articles published within the last ten years were selected, including those with free full-text access, including books and documents, clinical trials, meta-analyses, randomized controlled trials, and systematic reviews. Only articles published in the English language were included in the selection process.

Results: The brain methylome consists of DNA methylation marks at cytosine and guanosine separated by phosphate group (CpG) sites in the brain's genome, which regulate gene expression without altering the DNA sequence. This modification influences cellular processes like gene activity, development, and memory. Dysregulation of gene expression, particularly in the prefrontal cortex (PFC), contributes to schizophrenia's pathophysiology, impacting neurotransmission, myelination, metabolism, and immune signalling.

Histone modifications (acetylation, deacetylation, methylation, phosphorylation) also regulate gene expression, with reduced Histone Deacetylase 2 (HDAC2) expression seen in the dorsolateral PFC of schizophrenia patients. Additionally, microRNAs (miRNAs) and long non-coding RNAs (lncRNAs) are implicated in gene expression dysregulation in schizophrenia, influencing processes like synaptic plasticity and neural differentiation.

Epigenetic changes in peripheral tissues, such as blood and saliva, may serve as biomarkers for schizophrenia.

A comprehensive approach integrates genotyping, epigenotyping, and deep phenotyping to enhance understanding of an individual's health and treatment responses. Early therapeutic interventions may reverse epigenetic changes, improving outcomes. Incorporating molecular endophenotypes and neuroimaging biomarkers aids in identifying schizophrenia subgroups and enhancing treatment predictions. Omics integration (genomics, transcriptomics, proteomics, metabolomics) increases the precision of schizophrenia risk stratification.

There are various advancements in DNA methylation analysis include high density CpG array system (850,000 sites), whole genome bisulphite sequencing (better resolution but costly), targeted bisulphite sequencing (cost-effective), and emerging single molecule/nanopore sequencing technologies.

Conclusion: Current research in schizophrenia reveals interactions between genetic, environmental, and epigenetic factors. While significant advancements have been made in understanding the role of DNA methylation, histone modifications, and non-coding RNAs, further studies with larger sample size and more robust structure along with using multi-omic approach are desirable for understanding the disease pathophysiology and to deliver personalized treatment.

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H-MRS Correlates of Deep TMS in Schizophrenia: Insights From a Randomized Sham-Controlled Study on Negative Symptoms

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Aims: Negative symptoms of schizophrenia are disabling and often show inadequate response to antipsychotic treatment. Dysfunction in cortical regions such as the anterior cingulate cortex (ACC) and medial prefrontal cortex (mPFC) has been implicated in these symptoms. While repetitive transcranial magnetic stimulation (rTMS) has shown efficacy, deep transcranial magnetic stimulation (dTMS) offers the advantage of targeting deeper brain structures.

To assess the efficacy of high-frequency dTMS in improving negative symptoms of schizophrenia and to examine its effects as measured by proton magnetic resonance spectroscopy (h-MRS).

Methods: This sham-controlled, double-blind study randomized 46 patients with schizophrenia into active and sham dTMS groups. Participants received 10 sessions of high-frequency (10 Hz) dTMS at 100% of the resting motor threshold using an H7 coil over 2 weeks. Symptom severity was assessed using the Positive and Negative Syndrome for the Assessment of Negative Symptoms (SANS), and Clinical Global Impression (CGI) at baseline, 2 weeks, and 4 weeks post-treatment. h-MRS of the ACC and mPFC was performed at baseline and after 2 weeks of treatment.

Results: A total of 43 patients completed the study. While both groups showed improvement over time, the active dTMS group demonstrated significantly greater improvement in negative symptoms, as reflected by a reduction in SANS scores compared with the sham group ($p=0.003$) and improvement in the negative subscale of PANSS ($p=0.044$). h-MRS analysis revealed a positive correlation between ACC total N-acetylaspartate (tNAA) levels after 2 weeks of treatment and baseline SANS anhedonia subdomain scores.

Conclusion: High-frequency dTMS significantly improves negative symptoms and overall illness severity in schizophrenia. These findings highlight the potential role of dTMS as an adjunctive treatment and suggest that h-MRS may serve as a valuable biomarker for treatment response. Future studies with larger sample sizes are needed to further explore the therapeutic and neurobiological effects of dTMS.

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9-Year Trajectory of Depressive and Anxiety Symptoms in Community – the Hong Kong Mental Morbidity Survey Follow Up Studies

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Aims: Depression and anxiety are common in every community. Appreciation of the long-term trajectories of these symptoms will inform more targeted interventions for reduction of disease burden. We evaluated the 7th and 9th year episode onset and remission rates of common mental disorders (CMD) in participants of the Hong Kong Mental Morbidity Survey (HKMMS) at baseline (2010–2023), who were reassessed at 7th and 9th years follow up.

Methods: The HKMMS and follow up studies were commissioned by the Medical and Health Research Fund in Hong Kong. Baseline study was conducted from 2010–2013 (n=5,719). We reassessed 1,392 subjects at 7th (2019–2021, COVID pandemic) and 9th (2020–2023, late to post-COVID) years. Depression and anxiety symptoms, episode onset and remission rates of CMD were evaluated with the Clinical Interview Schedule – Revised scores at baseline and follow up. Repeated measures ANCOVA computed factors affecting CISR scores over time.