SmartGene introduces a new Fungal 25-28S Reference Database for D1-D2 sequencing

Zug, Switzerland: 12th September, 2019: Prompted by its ongoing efforts to create and maintain meaningful sequence reference databases for its customers, SmartGene has released a new IDNS® Fungi 25-28S Reference Database.

The rationale for this work is the complexity of this target, which is used mainly for identifying environmental fungal species. The large ribosomal sub-unit in fungi (25-28S) is indeed variable in length; the gene comprises approximately 3'500 bp and is rarely sequenced in its entirety. We observe that the 25-28S sequences present in the public repositories reflect highly variable coverage of the gene, with a preference for the D1-D2 region. Many labs choose indeed the D1-D2 region for identification of environmental fungal species, sequencing a fragment of roughly 500 bp; this region is at the 5' end of the gene, within the first 1'000 bp of the 25-28S.

Our new IDNS® Fungi 25-28S Reference Database is constructed for optimal coverage and representation of fungal species, in view of the more common sequencing of the D1-D2 region. Employing an adjusted and focused profile-based extraction process with quality filters, we recovered valid sequences for 30'224 fungal species from Genbank/ENA.

As a result of this activity, SmartGene created two reference data sets:

- One for alignment and editing purposes (e.g. in the IDNS®-ProofReader), containing long sequences spanning both D1 and D2, and covering 23'105 species (due to the exclusion of shorter entries).
- The other one as the new IDNS® Fungi 25-28S Reference Database, which contains sequences spanning at least D1 of the fungal 25-28S gene, with a minimum length of 450 bp; as of July 2019, this database covers currently 30'224 fungal species and is now available in our Fungi Modules, to enhance the resolution of fungal identification when sequencing the D1-D2 region of the 25-28S LSU.

These new data sets will be the basis for the new IDNS® Fungal 25-28S Centroid reference database and annotation, which SmartGene plans to introduce later this year.

For further information please contact your local SmartGene representative or

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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, molecular epidemiology of viruses and bacteria, and HIV, HCV, and Influenza genotyping and drug resistance analysis. SmartGene provides specific medical, clinical research, industrial and epidemiological surveillance applications designed for routine workflows from raw 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 which are CE-IVD labeled and compatible with the requirements of 21 CFR Part 11. Find out more at: www.smartgene.com.