Introduction:
Adequate animal models are clearly needed for the development of truly effective clinical strategies for the treatment of sepsis. The recently accepted recommendations (Minimum Quality Threshold in Pre-Clinical Sepsis Studies - MQTiPSS, Osuchowski et al. Shock 2018) are defining several aspects of rodent sepsis models, but the microbiological background received relatively less attention. In this line our aim was to explore the significance of microbial profile in the outcome of peritonitis-induced sepsis models.

Methods:
Fecal peritonitis was induced in Sprague-Dawley rats (n=22, with 1.22×10^6 – 5.9×10^6 CFU ip) and Vietnamese minipigs (n=18. with 3.8×10^7-6.2×10^9 CFU). Invasive hemodynamic monitoring and blood gas analyses were performed on anaesthetized animals between 18-24h of sepsis. The respiratory, cardiovascular, renal, hepatic and metabolic dysfunctions were evaluated with the species-specific Sequential Organ Failure Assessment (ssSOFA) score, the microbial profile was determined with selective media and MALDI-TOF MS in the initial inoculum and in the abdominal fluid taken 20h after sepsis induction.

Results:
Strong correlation was found between the initial dose of the inoculum (CFU) and the ssSOFA scores for organ dysfunction (rats: r = 0.656, P=0.0186; pigs: r=0.570, P = 0.0391). Similar to the human microbiota Protebacteria (rat: 53%; pig: 27%) and Firmicutes (rat: 40%; pig: 55%) were the predominant phyla in the induction inoculum in both model.

Conclusion:
Taxonomical similarity was present in both peritonitis model with human microbiota and the severity of organ dysfunction was associated with the initial bacterial concentration in both species. These findings can advance the process of refining the animal models to follow the latest guidelines.

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