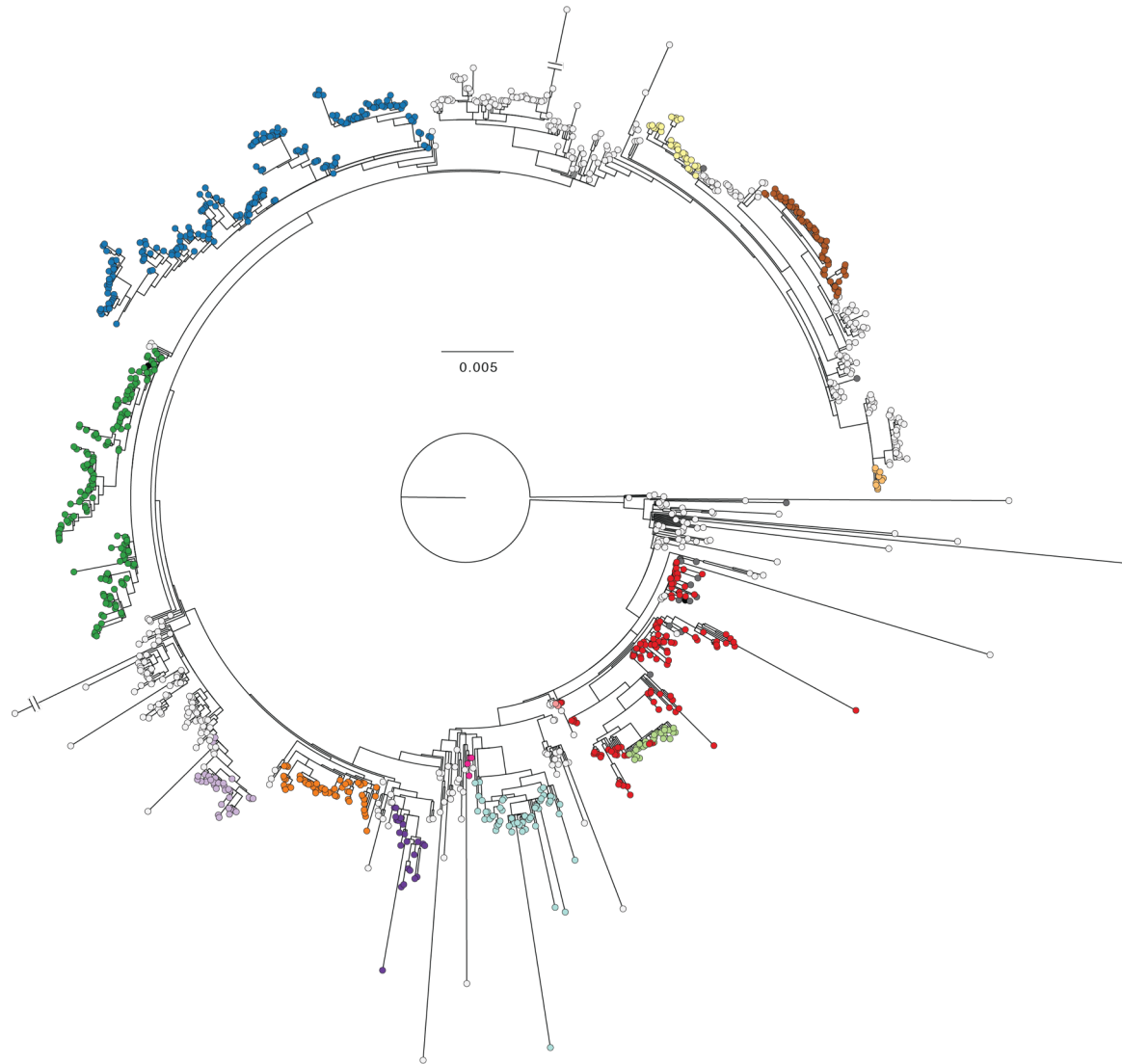


# Long read whole genome sequencing of *Vibrio cholerae* isolates from