Conclusions: Our results indicate several important novel SNPs associated with suicidal ideation when considered in interaction with the effect of childhood adversities. Furthermore, gene-based analyses replicate several genes playing a key role in central nervous system function such as *GRM7* (encoding metabotropic glutamate receptor 7) or previously implicated in association with suicide (*CDH13*) or suicide-related factors such as aggression (*RBFOX1*).
Funding: NAP2022-I-4/2022, K143391, 2019-2.1.7-ERA-NET-2020-00005, TKP2021-EGA-25

Disclosure of Interest: None Declared

EPP0587

Can compassion impact us on a cellular level? Preliminary findings on the effects of a compassion focused intervention on immunological markers and CTRA gene expression

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doi: 10.1192/j.eurpsy.2024.696

Introduction: Addressing mental and physical health problems and promoting wellbeing in educational settings is a global priority. Teachers present a high risk of stress and burnout, which negatively impacts their professional performance as well as their mental and physical health. Compassion-based interventions have been found effective in promoting psychosocial and physiological wellbeing.
Objectives: The current paper presents preliminary findings of the impact of a 6-module Compassionate Mind Training intervention for Teachers (CMT-T) on immunological markers and the Conserved Transcriptional Response to Adversity (CTRA; a gene expression signature that involves a group of 53 genes: pro-inflammatory genes, type I interferon response and genes related to antibody synthesis).
Methods: A pilot non-controlled study was conducted in a sample of public-school teachers in Portugal (n=36). Participants were assessed at 4 time-points: 1) Extended Baseline Control_M0, in order to establish a within-subjects psychological and biophysiological baseline (8 weeks before the start of the CMT-T); 2) Pre-intervention_M1 (8-weeks after M0); 3) Post-intervention_M2 (8-weeks after M1); and 4) Follow-up_M3 (3 months after the CMT-T end). In all assessment moments, participants completed a set of psychological self-report measures and were assessed in immunological and epigenetic biological markers through the collection of blood. After M1, teachers completed the 8-week group CMT-T intervention and given access to its resources and materials. They were instructed to practice daily and incorporate the teachings in their personal and professional lives. All assessments and the CMT-T intervention took place at the schools.
Results: Preliminary data on the impact of CMT-T on Immune Response Profiling revealed that teachers' Natural Killer (i.e., NK) cells were decreased after the CMT-T intervention. In regard to the CTRA gene expression, results showed that type one interferon response genes (e.g., IFI16, IFI27L2, IFITM2, IFITM3, IFITM4P) were decreased after the intervention. In addition, we observed that the gene c-Jun, a pro-inflammatory gene, had a decreased expression after the CMT-T intervention.
Conclusions: These preliminary findings seem to corroborate previous studies involving the type one interferon response, the pro-inflammatory genes and antibody synthesis genes in a signature involving 53 genes previously described as the CTRA gene signature. Furthermore, our results suggest that cultivating compassion using a compassion focused intervention may have a positive impact on markers of the immune system response, associated with how our bodies respond to stress, infection and cancer, as well as, on reducing the expression of genes related to our bodies' response to stress and inflammation.

Disclosure of Interest: None Declared

EPP0588

ASCL1 dysfunction contributes to the pathogenesis of schizophrenia by regulating genes associated with neuronal signature formation and neuroplasticity

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doi: 10.1192/j.eurpsy.2024.697

Introduction: ASCL1 (Achaete-scute homolog 1) is a neuron-specific transcription factor involved in CNS maturation in the mammalian brain. It has been shown to be associated with schizophrenia (SZ), Parkinson's disease, and the development of brain tumors. ASCL1 is expressed in the neuroblastoma cell line SH-SY5Y, which is a widely used model for the study of neurodevelopmental diseases, including SZ.
Objectives: The aim of this work was to study the effect of functional *ASCL1* knockout on the transcriptional landscape of SH-SY5Y cells in undifferentiated and neuron-like phenotypes.
Methods: For ASCL1 deletion, SH-SY5Y was sequentially transduced with two lentiviral vectors. One pLV-rtTA-Cas9-(nls)-pCMV-eGFP-PuroR-T2A-rTetR (derived from pCW-Cas9 and pEGFP-Puro) construct encoded Cas9. Stably transduced lines were selected for 3-5 days on puromycin (2 g/L). The inducibility of Cas9 expression was checked after adding the inducer oxytetracycline to the culture medium. The second construct (based on pLK05-tagRFP) encoded, a pair of guide RNAs targeting the start