Conclusions: Although results cannot be generalized due to a small sample, surgeons adopted different postures during the intervention while using each type of laparoscopic needle holder.

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Intestinal microbiota transplantation to germ-free mice in a in vivo model of nafld associated with a quercetin treatment

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Background: Gut microbiota is involved in obesity, metabolic syndrome (MS) and nonalcoholic fatty liver disease (NAFLD).

Objectives: To select mice donors for intestinal microbiota transplantation based on its metabolic phenotype in response to a high fat diet (HFD) and quercetin treatment (Q). Intestinal microbiota transplantation from donors to germ-free mice under the same experimental model.

Methods: HFD with or without quercetin feeding C57BL/6J mice were euthanized after 16 weeks, and blood, liver, and caecal samples were collected. Liver histological studies were carried out. Liver function and plasma lipid and glucose levels were analyzed.

Results: HFD mice showed typical pathophysiological features of NAFLD, with obesity, MS, steatosis and liver damage. HFD caused dysbiosis as indicated by the reduction of total number of bacteria and *Firmitutes/Bacteroidetes* rate increase. Quercetin tended to normalize these parameters, showing prebiotic capacity. Donors of intestinal microbiota were selected on the basis of body weight gain, MS, histological findings and altered gut-liver axis. Mice responder (HFD+) and non-responder (HFD-) to HFD together with a control, a ControlQ, and a HFDQ (responder to quercetin) were selected as donors. Germ-free mice were colonised with gut microbiota from donors and divided into 20 groups according to the transplanted feces and diets (Control, ControlQ, HFD or HFDQ) in order to establish the metabolic phenotype transfer in response to the HFD diet and quercetin.

Conclusions HFD induced different metabolic phenotypes allowing to the selection of donors of intestinal microbiota from HFD responders and non-responders. Also, quercetin supplementation modified the metabolic phenotype of HFD mice.

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Pressure ulcers treatment in paraplegic patients using bone-marrow autologous mononuclear cells vs combined with platelet-rich plasma

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Objectives: Pressure ulcers are a major health problem for bedridden patients or persons with reduced mobility. In patients with SCI, ulcers are often a chronic problem and approximately 85% of these patients will develop pressure ulcers sometime during their lives. Pressure ulcers are difficult to treat with standard medical therapy and often they recur. Taking into account preliminary positive results obtained with autologous bone marrow mononuclear cells (BM-MNCs) and published by our group, an alternative approach was considered in order to heal ulcers that are not able to be treated with this method due to their area and/or dimensions.

Methods: 29 patients with type IV chronic pressure ulcers were included in the study. All these patients had undergone prior surgery with a lack of response. The bursa was washed with saline solution and the wound was debrided. After this intervention the patients were divided into two groups depending on the pressure ulcer characteristics. One group named BM-MNCs (n = 11, x = 51·09 years) received a MNCs suspension obtained from autologous bone marrow. A second group called PRP (n = 18, x = 55,27) received a combination of autologous BM-MNCs and PRP obtained from peripheral blood from the same patient. Finally, the ulcer margins were revitalized and the wound closed by a purse-string silk suture.

Results: The mean number of MNCs infused in each group was $104{,}44 \cdot 10^6$ for BM-MNCs y $123{,}25 \cdot 10^6$ for PRP group. Ulcer resolution was 72·72% for the first group and 78·95% for the second group. The mean time to complete closure was 37,66 days in the BM-MNCs group and 44,23 days for PRP group. During follow-up (44 months) none of the patients whose wounds had resolved underwent ulcer recurrence.

Conclusions: Cell therapy using autologous BM-MNCs combined with PRP seems to be an adequate option to treat type IV chronic pressure ulcers whose particular morphology needs an alternative method. Moreover, the mean time period to achieve the wound closure is similar in the two groups.

Genetic changes in a new animal model of human pancreatic cancer based on mesenchymal cells versus a classic model based on peritumoral fibroblasts

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Objectives: We have described two animal models of human pancreatic cancer developed by orthotopic transplantation. The new model uses immortalized human mesenchymal cells (IHBMMC), whereas peritumoral fibroblasts (FPT) were used for the classic model. Both models show large tumor growth with metastatic dissemination. In this paper, we try to determine the differences between both xenograft models in the expression of human genes involved in tumor development of Hedgehog signaling pathway and the epithelial-mesenchymal transition (EMT) process.

Methods: Five experimental groups of severe combined immunodeficiency (SCID) transplant recipient mice were established with: IHBMMC (Group I), FPT (Group II), Capan-1 tumor cells (Group III), IHBMMC and Capan-1 (Group IV), and FPT and Capan-1 (group V). From 24 pancreas tissue samples, mRNA expression levels were determined by qPCR of the Hedgehog and EMT pathways.

Results: Statistical analysis of the data in the new model, based on the co-transplantation IHBMMC and Capan-1, shows that Hedgehog pathway *SHH* and EMT process *SNAI1* genes are overexpressed when compared to the levels detected in recipient mice Capan-1. In the classical model based on FPT and Capan-1, the expression profile is similar, although the aforementioned genes fail to be overexpressed.

Conclusions: The gene expression pattern of the new animal model of pancreatic cancer obtained using immortalized mesenchymal cells is different from that generated with peritumoral fibroblasts. Specifically, the co-transplant of IHBMMC and Capan-1 cells stimulates the expression of *SHH* and *SNAIL* genes.

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