The New Molecular Microbiology: Impact on Understanding of Diabetic Foot Infections

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Chronic wounds represent a significant clinical burden in the US, directly impacting the quality of life for patients. It is estimated that the treatment of diabetic foot ulcers (DFUs) alone costs nearly 17 billion dollars per year. Moreover, more than 60,000 limb amputations are performed per year as a result of chronic DFUs that are unresponsive to treatment leading to high costs for hospitalization and increased morbidity and mortality. Currently, diagnosis is only possible using standard culture-based methods in 20-50% of DFUs. Lack of diagnosis leaves clinicians with no choice but to use empirically based antibiotic regimens that can be ineffective and contribute to the rise of antibiotic resistance (as seen in the rise of MRSA and carbapenem superbugs) with serious worldwide health implications. Developing strategies for faster diagnosis, directed treatment of microbial infection, and rapid wound healing is critical for effective patient care. The advent of low cost next generation sequencing makes it possible to perform whole genome sequencing of polymicrobial samples. Moreover, emerging “big data” technologies allow for efficient data mining to convert large-scale next-generation sequence datasets and clinical factors into specific diagnoses; not only identifying and quantifying the species present, but also genes of clinical importance (e.g. resistance genes and virulence factors). Yet currently, little is known about the diversity, composition and proportions of microbial communities in wounds therefore inhibiting our ability to understand why infections become chronic or heal. This work shows the impact of new molecular microbiology on understanding of diabetic foot ulcers, provides a glimpse into comparisons between 16S rRNA and Whole Genome Shotgun (WGS) methods. Having knowledge of the wound flora and their inherent resistance and virulence in DFUs, will allow clinicians to make fact-based decisions about treatment options.