Malawi

Shirlee Wohl

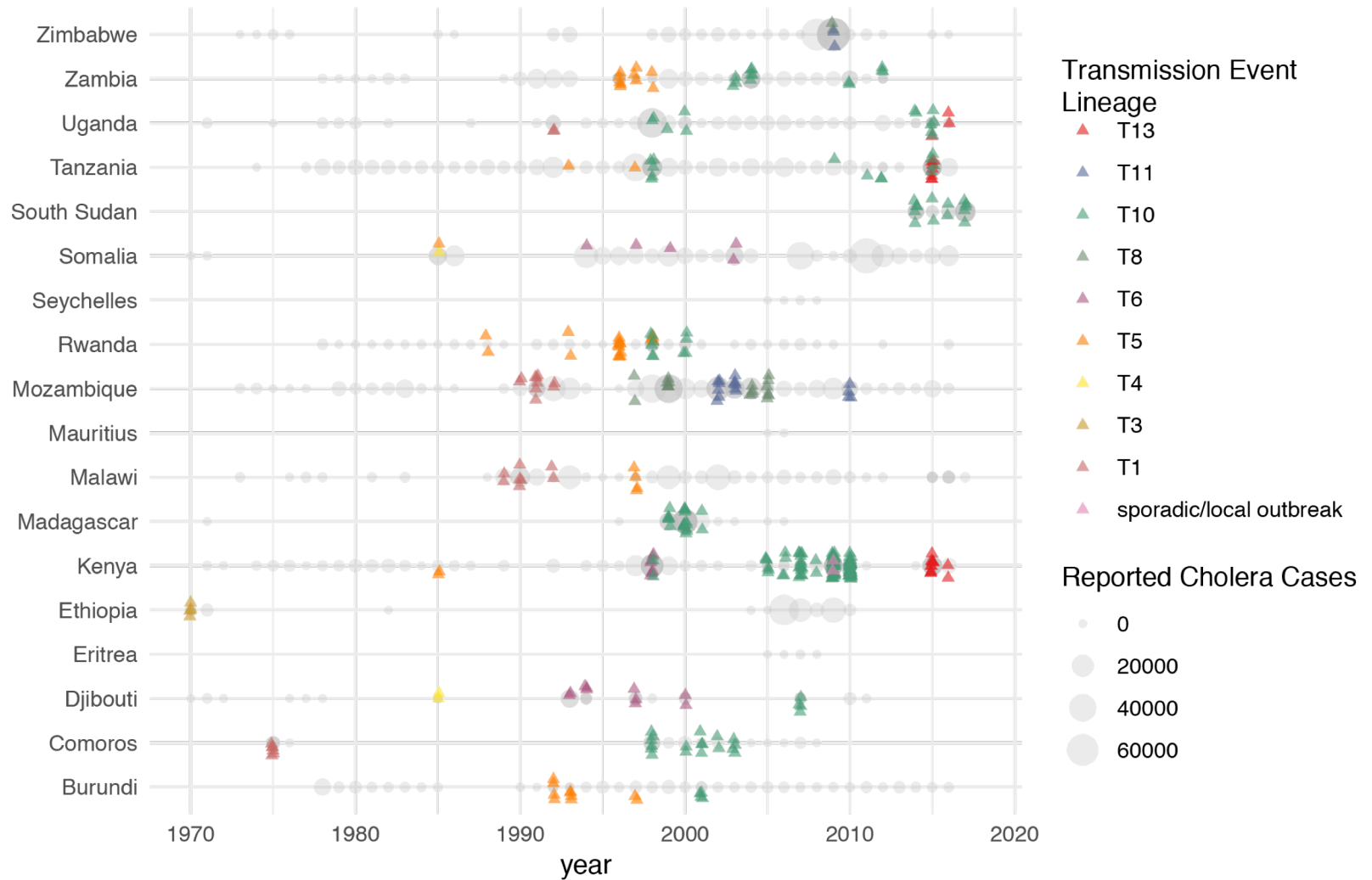
Johns Hopkins Bloomberg School of Public Health

