HYPERTROPHIC CARDIOMYOPATHY EXPRESSION: ROLE OF EPIGENETICS AND ENVIRONMENTAL FACTORS.

Repetti et al. (PNAS, 2021) report nine identical twin pairs with sarcomere protein gene variants and two with unknown disease aetiologies who were discordant for morphological expression of a Hypertrophic CardioMyopathy (HCM). The authors conclude that epigenetics and environmental factors contribute to the progression of the disease. These factors might include microbial infection, diet or exercise.

Chen et al. (Nature Biotechnology, 2016) reported "A comprehensive screen of 874 genes in 589,306 genomes led to the identification of 13 adults harbouring mutations for 8 severe Mendelian conditions, with no reported clinical manifestation of the indicated disease". The interpretation was that there was something in their genomes that was buffering the effects of these deleterious mutations. A paradigmatic example in this respect is the mutation that causes the persistence of foetal haemoglobin (HbF) which substantially attenuates beta-hemoglobinopathies.

The report by Repetti et al. suggests that genome identity is not enough! The complexity of our genome is complex ☺