## P-369 Comparing the sensitivity and specificity of otoacoustic emission screeners in diagnosing noise-induced hearing loss from air conduction pure tone audiogram in a hearing conservation programme

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One of the key components of hearing conservation programme is the yearly pure tone audiogram (PTA) obtained from workers who are at risk of developing noise-induced hearing loss from occupational noise exposure. Although it is the current gold-standard for assessing one's hearing threshold, a number of limitations are associated with the PTA. It is not an objective test, it is time consuming, it needs trained technician and a sound-proof room (or at least a very quiet ambience) and it is deemed not sensitive enough to detect subtle changes in the cochlea due to early exposure to noise as it assesses the whole auditory pathway and not just the cochlea, where damage from noise mainly occur. A likely alternative would be otoacoustic emission (OAE), an objective test that measures the emission of outer hair cells which ideally would reflect early damages from sound, and takes only fraction of the time to do PTA to complete. Our objective is to see whether screening OAE can be used instead of PTA for early detection of NIHL. A total of 72 workers from a quarry in Kuantan recently underwent PTA, TEOAE, DPOAE and DDPOAE. The association between PTA and OAE (right and left ear) was tested using McNemar's test and the proportion between the pass and refer cases of OAE and PTA findings was noted to be significant. We will then report on the sensitivity and specificity of different types of OAE as stated above when compared to PTA as gold-standard.

## P-372 Molecular Study of Hepatitis C Viral RNA Extracted From Local Isolates in Pahang, Malaysia: Genotyping, Subtyping and Base Sequencing

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Hepatitis C virus infection affects approximately 170 million individuals constituting about 3% of the world's population. Most of those infected face the risk of developing liver cirrhosis and/or liver cancer. In Malaysia, hepatitis C prevalence is 1.6% and is still the foremost infection among multiple blood transfusion groups. The current mainstay treatment of HCV is pegylated alpha-interferon in combination with ribavirin, incurring considerable expense on local health services. In fact, less than 50% of treated patients respond favorably to the given therapy. Understanding the characteristics of the RNA genome of the local HCV genotypes can serve as foundation for future development of rapid diagnostic techniques. In addition, it has the potential for helping in designing small interfering RNA (siRNA) to be utilized in studies related to specific silencing of vital viral genes. However, despite the plethora of global HCV studies, there is relative scarcity HCV research in Malaysia. In this present study, HCV isolates from infected haemodialysis patients were studied, focusing on the characterization of their genomes, by genotyping and base-sequencing. The nucleotide sequence of the conserved 5'UTR region of HCV genome revealed several sequence patterns across the 4 main HCV genotypes available in the study panel. Phylogenetic analysis of the NS5B region showed a predominance of HCV genotype 3a. The revealed sequence patterns have the potential for designing probes that could differentiate the predominant HCV genotype 3 from other genotypes. Analysis of the secondary structure of genotype 3a showed conserved loop structures that could be targeted by small interfering RNA molecules. In conclusion, molecular studies of local HCV strains provide a new dimension for the improvement of current HCV detection and genotyping methods, aid in better understanding of the molecular epidemiology of the virus infection and may form the basis for future in-vitro studies on viral molecular pathogenetic mechanisms and