www.health.gov.il
המדען הראשי
Chief Scientist Office
משרד הבריאות
לחיים בריאים יותר

מרץ, 2019

Israeli Medical Abstracts Repository (IMAR)

Research Number: 3-0000-12908
Title: The interplay between milk and the gut microbiome in IgE-CMA patients in the context of oral immunotherapy
Principal Investigator: Michael Goldberg, MD, PhD
PI's Institute: Shamir Medical Center (formerly Assaf Harofeh)
Other Author(s): Arnon Elizur[1], MD; Ilan Youngster[1], MD; Liat Nachshon[1], MD; Omry Koren[2], PhD
Institute(s): [1]Shamir Medical Center (formerly Assaf Harofeh); [2]Faculty of Medicine, Bar Ilan U.
Year (Start): Jan 1 2017 Year (End): Dec 31_2017

Background: It is increasingly being recognized that the enteric organisms that live in the gut (termed gut microbiota) have a profound influence on the metabolism and immune system of their host, and are themselves highly influenced in turn by the host's diet. Oral immunotherapy (OIT) is a novel therapeutic regimen which desensitizes food-allergic individuals by slowly exposing them to increasing amounts of allergen. Thus, OIT, for treatment of milk allergy provides a unique opportunity to study the contribution of ingested milk to the host microbiota and how it modulates the immune system leading to allergic desensitization.
Research Hypothesis: Consumption of milk has an effect on the gut microbiota, which can be discerned in a IgE-mediated cow's milk allergy (IgE-CMA) context.
Aim 1: To compare the gut microbiota of IgE-CMA patients to those of patients with other IgE-mediated food allergies.
Aim 2:. To examine the effects of milk in a temporal fashion, on the gut microbiota, of CMA patients undergoing milk oral immunotherapy (OIT).
Aim 3: To explore the use of intra-patient microbiota changes associated with OIT (aim 2) as predictors for successful treatment, and for reaction frequency and severity during therapy.
Methods: Fecal samples were collected from milk-allergic patients undergoing oral immunotherapy, and from patients allergic to other foods. DNA was extracted, and the 16SrRNA genes amplified and sequenced, facilitating the characterization of the gut microbiota.
Results: Distinct microbial signatures were noted for FA to different foods. SCFAs levels were significantly higher in the non-allergic compared to the FA groups. Among milk-allergic patients undergoing milk-OIT, the abundance and evenness of the taxa present were different among those who failed the desensitization program as compared to those successfully desensitized.
Discussion: The location and scope of the human gut microbiota uniquely situate it to exert influence on the progression and establishment, and potential for resolution of of food allergy.
Conclusions: Our results demonstrate a link between IgE-mediated FA and the composition and metabolic activity of the gut microbiota.

Key words (Up to 5): Microbiome; Food Allergy; Oral Immunotherapy

מרץ, 2019

Israeli Medical Abstracts Repository (IMAR)

Publications associated with the project (PubMed Format):

1. Distinctive Gut Microbiota Signature in Persistent IgE-mediated Food Allergy
   Goldberg, MR Hadar Gershon, Appel M et al. Journal of Allergy and Clinical Immunology, Volume 143, Issue 2, AB189.

2. Goldberg MR, Mor H, Magid Neriya D, et al. Microbial signature in IgE-mediated food allergies. Genome Med. 2020 Oct 27;12(1):92. doi: 10.1186/s13073-020-00789-4. PMID: 33109272; PMCID: PMC7592384.
   https://doi.org/10.1186/s13073-020-00789-4