# Whole genome sequencing of *Vibrio cholerae*

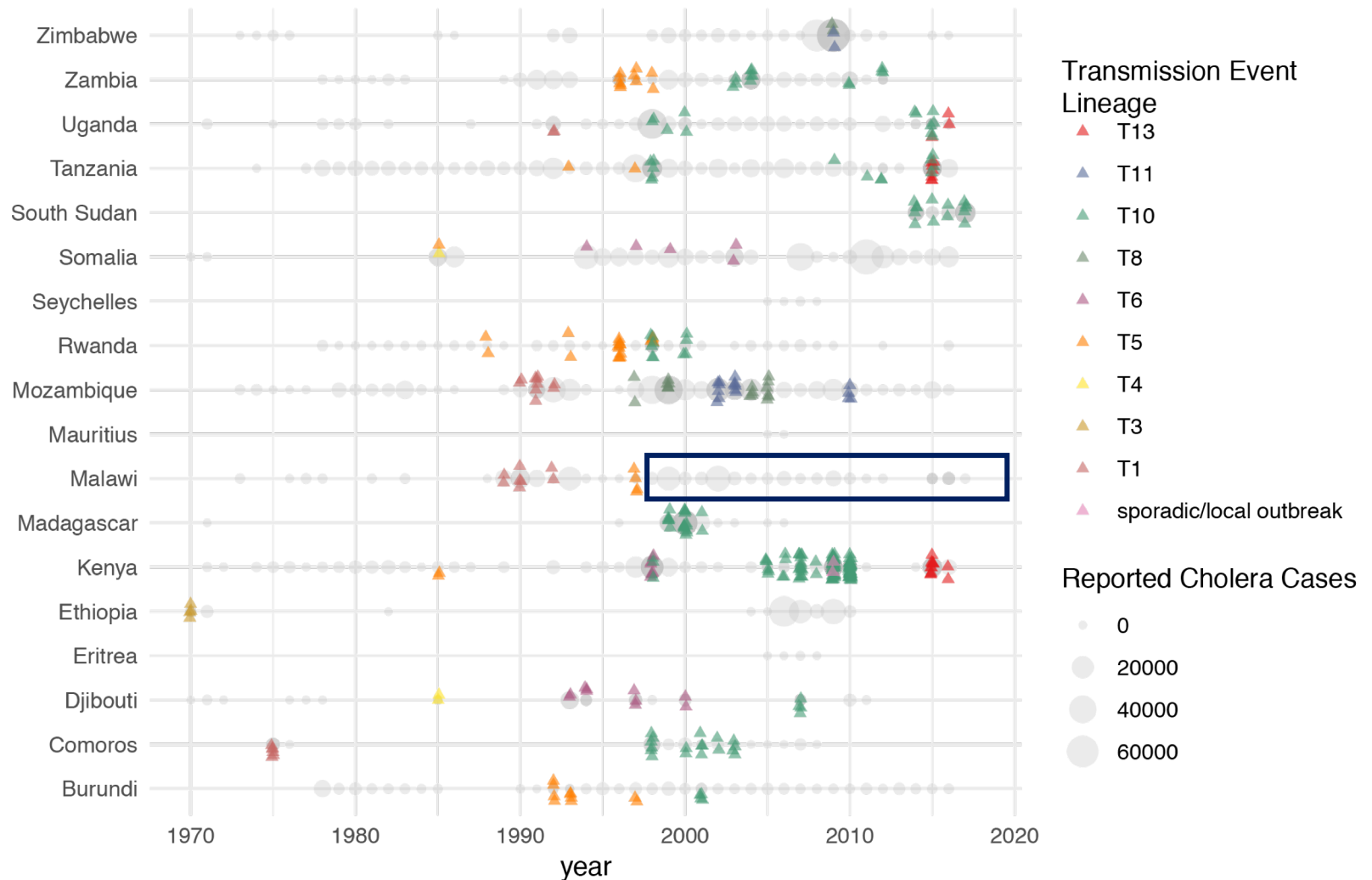


Adapted from data presented in Weill et al. *Nature* 2019.

