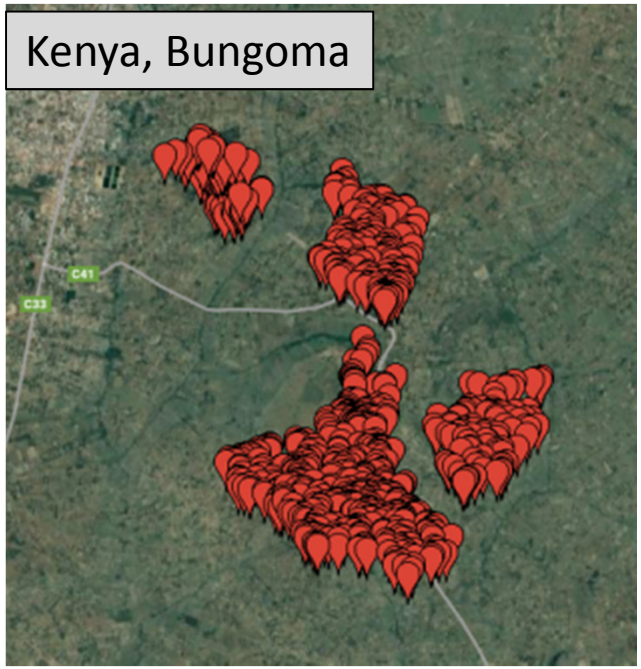


1.288 billion treatments were delivered to 998 million people in 2015

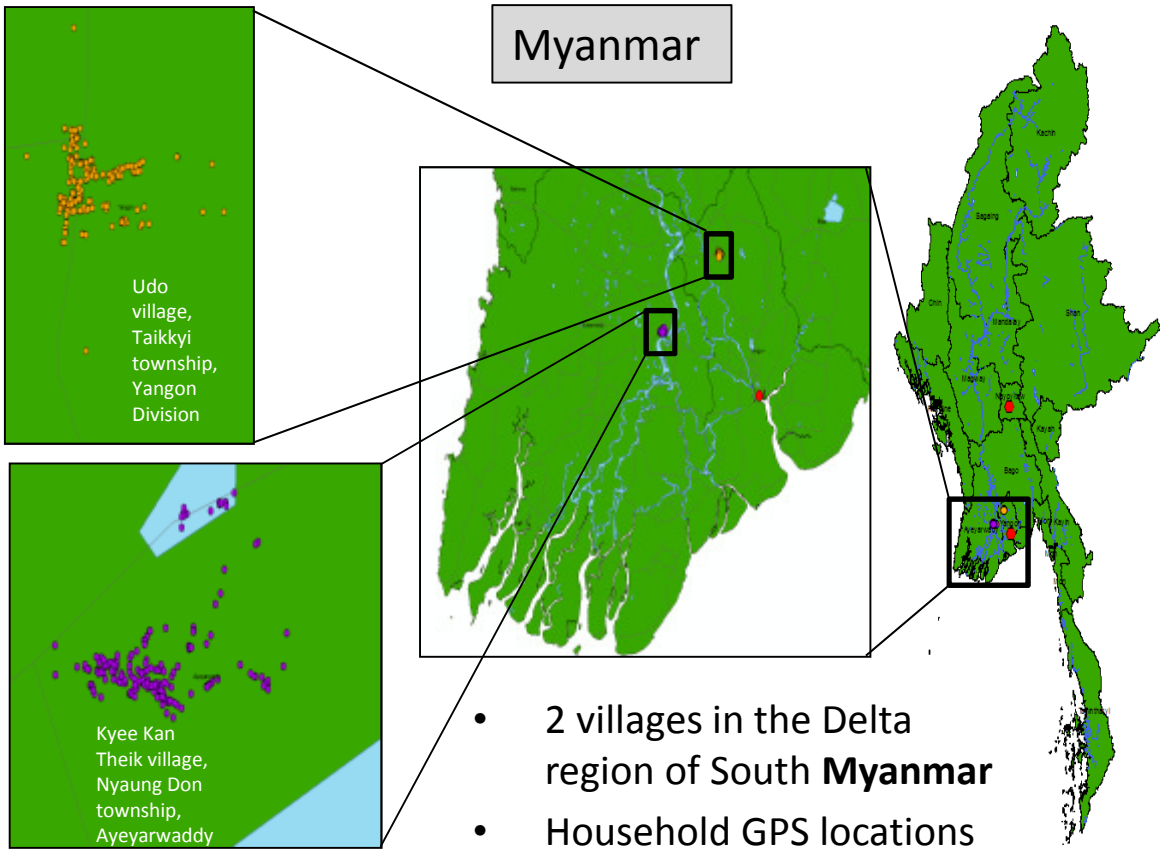
The effect of mass drug treatment on the intensity of infection – bounce back if breakpoint is not crossed – no acquired immunity



