

Deciphering epigenetic changes related to the SARS-CoV-2 pandemic in a genetically informative, longitudinal twin family study:

The TwinLife Epigenetic Change Satellite (TECS) project

Binder, E., Diwald, M., Forstner, A. J., Kandler, C., Nöthen, M.M., Spinath, F.M.



COVID-19 and Epigenetic Change in TECS

- Covid-19 pandemic has brought a lot of change in peoples' day-to-day lives, for example at work, in school, or with childcare. New strains and stressors emerged and those which already existed potentially intensified.
- *TwinLife Epigenetic Change Satellite project (TECS)* analyzes how these experiences have impacted peoples lives and their epigenetic structure.
- To disentangle the link between *experiences of pandemic stress and strain with changes in epigenetic activity* (DNA methylation), the TwinLife team cooperates with the Institute for Human Genetics of the University Hospital Bonn and the Max-Planck Institute for Psychiatry in Munich.

Epigenetic gene regulation

DNA methylation is an epigenetic mechanism, a process regulated by molecules, where gene expression is typically repressed; it is assumed to be altered by environmental risk factors, such as pandemic stress and strain

COVID-19 Supplementary Questionnaire in TwinLife

- *TwinLife* is a multi-disciplinary twin study, that enables to investigate the development of *differences in life chances*.
- Cross-sequential survey design with *4,000 twin families*, a time span of 9 years (2014 to 2023) and *four age cohorts* (early childhood, late childhood, adolescence, early adulthood).
- *Face-to-face interviews* (F2F) and *telephone interviews* (CATI) for *two sub-samples A and B*.
- *Three supplementary surveys* (short: Cov; Summer 2020, Winter 2020 to Spring 2021, Autumn 2021) were conducted. The survey covered the following topics:
 - Health during the COVID-19 pandemic and psychological impairment
 - Socioeconomic changes
 - COVID-19 related behavioral changes
 - Resilience
 - Perceived threats, stress and burdens
 - Evaluation of governmental restrictions

Saliva Samples

- *Three saliva samples of TwinLife panel participants*: The comparison of saliva samples allows to identify changes in DNA methylation.
- The genotyping of the *first saliva sample* has been completed; data for GWAS (Genome Wide Association Studies) and polygenic risk scores are being prepared.
- Collection of the *second saliva sample* is ongoing.
- A *third saliva sample* is planned for the fifth face-to-face interview.
- Genetic information and DNA methylation of the saliva samples is analyzed by the Institute for Human Genetics of the University Hospital Bonn. Statistical analyses in combination with the TwinLife data are expected to start in early/mid 2022.

Research Goals and Objectives

- *Identification of resilient versus risk groups*: Not all individuals will be similarly affected by the pandemic stressors on a symptom level. We will explore whether risk or resilience to specific symptoms (psychological, psychiatry, and medical) are associated with specific epigenetic patterns.
- *Identification of transactions and change patterns over time*: On the long run, the longitudinal design enables an investigation of the dynamic interplay between SARS-CoV-2 associated stressors and epigenetic changes over time and the associated change patterns with their short-term or long-term effects.
- *Identification of moderating factors*: Existing molecular genetic (e.g., polygenic risk scores), constitutional (e.g., physical health), psychological (e.g., personality), socio-demographic (e.g., SES), and social variables (e.g., social support) from individuals and the family captured in TwinLife may moderate the impact of the pandemic stressor on the epigenome.

For more information on the study, visit:

www.twin-life.de/documentation

Data of the *first COVID-19 supplementary survey* (Summer 2020) are available to the research community, doi: 10.4232/1.13747

