# Newer investigative tools for expansion of the spectrum of isolation list of infective microorganism in Orthopaedic surgery

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Infection is common and major complications of elective orthopaedic surgery. Therefore diagnosis of infection and identification of pathogen and their elimination is the primary and basic management prior to any elective orthopaedic surgey, but unfortunately, the standard investigation tools are not sufficient enough to isolate the infecting organism in the spite of several measures including withholding antibiotics for two to three weeks prior to the collection of samples for culture, increasing the number of specimens in different sites of affected area etc. In already implanted prosthesis or metals, the presence of bioflims attached with the prosthesis or metals with less number of organism in the surrounding tissues result in failure of their detection by standard investigation tools. If the implants are removed then , these can be processed in solid containers with addition of vortexing step followed by sonication which can diagnose by isolating infective organism in spite of taking antimicrobials within two weeks of the surgery ( Trampuz A et al 2007), but in others, culture negative organism remains between 27% and 55% in spite of standard investigations of synovial fluids including C reactive protein, human neutrophil elastase, total neutrophil count, alfa defensin and culture. Species specific polymerase chain reaction (PCR) only detect presence of one organism which advocate multiplex PCR and broad – range PCR to broaden the range of infective organism with limited success. In this scenario next generation sequencing can be as promising solution to detect culture negative organism. Here initially, a conventional PCR reaction is used to amplify the microbial DNA. The amplified DNA is marked with unique tags for their identification and loaded onto beads for the emulsion PCR for microbial isolation using a statistical analysis, by this technique the culture negative organism can be isolated with higher degree (96.1%) of corcordance. Therefore the next generation sequencing may be the useful investigative tool to diagnose infective organism in culture – negative scenario.

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