Study sites 1 & 2 in Kenya, Bungoma [who infects whom], and South Myanmar (transmission in heavily treated communities)



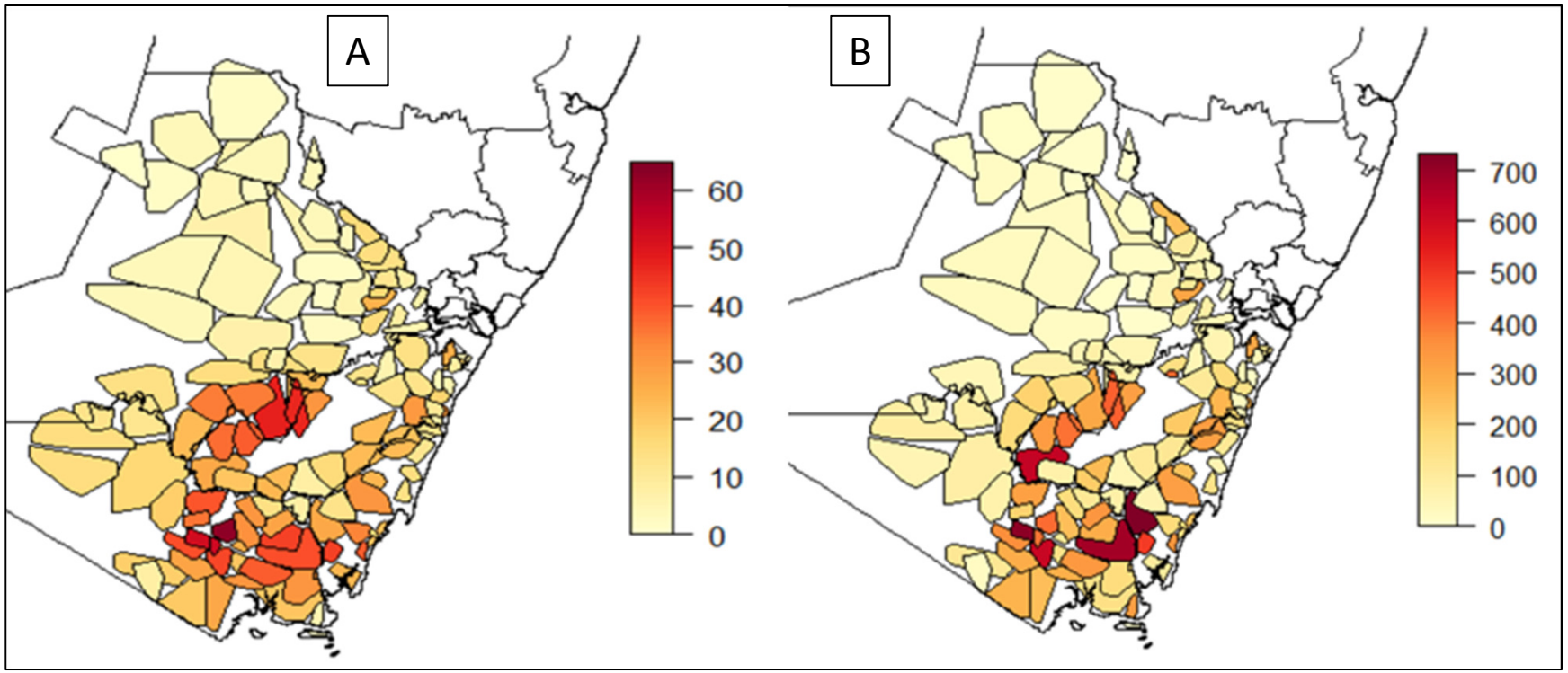
- 5 villages in rural Western **Kenya**
- Household GPS locations mapped



