

IDENTIFICATION OF EPIGENETIC SIGNATURES IN SUBJECTS EXPOSED TO ENVIRONMENT STRESSORS

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Introduction: Human well-being is changing due to dramatic warming situation. There are rising evidence of environmental disasters, such as floods and fires, which led many animals and insect to migrate, becoming vectors of unknown pathologies in cities. All these things (and others) have important side effects on all those diseases affected by environment, for instance, multifactorial pathologies like allergies¹. Epigenetic is known to be the linker between human genetics and environment influence on DNA, so it is rising importance to know how and which climate changing is responsible for certain human disease ².

Aim: the purpose of this project is to evaluate if there are any epigenetic differences in individuals affected by allergic disease, more thoroughly, investigate whether there are pleomorphic phenotypes related to epigenetic differences. Before doing this, is necessary to do an in-depth analysis of literature to identify the major genes shared between allergic disease, thus making possible to set an EWAS³ analysis and then find the stressors which cause the arising of allergic disease and serological markers.

Methods: the first step will be the literature study, in order to determine the candidate genes to rhinitis, asthma and atopic dermatitis. Then the collection of patients biological sample, prior to ethical committee approved, will enable us to sequencing the genes of interest, take notes of the variants and epigenetic divergence. Finally, try to propose a model *in vitro* with the purpose to confirm the major environmental stressors. Patients' samples will correlate with anamnestic evaluation, then will be extracted nucleic acid (DNA, RNA) following by PCR, sequencing and bioinformatical analysis to predict the function of the founded epigenetic variations.

Conclusion: the challenge of this project is to find out or predict a direction for human well-being, related to the exposition to xenobiotic particles, coming from anthropic activities. Trying to fill up the gap of knowledge on the epigenetic conditions in complex multifactorial disease, like allergy. The latest goal is to create patients' groups of risk which correlates with the exposure to specific environment stressor.

References:

- 1. Abdelzaher H et al. (2022) Climate change, human health, and the exposome: Utilizing OMIC technologies to navigate an era of uncertainty. *Front Public Health*. 10: 973000. doi:10.3389/FPUBH.2022.973000
- 2. Ray C & Ming X (2020) Climate Change and Human Health: A Review of Allergies, Autoimmunity and the Microbiome. *Int J Environ Res Public Health*. 17:1-7. doi:10.3390/IJERPH17134814
- 3. De Lillo Aet al. (2020) Epigenetic profiling of Italian patients identified methylation sites associated with hereditary transthyretin amyloidosis. *Clin Epigenetics*. 12, 176 doi.org/10.1186/s13148-020-00967-6