analysis shows that high HSBP1 may be involved in the regulation of nucleotide excision and repair, spliceosome, proteasome and other pathways (IDDF2021-ABS-0106 Figure 4). The analysis of immune checkpoint results showed that patients with high HSBP1 expression had increased immune checkpoint molecules CLAG3 and TIGIT (IDDF2021-ABS-0106 Figure 5).

Conclusions The iron death-related gene HSBP1 may be involved in the occurrence and development of esophageal squamous cell carcinoma and the regulation of immune checkpoints. This study provides a new research direction for future HSBP1-related esophageal squamous cell carcinoma research and treatment targets.

IDDF2021-ABS-0108 ENTEROBACTERIACEAE – DECIPHERING THE CULPRIT GUT BACTERIA CAUSING NECROTIZING ENTEROCOLITIS IN INFANTS

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Background Necrotizing enterocolitis (NEC) is a lethal gastrointestinal illness primarily affecting preterm infants, causing inflammation and necrosis of the intestines. It is apparent that the colonization of certain bacteria in the gastrointestinal tract had contributed to NEC pathogenesis. This research aims to investigate the association of gut pathogens from family Enterobacteriaceae and the development of NEC.

Methods A systematic literature search was performed according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guideline across three databases

(Ovid MEDLINE, ProQuest, and Scopus; dated to 31st May 2021). The research was conducted using MeSH terms: ('gut' OR 'intestinal') AND ('Enterobacteriaceae' OR 'pathogen') AND ('neonate' OR 'neonatal' OR 'infant') AND 'enterocolitis'. Studies involved the analysis of the gut microbiome of infants with NEC as compared to those of non-NEC/healthy controls were included. Studies that are irrelevant at the title/abstract level or without experimental intervention (e.g., reviews) were excluded.

Results Twenty-one studies were identified for qualitative analysis, which amounted to 361 NEC cases. The majority of NEC cases were diagnosed in preterm infants, and the gut microbiome was determined by analyzing fecal/intestinal tract samples using microbial culture or culture-independent molecular techniques. The main findings demonstrated a significant increase in abundance of Enterobacteriaceae colonizing the gut of NEC infants than those of controls. *Klebsiella* spp. (*Klebsiella pneumoniae*, *Klebsiella oxytoca*), *Shigella dysenteriae*, *Escherichia coli*, and *Citrobacter koseri* were identified as the dominating taxa present in the gut of NEC infants (IDDF2021-ABS-0108 Figure 1). Enterobacteriaceae colonizing the gut of NEC infants). However, some studies reported contradicting results due to the inability to pinpoint clear signatures of gut microbial composition causing NEC. Dysbiosis of the gut microbiota caused by a higher abundance of Enterobacteriaceae can be a factor triggering an inflammatory response in premature infants. Preterm infants have immature intestinal host defenses that could expose them to a higher risk of intestinal diseases.

Conclusions The outcome of this systematic review revealed an important trend of increased abundance of intestinal Enterobacteriaceae in NEC. Nevertheless, the role of Enterobacteriaceae in the development of NEC warrants further investigation. A better understanding of NEC is crucial for effective prophylactic and therapeutic interventions.

Abstract IDDF2021-ABS-0108 Figure 1