Stenotrophomonas maltophilia virulence and phenotypic properties of clinical relevance

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Introduction
Stenotrophomonas maltophilia is a genetically highly versatile bacterial species, belonging to the γ-β subclades of Proteobacteria. It is ubiquitously distributed in the environment but recently gaining evidence as causal agent of nosocomial infections [1]. According to their gyrB gene sequences the S. maltophilia isolates could be classified into ten different genomic subgroups (gyrB gene phylogenetic tree as seen below). To have a look at the S. maltophilia physiological properties, we used 51 isolates of clinical and environmental origin for the genetic groups A-J, and some isolates belonging to none of the groups. Phenotypic properties of clinical relevance were tested, thereby major focus lied on the establishment of an assay with Dictyostelium discoideum as host organisms to measure bacterial virulence.

Virulence assayed by amoebae as host organisms
Plate killing assay
In order to assess bacterial virulence the amoebae Dictyostelium discoideum and Acanthamoeba castellanii were used as model organisms in a plate killing assay. 5 µl droplets containing defined numbers of amoebae (10,000, 5,000, 2,500…5) were spotted on a bacterial lawn. Plates were incubated at 30°C for 3 days with A. castellanii, and for 5 days at 22,5°C with D. discoideum. After that, bacterial virulence was measured as the count of amoebae necessary to form a plaque on the bacterial lawn.

Biofilm formation and Motility
Biofilm formation was monitored after 24 hours growth at 30°C in polystyrene microtiter plates. The optical density was measured at 595 nm of the crystal violet stained biofilm diluted 1:10 in 70% ethanol.

Exotoxins/Exoenzymes
Hemolysis of erythrocytes was observed for 45 of the 51 tested isolates. Five strains that did not produce hemolysins originated from infected patients. Thereby, no specific genetic group or isolation site was preferred.

Antibiotic resistance (MIC= minimum inhibitory concentration) to Vancomycin, Gentamicin, Tetracycline, Norfloxacine, and Co-trimoxazole was determined for the 51 strains (43 isolates) were resistant to Gentamicin (>512 µg/ml). Five strains that did not produce hemolysins originated from infected patients. Thereby, no specific genetic group or isolation site was preferred.

Conclusions
Stenotrophomonas maltophilia was shown to be a highly versatile species, on a physiologic level. Most phenotypic properties could neither be ascribed to the appearance in clinical or environmental surroundings nor to their genetic subgroups. We were able to show that virulence in an amoeba model could be correlated to their genetic groups. Genetic groups including respiratory tract isolates from cystic fibrosis patients thereby tend to show no virulence to the amoeba.

Literature

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