"GUT MICROBIOTA IS IMPLICATED IN CANCER-INDUCED CACHEXIA"

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ABSTRACT

BACKGROUND AND AIMS: We know that the gut microbiota is implicated in energy metabolism and its role has been mostly studied upon obesity. Here we set the hypothesis that the gut microbiota could also be implicated in metabolic alterations associated with cancer, cachexia. METHODS: This hypothesis was assessed in BALB/c mice intravenously injected with mouse proB BAF3 cells transfected with BCR-ABL gene in order to allow the development of chronic myelogenous leukemia (CML). Muscles (tibialis, gastrocnemius), liver, intestine and adipose tissues were withdrawn 2 weeks after injection for further biochemical and histological analysis. Gut microbiota composition was assessed by RT-qPCR. RESULTS: BCR-ABL expressing CML constitutes a new model of cancer cachexia, as proven by a decrease in adipose and muscle tissue weights. In both male and female, Lactobacillus spp. levels in caecal content drastically decrease, independently of food intake (p<0.001). Moreover, this decrease is highl...

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BACKGROUND AND AIMS: We know that the gut microbiota is implicated in energy metabolism and its role has been mostly studied upon obesity. Here we set the hypothesis that the gut microbiota could also be implicated in metabolic alterations associated with cancer, cachexia.

METHODS: This hypothesis was assessed in BALB/c mice intravenously injected with mouse proB BAF3 cells transfected with BCR-ABL gene in order to allow the development of chronic myelogenous leukemia (CML). Muscles (tibialis, gastrocnemius), liver, intestine and adipose tissues were withdrawn 2 weeks after injection for further biochemical and histological analysis. Gut microbiota composition was assessed by RT-qPCR.

RESULTS: BCR-ABL expressing CML constitutes a new model of cancer cachexia, as proven by a decrease in adipose and muscle tissue weights. In both male and female, Lactobacillus spp. levels in caecal content drastically decrease, independently of food intake (p<0.001). Moreover, this decrease is highly correlated to muscle markers of atrophy, such as Atrogin-1 mRNA (r = -0.8885, p<0.0001). Finally, increasing the level of Lactobacillus spp. levels by dietary prebiotics allows to lessen Atrogin-1 mRNA induction in the muscle.

CONCLUSIONS: In this new model of cancer cachexia, we highlight two important facts: first, gut microbiota modification is associated with cancer-induced cachexia; second, modulation of gut microbiota counteracts markers of muscle atrophy. Therefore, we suggest that gut microbiota is implicated in cancer cachexia and may constitute a new target in the treatment of this metabolic disease.
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