# Gaps in cholera sequences from Eastern Africa



# Gaps in cholera sequences from Eastern Africa





# Whole genome sequencing with Oxford Nanopore

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# Whole genome sequencing with Oxford Nanopore

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**PRO** Low cost instrument, minimal equipment needed for library prep



# Whole genome sequencing with Oxford Nanopore



**PRO** Low cost instrument, minimal equipment needed for library prep

**PRO** Long reads can capture repeat regions and complex genome structure

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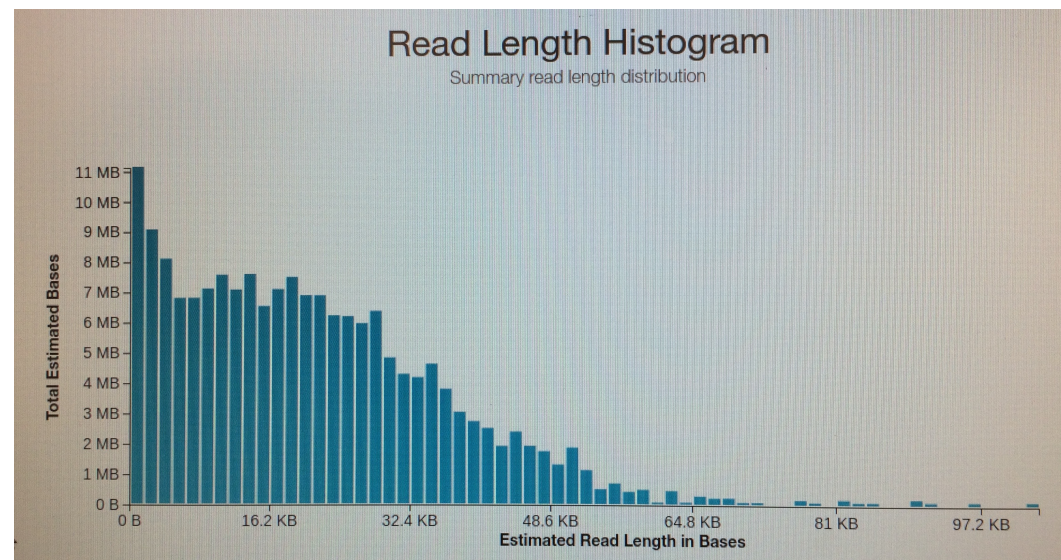
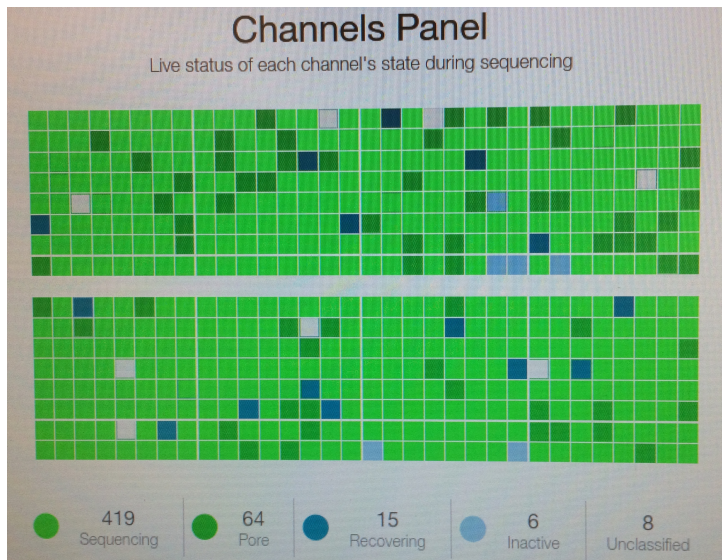
# Whole genome sequencing with Oxford Nanopore



**PRO** Low cost instrument, minimal equipment needed for library prep

**PRO** Long reads can capture repeat regions and complex genome structure

**PRO** Real-time analysis of sequencing reads



# Whole genome sequencing with Oxford Nanopore

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**PRO** Low cost instrument, minimal equipment needed for library prep

