S208
Symposium
Rapid genome sequencing: applications and limitations

The advent of ultra high-throughput sequencing (UHTS) technologies offered large promise for clinical and basic research laboratories. With the associated decrease in costs, from 10’000$ to roughly 200$ per microbial genome and the shortening of sequencing time, from a few days to 3h, bacterial whole genome sequencing is developing into a primary analysis for diagnostic laboratories. These UHTS technologies opens wide opportunities to diagnostic labs and applied research for (i) strain taxonomical classification, (ii) epidemiological typing, (iii) outbreak monitoring and examination of transmission history, (iv) investigation of biological properties such as the resistome or the presence of toxins, as well as (v) clinical metagenomics. Recent developments such as the sequencing of single cells unlock new possibilities by reaching a previously unattained precision. Although most applications still requires a first culture step, done in routine in clinical laboratories, a culture-independent processing of samples is developing, thus providing a gain in time and allowing the detection of unculturable bacteria. The scientific community is now facing new challenges to extract biologically relevant information from the increasing amount of sequence data. Data interpretation which is currently performed by a highly skilled workforce must be transferred to a mainly automatized pipeline. Moreover, highly harmonized procedures are required to allow inter-laboratory comparisons. Finally, new solutions for worldwide databases have to be found to stock not only genome sequence information but also associated so called meta-data on resistance profile and disease characteristics.