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Prognostic utility of whole genome sequencing and polymerase chain reaction tests of ocular fluids in post-procedural endophthalmitis

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Purpose:
To correlate detection of potential pathogen DNA in endophthalmitis with clinical outcomes

Methods:
Patients diagnosed with endophthalmitis following an intraocular procedure were recruited. Clinical outcome data from baseline, week 1, month 1 and month 3 visits were collected. Intraocular biopsy samples were cultured by standard methods. Quantitative polymerase chain reaction (qPCR) for specific pathogens and whole genome sequencing (WGS) were performed.

Results:
A total of 50 patients (mean age 72, 52% male) were enrolled. Twenty-four cases were culture-positive and 26 were culture-negative. WGS identified the cultured organism in 76% of culture-positive cases and identified potential pathogens in 33% of culture-negative cases. Month 1 and 3 visual acuities did not vary by pathogen-positive vs pathogen-negative cases as detected by either culture or WGS. Visual outcomes of S. epidermidis endophthalmitis were no different than those of pathogen-negative cases, while the patients infected with other pathogens showed worse outcome. Higher baseline bacterial DNA loads of bacteria other than S.epidermidis detected by WGS were associated with worse month 1 and 3 visual acuity, while the S.epidermidis loads did not appear to influence outcomes. Torque teno virus (TTV) and Merkel cell polyomavirus (MCV) were detected by qPCR in 49% and 19% of cases, respectively. Presence of TTV at presentation was associated with a higher rate of secondary PPV (p=0.009) and retinal detachment (p=0.022).

Conclusions:
Presence and higher load of bacteria other than S. epidermidis detected by WGS or DNA from TTV by qPCR in ocular fluids is associated with worse outcomes in post-procedure endophthalmitis.