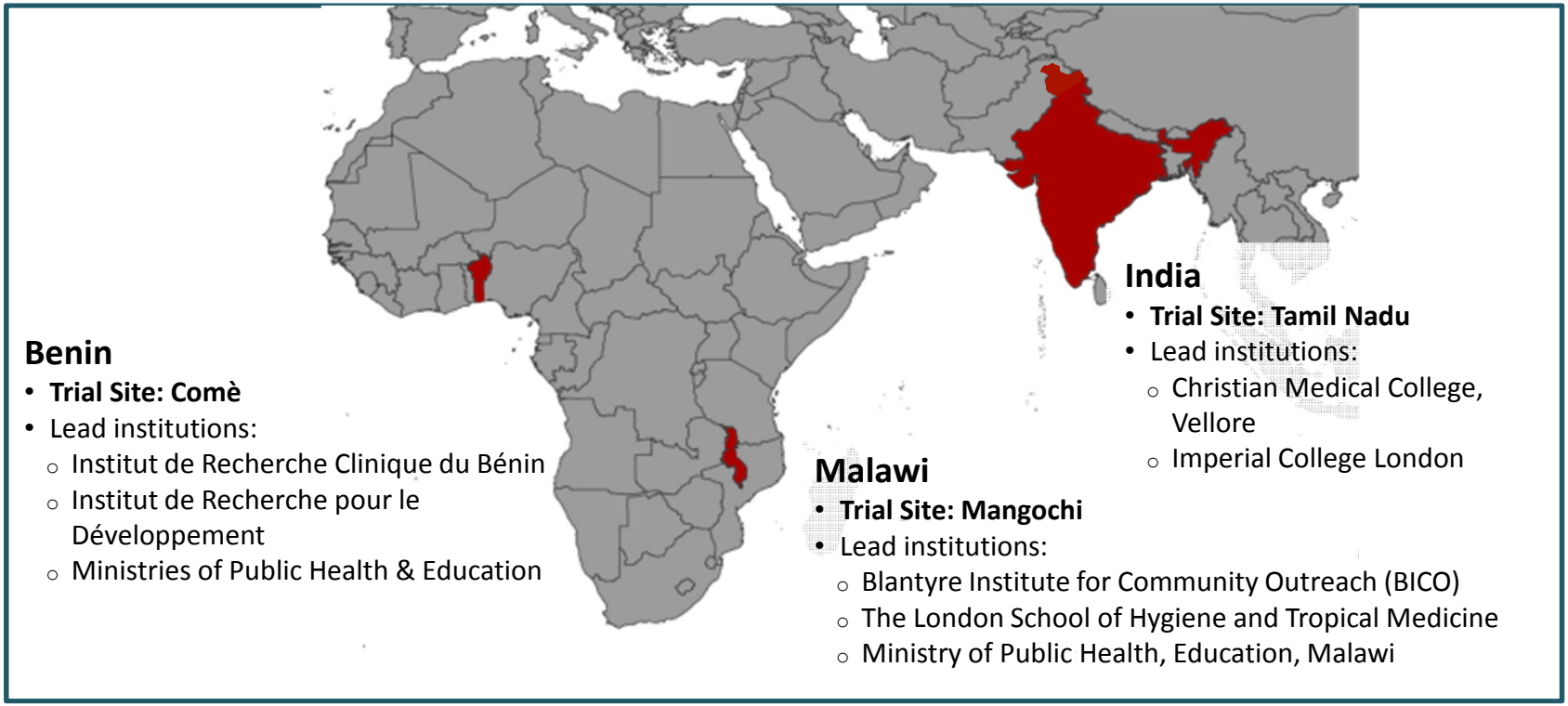
- 2 villages in the Delta region of South **Myanmar**
- Household GPS locations mapped

Study site 4 - the Tumikia project in South East Kenya (Pullen et al 2017)