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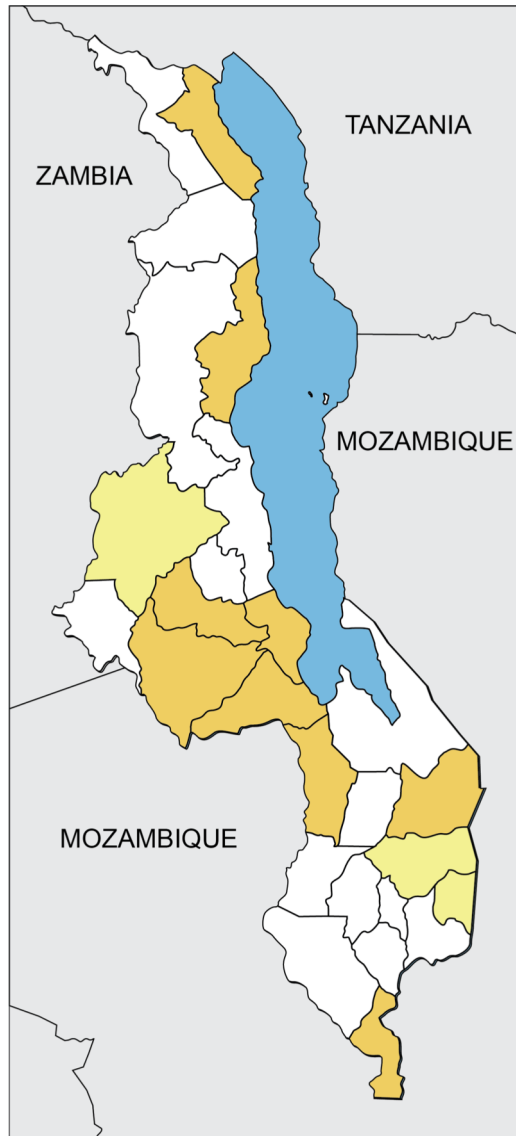
**PRO** Real-time analysis of sequencing reads

