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SmartGene's Scientists Co-Author a Comprehensive Publication in ASM's *Clinical Microbiology Reviews* Addressing Pathogen Sequencing

Zug, Switzerland: 04 November 2020: SmartGene announces that its scientists are co-authors of an important, wide-ranging article which broadly addresses the role of gene sequencing for the specific identification and characterization of bacteria. Published by the **American Society for Microbiology** in ***Clinical Microbiology Reviews***, the article is entitled: ***Performance and Application of 16S rRNA Gene Cycle Sequencing for Routine Identification of Bacteria in the Clinical Microbiology Laboratory***.

Starting with a description of Sanger sequencing of the 16S rRNA gene in today's routine, clinical microbiology laboratory, the Review focuses on the importance of proper data analyses and interpretation of sequences for reliable identification of bacteria. This comprehensive evaluation is underpinned by the presentation of extensive, genus-specific, multiple alignments of 16S sequences. The multiyear experience of a large, regional, clinical microbiology service is presented, showing the use of direct 16S broad-range PCR followed by cycle sequencing as a complement to MALDI-TOF (matrix-assisted laser desorption ionization - time of flight) proteomics. Finally, the article discusses the potential for next generation sequencing (NGS) methods to replace 16S cycle sequencing for several routine diagnostic applications while highlighting the barriers which must be overcome to implement newer genomic techniques fully into clinical microbiology.

"Leading clinical laboratories around the world adopt sequence-based, bacterial identification as a routine procedure to complement their MALDI-based approach," stated Stefan Emler, MD, CEO of SmartGene and a main author of the Review. Emler further stated, "Broad implementation of sequencing by diagnostic labs has been hampered by a lack of standards for the interpretation of sequence data and results. The Clinical and Laboratory Standards Institute took up this issue in the second edition of the **CLSI Guideline MM18** *Interpretive Criteria for Identification of Bacteria and Fungi by Targeted DNA Sequencing* (2018). Professor Church, Dr. Zelazny, and I worked together on that Guideline, and this new Review Article presents some of the detailed analysis which informed our drafting of that Standard."

In closing, Dr. Emler noted that: "While this Review was written to reflect the current state of the art and to complement the CLSI guideline, it also provides a vision of sequence-based identification of microorganisms for the future. Issues of species diversity, sequence quality, and proper maintenance of reference databases are all just as relevant to NGS-based approaches. We at SmartGene look forward to working with our users to tackle the challenges of translating vast NGS microbial data sets into precise, actionable information which will inform clinical decision making and improve patient care."

About SmartGene

SmartGene is a bioinformatics application service provider (ASP) delivering secure, integrated, software solutions (SaaS) for the analysis, interpretation, and data management of genetic sequences. Customers worldwide use SmartGene's cloud-based modules for multiple applications, including bacterial and fungal identification, microbiome analysis, strain typing, HIV, HCV, and Influenza genotyping and drug resistance analysis, Coronavirus sequencing, plus molecular epidemiology of viruses and bacteria. SmartGene provides specific applications designed for routine workflows from raw sequencing data (Sanger, NGS) to comprehensive reports. Frequently updated, quality-controlled, reference databases, interpretative algorithms, specifically parameterized bioinformatics tools, and customized, searchable, sequence databases are integrated within SmartGene's solutions. Find out more at www.smartgene.com.