Paper #17

Familial Clustering in Periprosthetic Joint Infection: A Population-Based Cohort Study

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Introduction: Recent reports suggest a genetic susceptibility towards PJI; however, there is limited data to support this. Thus, we performed a population-based, retrospective-cohort study to determine if familial clustering of PJI was observed.

Methods: The cohort was obtained by querying the UPDB for all patients who underwent TJA between January 1, 1996 to December 31, 2013. From this cohort, we identified patients who experienced subsequent PJI using an isolated ICD-9 code (996.66). The magnitude of familial risk was estimated by hazards ratios (HR) from Cox regression models to assess the relative risk of PJI in relatives and spouses. Using quantiles for age strata, we adjusted for sex, BMI ≥30, a history of smoking, diabetes and/or end-stage renal disease (ESRD). Additionally, we identified families with an excess clustering of PJI above that expected in the population using the familial standardized incidence ratio (FSIR).

Results: We identified 66,985 patients that underwent TJA, of which 1,530 experienced a PJI (2.3%). The risk of PJI was elevated in first degree relatives (HR 2.16, 95% CI 1.29-3.59) and combined first and/or second degree relatives (HR 1.79, 95% CI 1.22-2.62) of PJI patients. There was no difference in PJI risk in spouses of PJI patients that also underwent TJA compared to their controls (HR 0.74, 95% CI 0.20–2.78). Further, 116 high-risk pedigrees with a FSIR >2 and p-value <0.05 were identified and nine were selected for future genotyping studies.

Conclusions: Familial clustering was confirmed in patients experiencing PJI. We found the adjusted HR of PJI in first degree relatives exceeds the individual hazard ratios of PJI for morbid obesity, diabetes, sex, age, smoking and approached that of end stage renal disease. This data supports the importance of genotyping studies and emphasizes the need to obtain a family history of PJI preoperatively in TJA candidates.

