

ISOLATE-SPECIFIC DIFFERENCES IN MACROPHAGE RESPONSE TO GROUP B *STREPTOCOCCUS*

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Although *Streptococcus agalactiae* (Group B *Streptococcus*, GBS) is primarily an opportunistic pathogen that colonizes the gastrointestinal and genitourinary tracts of 15-30 % of healthy individuals, it remains a major cause of invasive disease in neonates [1]. The latter can occur in the first week of life and usually manifest as sepsis or pneumonia (i.e., early-onset-disease), or at 1 week to 3 months of age, which usually manifests as meningitis (i.e., late onset disease) [2]. To date, 10 different serotypes (Ia, Ib, II – IX) have been described, distinguished by their virulence and the immune response they elicit [3]. Since intrapartum antibiotic prophylaxis can only prevent early-onset, but not late-onset disease and infections in the elderly and immunocompromised individuals, further studies are needed to investigate GBS-associated pathogenesis. Because adaptive immunity is underdeveloped in neonates, cells of innate immunity play a critical role in protection against pathogens [4]. Of the latter, macrophages are particularly important as they are involved in pathogen recognition, phagocytosis, and elimination [5]. Because disease severity depends on both the GBS isolate and the immune status of the individual, we investigated possible isolate-specific differences in the immune response of THP-1 macrophages to 12 different previously genotyped GBS isolates [6]. Significant isolate-specific differences were observed in phagocytic uptake and expression of macrophage polarization markers [7]. Furthermore, by measuring inflammatory and anti-inflammatory cytokines and chemokines at the protein level, as well as expression of genes involved in antimicrobial activity and inflammation at different time points, we observed that different isolates have different potential to become invasive or remain colonizing. In addition, by measuring IL-1B, IL-18, and caspases 1 and 3 at the mRNA and protein levels, LDH secretion, and caspase-1 activity, we demonstrated that some isolates were significantly more cytotoxic to macrophages and induced pyroptosis. By measuring glycolysis and oxidative phosphorylation using Seahorse extracellular flux analyzer and analyzing the expression of glycolytic genes, we have shown that different GBS isolates activate macrophage metabolism differently and that differences in metabolism lead to differences in macrophage effector functions [7].

References:

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