**CON** High basecalling error rate

**CON** More difficult to multiplex large numbers of samples

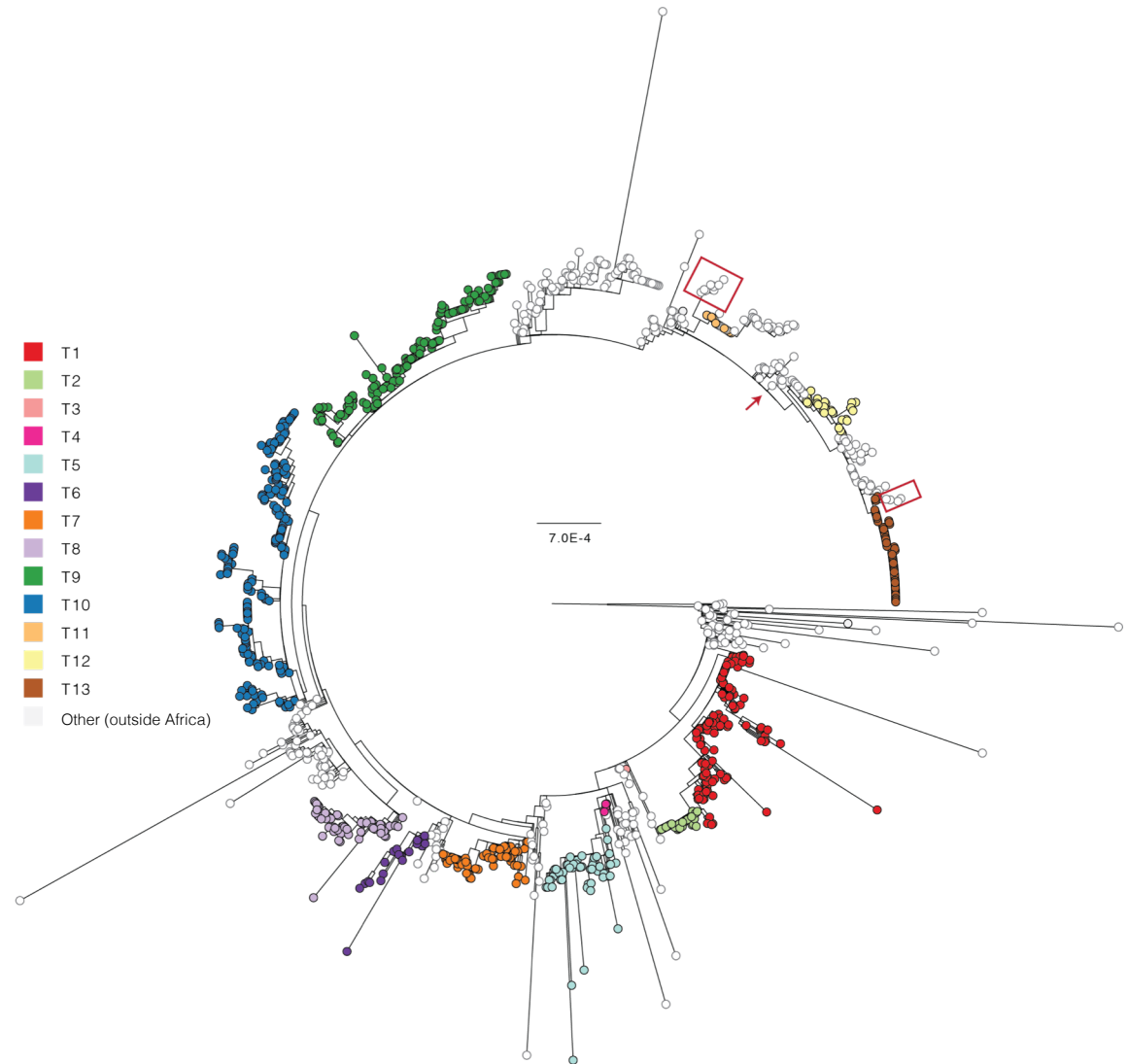
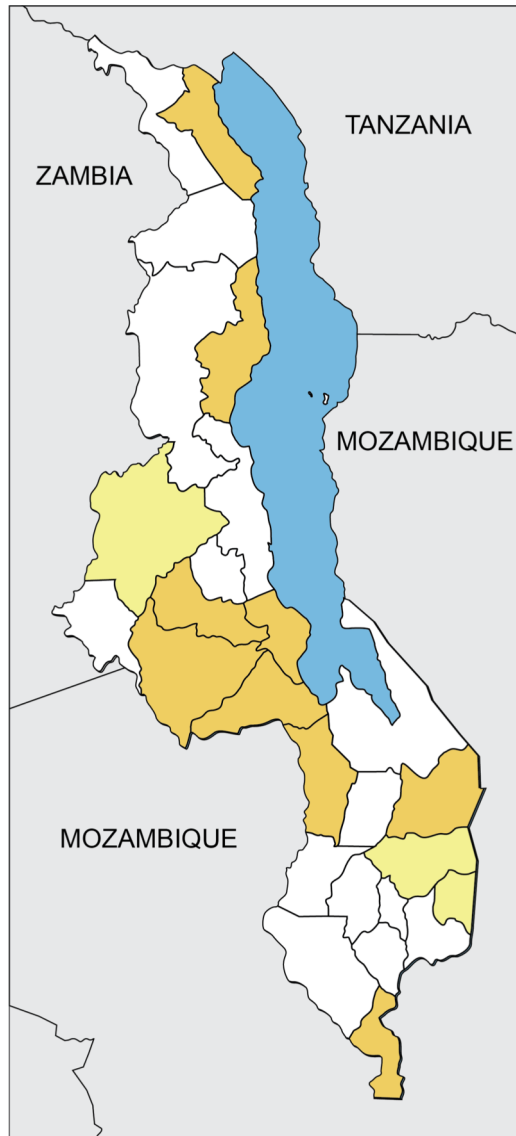


