The Meningitis Vaccine Project partners hope to vaccinate some 300 million people throughout the African ‘meningitis belt’ by 2015, thereby ridding the region of a disease that has caused havoc for more than a century.

Bacterial meningitis (meningococcal disease) kills 1 in 10 patients within 48 hours, even when antibiotics are started early. Patients that survive often have permanent disabilities like paralysis, blindness, hearing loss, or seizures. Meningococcal disease threatens the lives of millions of people across sub-Saharan Africa’s “meningitis belt.”

A vaccine (MenAfriVac) was introduced in 2010 to prevent the most common strain of meningococcal disease in Africa (serogroup A). But even with this vaccine still many questions and challenges remain. For instance, what if other strains in circulation in the region (serogroups X and W) start causing more disease? Evidence already suggests that this may be happening. How dangerous are those strains? Are they genetically linked to other strains? And most important, are currently available vaccines effective against these other strains?

To answer these questions, CDC is using whole genome sequencing analysis on hundreds of African meningococci specimens. CDC will compare these specimens to strains causing sporadic disease and other outbreaks worldwide. Using new tools, CDC’s laboratory scientists will compare how closely related the strains are and find markers for how likely they are to cause epidemics.

Using whole genome sequencing analysis, meningitis experts will be more effective in predicting meningococcal disease epidemics at an early stage and know if available vaccines are effective against these strains.

This vital information will help ministries of health and policy makers in structuring vaccination decisions and maximize public health response.