The primary aim of this study was to determine if postoperative use of high flow nasal cannula (HFNC) and/or continuous positive airway pressure (CPAP) are independent risk factors for adverse postoperative outcomes after surgical repair of Esophageal Atresia (EA). Secondary aims were to determine other significant clinical risk factors associated with these adverse outcomes.

A retrospective chart review was conducted on all EA neonates repaired and managed postoperatively between 2007–2020 across two centres: Sydney Children’s Hospital (SCH) and The Royal Hospital for Women (RHW). The primary outcome measure was anastomotic leakage (AL), and other outcome measures included anastomotic stricture (AS), mediastinitis, sepsis, and pneumothorax. Significant associations were identified using Chi-square, and univariate and multivariate logistical regression models (p < 0.05).

We reviewed 104 charts. Post-repair, all were placed on invasive mechanical ventilation (IMV) (median of 119.50 hours). Of these, 45 (43.3%) were taken from lower part of the esophagus during endoscopy. Expression of IL-1β, TNFA, GATA3, TLR4, CD68 genes and mean esophageal pH.

In patients with erosive esophagitis, local expression of interleukin 18 and beta-2 macroglobulin genes in esophageal mucosa was assessed with ImmunonQuartet assays. Multichannel intraluminal esophageal pH-impedance (MII-pH) studies performed to all the participants. Diagnosis of GERD was confirmed by the results of MII-pH data. Patients were allocated to erosive esophagitis (EE) or non-erosive GERD groups (NERD). Non-symptomatic subjects with normal endoscopy and MII-pH results served as a control. Spearman rank correlation was used to assess association of genes expression and results of MII-pH.

Data of 60 patients with GERD and 10 subjects of the control group were available for the analysis. Higher expression of IL-1β (5.89 ± 0.4 vs 5.28 ± 1.1, p = 0.04) and GATA3 (3.82 ± 0.86 vs 2.23 ± 0.96, p = 0.03) genes was found in EE group compared to NERD. Expression of IL-1β, IL-18, TNFA, and TLR4 genes was lower (P < 0.05) in the control group compared to EE and NERD. Esophageal acid exposure correlated with the expression of IL-1β (R = 0.29), IL-18 (R = 0.31), TNFA (R = 0.35), GATA3 (R = 0.34), TLR4 (R = 0.29), CD68 (R = 0.37) genes. Mean esophageal pH correlated inversely with the expressions of IL-18, TNFA, GATA3, TLR4, CD68 genes.

In patients with erosive esophagitis, local expression of interleukin 18 and GATA3 transcription factor genes was higher compared to subjects with non-erosive form of gastroesophageal reflux disease. Esophageal acid exposure correlated directly with expression of IL-1β, IL-18, TNFA, TLR4, CD68 and B2M genes. Inverse correlation revealed between expression of IL-18, TNFA, GATA3, TLR4 CD68 genes and mean esophageal pH.