# Oxford Nanopore sequencing of cholera in Malawi

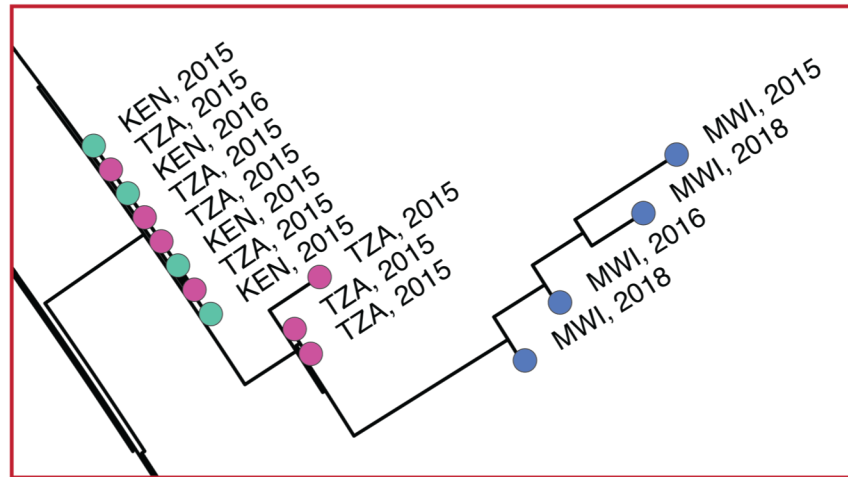
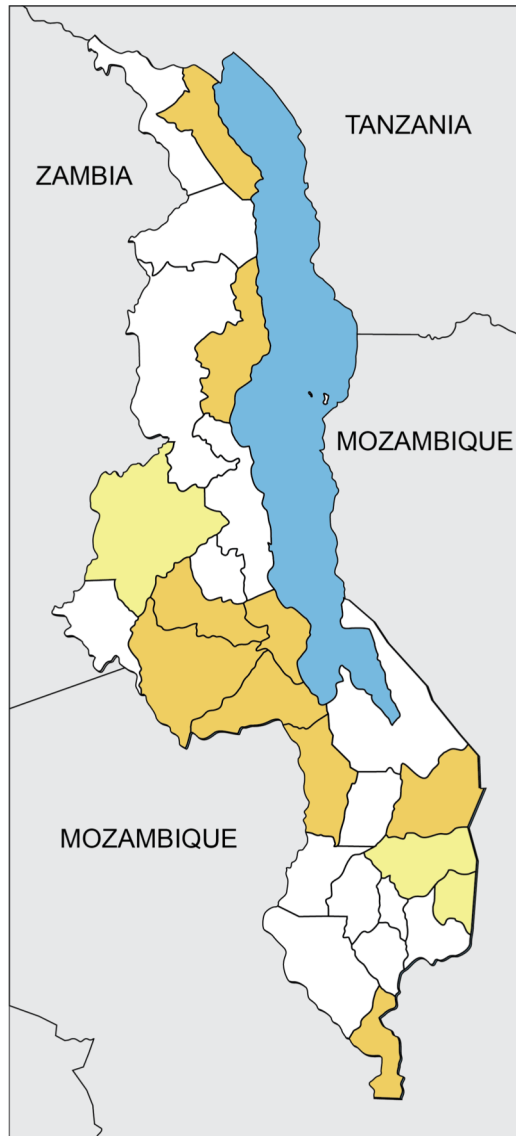


Watipaso Kasambara, Innocent Chibwe  
Amanda Debes, David Mohr  
Justin Lessler, Andrew Azman

