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Abstract (publication only)
Typing of Propionibacterium acnes by MALDI-TOF MS
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Objectives: P. acnes has been considered traditionally as a non-pathogenic member of the skin flora, however today it is accepted as an opportunistic pathogen associated with several diseases such as severe acne vulgaris, corneal ulceration, endophtalmitis, endocarditis, late-stage prostatic joint infection, and shunt-associated central nervous system infection. The aim of the present study was to evaluate the possibility to use MS-based typing for this important anaerobic species after routine identification by MALDI-TOF MS. Methods: P. acnes strains obtained from patients with severe acne, blood, joint infection or skin, were identified by conventional methods and by MALDI-TOF MS. After acquisition the mass spectra of P. acnes strains (MS Bruker Biotyper 2.0), the type of which were determined earlier as type I, II and III, mass spectrum sets were imported in the ClinProTools 2.2 software. Spectra were normalized and recalibrated using the respective functionalities of the software. Type characteristic peaks and peak shifts were searched. In addition, peak variations between the different types of P. acnes were investigated by using our FlexAnalysis 3.3 software. Out of the main spectra (MSP) of strains with known types, differentiating library was created for P. acnes type I (IA and IB), II and III and this library was challenged with spectra of further 60 P. acnes isolates with different origins. MLST analysis of the strains was also carried out. Results: By careful analyses of the mass spectra of 7 strains with known types of P. acnes, specific peaks and peak shifts were found in the range of 6800 and 7400 Da, which could be selected as characteristic peaks for type I, II and III. Even differentiation of types IA and IB was possible with a characteristic peak with 9950 Da present in type 1A P. acnes and missing in type IB strain. Using this approach out of the further 60 clinical P. acnes isolates 52 (86%) could be typed after identification by MALDI-TOF MS. MLST results were compared with the MS-based typing results. Conclusion: Since the introduction of MALDI-TOF MS for microbiological application, it has evolved from an experimental tool to a technology with significant benefit for routine microbiological laboratories first of all for the identification of bacteria and fungi. However careful evaluation of the MSP of well known bacteria may give a possibility to use this technique also for typing of bacteria such as presented here.