Epigenetic association studies at birth and the origin of lung function development

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Mukherjee and co-workers explore for the first time the association between blood DNA methylation patterns at birth and lung function trajectories from childhood to adulthood. The beneficial implications of this kind of research are promising. https://bit.ly/3qlytda

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Epigenome mechanisms, and in particular DNA methylation, have been suggested to mediate the association between environmental exposures, especially the ones taking place during early life, and later susceptibility to common complex diseases. Epigenome-wide association studies (EWAS) are a widely used approach to identify epigenetic markers associated with exposures, lifestyle factors or phenotypic traits in epidemiological settings [1]. Thanks to them, over the past decades DNA methylation markers have been studied with two main objectives: 1) the identification of biomarkers of exposure and disease risk, progression or response to treatment, that enables precision medicine; and 2) the understanding of disease mechanisms to develop not only pharmacological treatments but also environmental and lifestyle interventions that improve health outcomes (figure 1) [2].