

Scarlet fever pathogen draft genome sequence released

June 22 2011

Scarlet fever has revealed unusual high infect rate in Hong Kong this year. So far, 466 children were infected and 2 of them dead. Scarlet fever is caused by *Streptococcus pyogenes*, a gram-positive pathogen that can be transmitted via skin wound and airborne droplet.

Under the guidance of Hong Kong Center for Disease Control (HK [CDC](#)), Hong Kong University (HKU) and their partners today released the draft genome sequence of the *S. pyogenes* strain that was isolated from a scarlet fever patient (Sequence has been uploaded to NCBI AN: SRA038808 and is available for immediate download at <ftp://ftp.genomics.org.cn/pub/S.pyogenes/>). Current analysis results indicate that this strain belongs to M12 serotype, which was widely distributed in Europe, North America, South America, and Asia. No significant [virulence](#) characters were observed on this type of *S. pyogenes* strain. There is 95.2% genomic region of this strain can be aligned to two previously fully sequenced M12 [strains](#) and 4.8% (around 90 kbp) is specific to this strain. It is possible that the specific sequences in this strain may result in the increase of virulence and improved spread ability.

HKU and their collaborators are continuing on the intense research of this pathogen. The whole genome fine map of this *S. pyogenes* will be released within a week. The team will further explore the source of the specific virulent-related sequences and possible pathogenicity mechanism by comparing the previous *S. pyogenes* isolates in Hong Kong and the current sequenced strain. The research results will provide

scientific evidences to facilitate the control of the infectious rate as well to develop effective measures to prevent the spread of scarlet fever.

It is reported that the draft genome sequence and preliminary analysis results were accomplished by HKU and BGI-HongKong. Earlier this month, BGI-Shenzhen and University Medical Centre Hamburg-Eppendorf worked together to firstly develop the complete whole [genome sequence](#) of the Germany Escherichia coli outbreak strain.

Provided by Beijing Genomics Institute

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