Results

HOXC6 was overexpressed in RCC and associated with poor prognosis. Overexpression of HOXC6 promoted the migration and invasion of CRC cells in vitro and in vivo. Increase in CCL2 expression by upregulation of HOXC6 could attract more infiltrating M2 macrophages. IL6 secreted by M2 macrophages could induce EMT in tumor cells by upregulating HOXC6 and activating the Wnt/β-catenin signaling pathway via inhibition of DKK1 secretion.

Conclusions

Our study indicates that overexpression of HOXC6 induces EMT by regulating the DKK1/Wnt/β-catenin axis. The positive crosstalk between M2 macrophages and HOXC6 in tumors led to poor prognosis of RCC.

MALONDIALDEHYDE LEVELS IN THE LONG INTERGENIC NON-PROTEIN CODING GUT-SKIN AXIS: DECODING THE LINK

Muhammad Luthfi Adnan*, Dini Islamiana, Hilm Aryand Sudarto, Miranti Devi Pramantyanto, Undergraduate Program of Medicine, Faculty of Medicine, Universitas Islam Indonesia, Indonesia; Departement of Physiology, Faculty of Medicine, Universitas Islam Indonesia, Indonesia

Background

Hyperlipidemia can cause infertility due to cell damage to the testicular organs. Hyperlipidemia can induce lipid peroxidation, which results in the formation of malondialdehyde (MDA). Quail egg yolk is one of the many foods consumed by Asians that contain high lipid levels. The aim of this study was to determine the effect of quail egg yolk diet on MDA levels of testicular organ on the rat.

Methods

The subjects are male Wistar (Rattus norvegicus) strain rats 2–3 months with body weight 200–300 grams divided into two groups (K+ and K−). Group of K+ were given quail egg yolk for two weeks with a dose of 5 ml while group of K− were only given fed ad libium. All rats terminated to take the testicular organ to measure the level of MDA. All data were statistically analyzed with one-way ANOVA. Values were considered significant at p<0.05.

Results

Mean of MDA level (nmol/gram) in rats was 0.95 ± 0.25 in K− group and 8.64 ± 0.13 in K+ group. The one-way ANOVA test showed significant differences in activity between the group with p<0.001 and Post Hoc test p<0.001.

Conclusions

Quail egg yolk significantly increases MDA Levels between the group with p<0.001 and Post Hoc test p<0.001.

GUT-SKIN AXIS: DECODING THE LINK BETWEEN THE GUT MICROBIOME AND HIVES

Learn-Han Lee*, Vengadesh Letchumanan, Loh Teng-Hern Tan, Hooi-Leng Ser, Jodi Woan-Fei Lian. Novel Bacteria and Drug Discovery Research Group (NBDD), Microbiome and Bioresource Research Strength (MBRS), Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, Malaysia

Background

Urticaria (hives) is a rash affecting the skin and mucosa, often characterized by appearance wheals, angioedema, and pruritus. Chronic urticaria (CU) is classified by the occurrence of urticaria which exceeded six weeks (almost daily) without specific triggers and identifiable cause. CU is a common disease that has detrimental effects on quality of life. However, its aetiology remains unclear. There is increasing evidence that dysbiosis of the intestinal microbiota is associated with dermatologic conditions. The human gut microbiome has a significant role in the regulation of the immune system, which can be implicated in the development of immune-mediated diseases such as CU. This systematic review aims to investigate the relationship of gut bacteria and the development of CU.

Methods

The systematic literature search was executed in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guideline. Research commenced using MeSH terms relevant to the topic, (‘gut’ OR ‘microbiome’ OR ‘microbiota’ OR ‘microflora’) AND (‘urticaria’ OR ‘hives’) were performed on four databases (PubMed, EMBASE, ProQuest, Scopus; publication date limit to 29 February 2020). Titles and abstracts of all retrieved articles were screened for inclusion. Full-text articles were retrieved for in-depth evaluation.
studies were screened and refined by the inclusion and exclusion criteria. Studies involving gut microbiome and CU were considered for inclusion. Irrelevant articles based on title/abstract level, case reports, conference abstracts and other studies with no experimental intervention (reviews, book, commentaries) were excluded.

**Results**

Three studies were eligible for final qualitative analysis, with a total of 100 participants. Research findings have shown that CU patients have a significant decrease in abundance of Firmicutes (Lactobacillus; Faecalibacterium prausnitzii), Actinobacteria (Bifidobacterium), Bacteroidetes (Bacteroides fragilis, Bacteroides plebeius), whilst an increase in abundance of Proteobacteria. The research suggested that increased abundance of Proteobacteria might enhance the permeability of intestinal mucus inner layer and enable bacterial infiltration, causing inflammation of epithelium and impairment of gut barrier function which leads to the development of inflammatory skin diseases.

**Conclusions**

As a summary, this outcome provides a preliminary understanding of microbial composition in CU patients (figure 1). This offers a new avenue of research for potential CU treatment via maintaining gut health.

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**BUDDING ASSOCIATION BETWEEN GUT MICROBIOME IN THE DEVELOPMENT OF MYASTHENIA GRAVIS**

Lee Han, Jodi Woan-Fei Law, Loh Teng-Hern Tan, Hooi-Leng Ser, Vengadesh Letchumanan. Novel Bacteria and Drug Discovery Research Group (NBDD), Microbiome and Bioresource Research Strength (MBRS), Jeffrey Cheah School of Medicine and Health Sciences, Monash University Malaysia, Malaysia

**Background**

The human microbiome comprises of microbes that live on or within various sites of the human body. These diverse microbes have the potential to impact our physiology, both in health and disease. Recently, several autoimmune diseases have been associated with the alterations in patients' microbiota, including myasthenia gravis. Thus, this study aims...