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Predictive pathogen biology: Genome based prediction of pathogenic potential and counter measures targets

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Horizontal gene transfer (HGT) and recombination leads to the emergence of bacterial antibiotic resistance and pathogenic traits. Genetic changes range from acquisition of a large plasmid to insertion of transposon into a regulatory gene. HGT events can be identified by comparing a large number of fully sequenced genomes across a species or genus, define the phylogenetic range of HGT and find potential sources of new resistance genes. In-depth comparative phylogenomics can also identify subtle genome or plasmid structural changes or mutations associated with phenotypic changes. Comparative phylogenomics requires that accurately sequenced, complete and properly annotated genomes of the organism. Due to dramatic advances in "short read" sequencing technology, the raw sequence coverage needed for sequencing a bacterial genome now can be obtained in a couple of days for a few dollars sequencing costs, starting with only a few nanograms of genomic DNA. Assembling closed genomes requires additional mate-pair reads or "long read" sequencing data to accompany short read paired end data. To bring down the cost and time required of producing assembled genomes and annotating genome features that inform drug resistance and pathogenicity, we are analyzing the performance for genome assembly of data from the Illumina NextSeq, which has faster throughput than the Illumina HiSeq (~1-2 days versus ~1 week) and shorter reads (150 bp paired end versus 300 bp paired end) but higher capacity (150-400 M reads per run versus ~5-15 M) compared to the Illumina MiSeq. Bioinformatics improvements are also needed to make rapid, routine production of complete genomes a reality. Modern assemblers such as SPAdes 3.6.0 running on a standard Linux blade are capable in a few hours of converting mixes of reads from different library preps into high quality assemblies with only a few gaps. Remaining breaks in scaffolds are generally due to repeats (e.g., rRNA genes) are addressed by our software for gap closure techniques that avoid custom PCR or targeted sequencing. Our goal is to improve the understanding of emergence of pathogenesis using sequencing, comparative genomics and machine learning analysis of ~1000 pathogen genomes. Machine learning algorithms will be used to digest the diverse features (change in virulence genes, recombination, horizontal gene transfer & patient diagnostics). Temporal data and evolutionary models can thus determine whether the origin of a particular isolate is likely to have been from the environment (could it have evolved from previous isolates). It can be useful for comparing differences in virulence along or across the tree. More intriguing, it can test whether there is a direction to virulence strength. This would open new avenues in the prediction of uncharacterized clinical bugs and multidrug resistance evolution and pathogen emergence.

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A clinical and mycological study of onychomycosis

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Onychomycosis is a major public health problem with a high incidence. The aim of this study was to determine the prevalence of various causative agents of onychomycosis and to study the clinical and mycological patterns of onychomycosis. A prospective study was conducted from September 2015 to March 2016 in university hospital center of Tlemcen in Algeria. The nails were evaluated clinically and the nail samples were subjected to direct microscopy and culture. 73% samples were found to be positive by direct microscopy and culture. Toe nails were affected more frequently than finger nails and distolateral subungal onychomycosis was the most common clinical type of infection which was seen in 74.73% patients. The etiological agents were yeasts (63.33%) and dermatophytes (36.67%). Among dermatophytes, *T. rubrum* was the commonest etiological agent. In our study, the mycological examination is the key for the positive diagnostic of onychomycosis, although yeasts were the main causative agents.

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