# Oxford Nanopore sequencing of cholera in Malawi

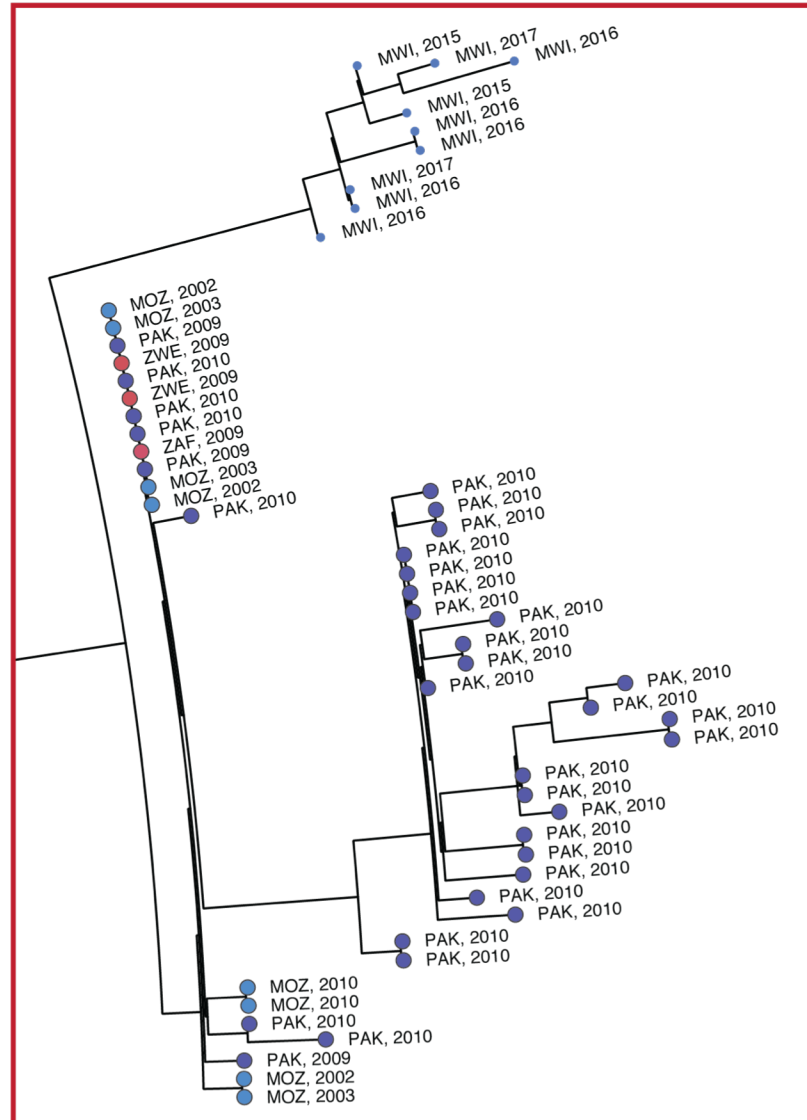
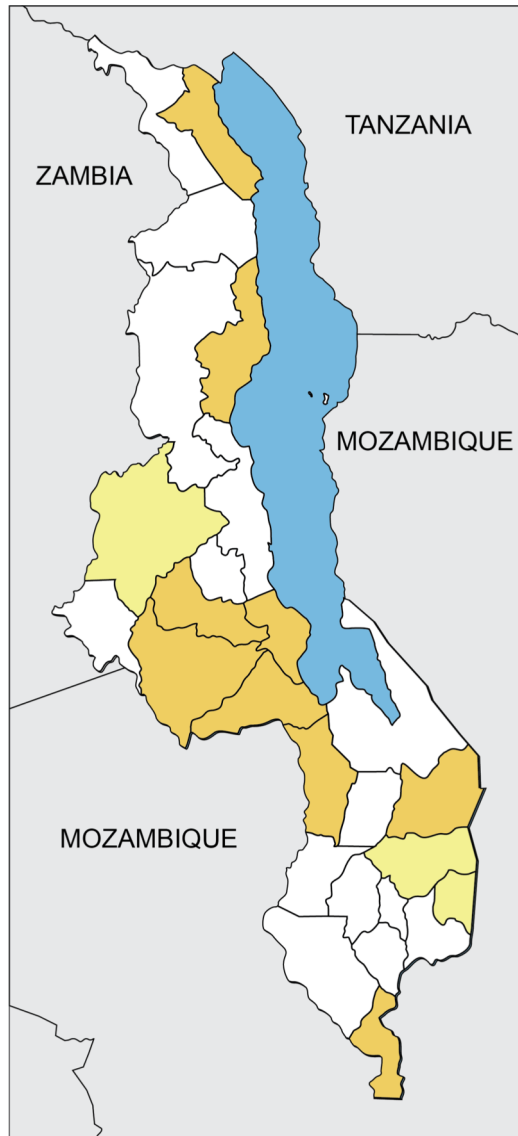


# Oxford Nanopore sequencing of cholera in Malawi





# Oxford Nanopore sequencing of cholera in Malawi



# Cholera sequences from Malawi fill in gaps