The cluster level prevalence (A) and mean intensity of hookworm infection, eggs per gram (B). **20,842 individuals aged 1 to 99 years**



Study sites 5, 6 & 7 - randomized cluster controlled trials of breaking transmission in BGMF project entitled DeWorm3 with different treatment strategies



Benin
- **Trial Site: Comè**
- Lead institutions:
  - Institut de Recherche Clinique du Bénin
  - Institut de Recherche pour le Développement
  - Ministries of Public Health & Education

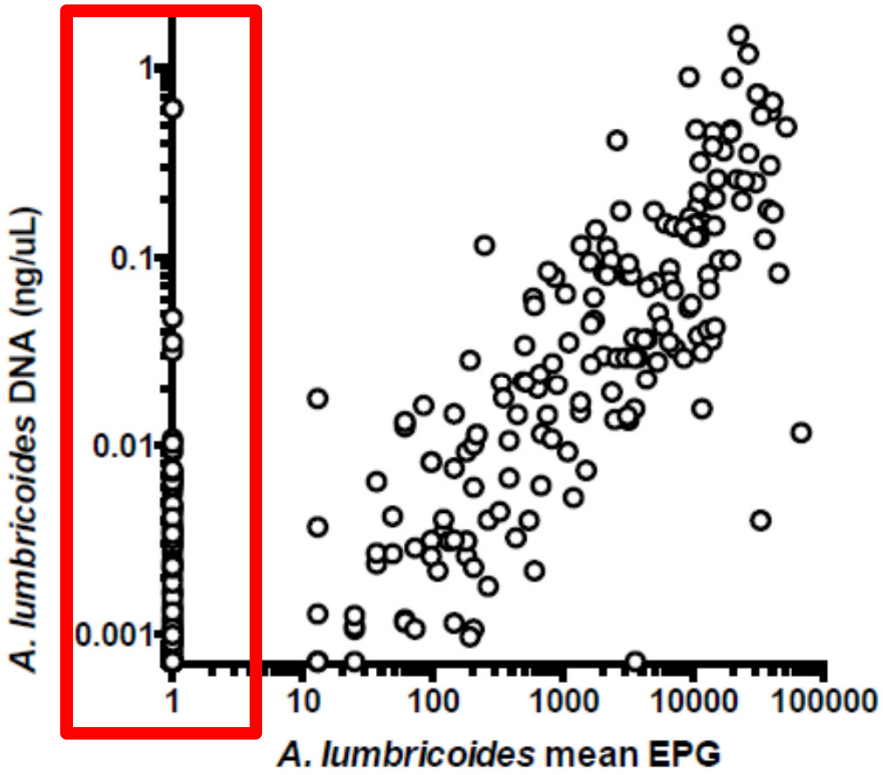
India
- **Trial Site: Tamil Nadu**
- Lead institutions:
  - Christian Medical College, Vellore
  - Imperial College London

Malawi
- **Trial Site: Mangochi**
- Lead institutions:
  - Blantyre Institute for Community Outreach (BICO)
  - The London School of Hygiene and Tropical Medicine
  - Ministry of Public Health, Education, Malawi

