Immune responses in a murine device-related infection model

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Introduction: Infection associated with orthopedic devices is one of the main causes for implant failure and the treatment of these infections remains a big challenge for surgeons. In this study, the MouseFix™ system (RISystem AG, Davos) [1, 2] was used to establish a murine device-related infection model. Implant associated osteomyelitis was developed in some groups using a clinical isolate of Staphylococcus epidermidis, one of the leading etiologic agents of orthopedic infections [3]. The development of infection over time and associated immune responses were assessed.

Methods: Titanium MouseFix™ plates, with or without Staphylococcus epidermidis (10^4 CFU) contamination, were used to fix a femoral osteotomy in C57Bl/6 mice (female, 20-28 weeks old). Mice were sacrificed at 3, 7 and 14 days after surgery (n=6-9 per group). Based on the observed results, IL-17A knockout (KO) C57Bl/6 mice (female, 20-28 weeks old) have recently been operated and sacrificed at day 14. Live bacteria from the implant, bone and soft-tissue were quantified. Bone cells were kept for mRNA analysis and stimulated to collect supernatants for cytokine and chemokine quantification. Lymph node and bone cells were characterized by flow cytometry.

Results: Three days post-operatively all animals were infected, with live bacteria recovered from bone, implant and soft tissue. At later time-points, the number of bacteria decreased in each location, particularly in the soft tissue adjacent to the implant. Furthermore, no bacteria were cultured from some animals, indicating the immune system was capable of clearing the infection. Infected animals presented an increase in inflammation markers compared to non-infected animals, which peaked at day 7. When studying the T-cell populations in lymph node, an increase of IL-17+ cells was detected, especially in those animals where bacteria were cleared.

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3. Montanaro, L., et al., Scenery of Staphylococcus implant infections in orthopedics. Future.Microbiol., 2011. 6(11): p. 1329-1349.