deworm3

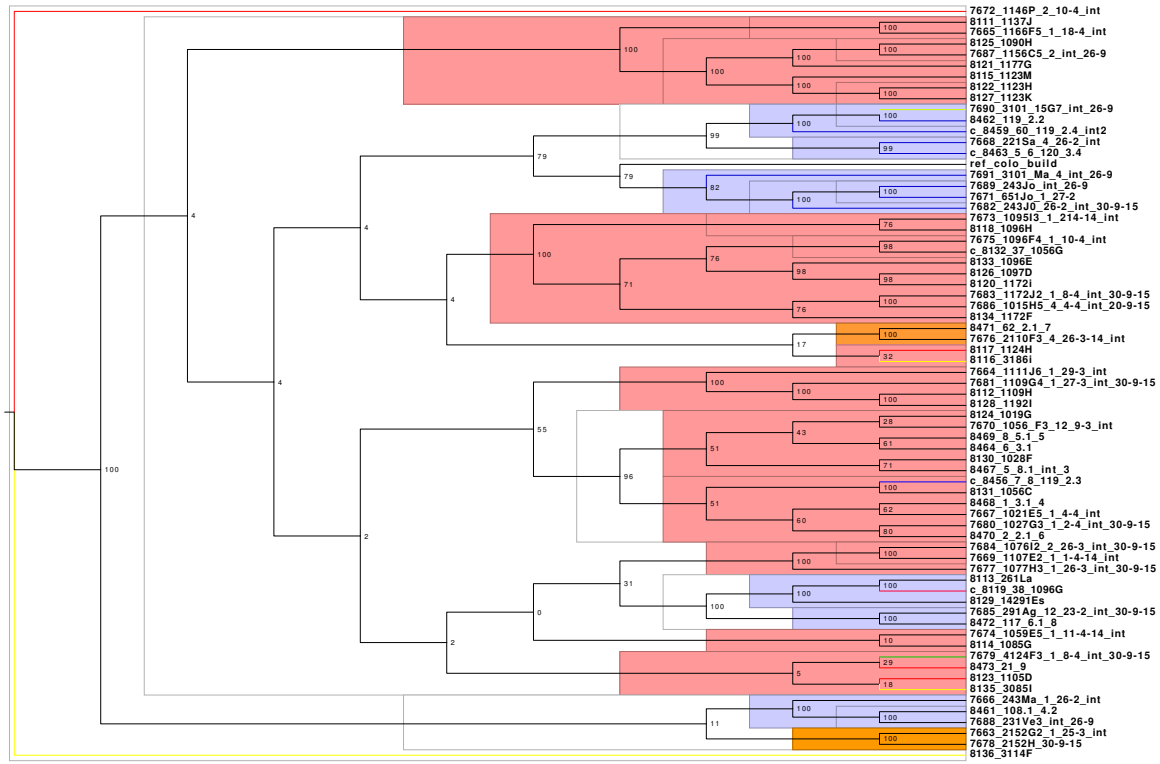
New diagnostic tools - Ascaris - Kato-Katz versus qPCR

(Easton et al 2016)



46% more positive samples when diagnosed with qPCR compared with Kato-Katz (2 slides)

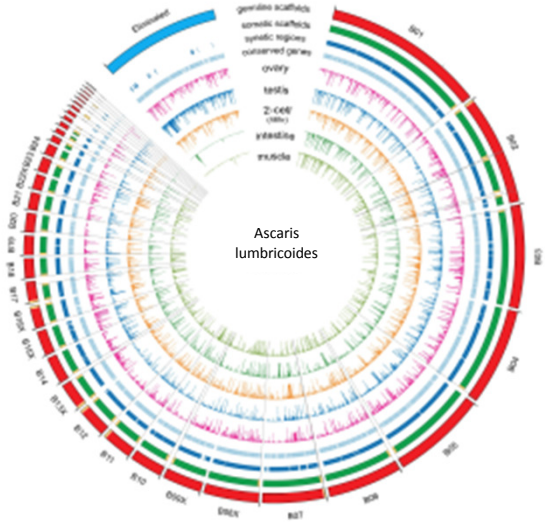
New genome methods help to determine 'who infects whom?'



Ecuador (only other genome sequence)

Village

1
2
3
4
5



- >99% identity with *A. suum*
  - Differ only by SNPs
  - Same DNA break regions in DNA elimination
- Combined sequencing to generate two genomes
- Improvement on previous *A. lumbricoides* genome: down to 415 scaffolds compared to 31,720

273 Mb – *Ascaris* genome
3234 Mb – human genome

Conclusions

The research of staff at LCNTDR have been central in helping to define policy for the control of NTDs.

- They have defined key epidemiological concepts and been a template for the design of community based randomised treatment clinical trials.
- These trials were designed to test predictions of detailed analyses – so far so good - but a long way to go before they complete in 2021.
- Parameter uncertainty a key issue – need for better quality epidemiological studies.
- In achieving MDA coverage required to break transmission individual compliance to treatment is key – as is its accurate measurement.
- In the 'End Game', new tools, such as molecular epidemiological methods, will be key to helping to understand how infection persist at very low prevalence – may dictate a policy change towards targeted treatment.