encodes an activator protein of D-amino acid oxidase (DAAO), a D-serine degrading enzyme, has been reported to associate with schizophrenia and bipolar disorders. To further elucidate the relationship between D-serine metabolism and psychiatric disorders, we recently examined by an ELISA technique the contents of G72 protein in plasma and CSF of Japanese patients with schizophrenia, MDD, and healthy controls. Both plasma and CSF G72 protein levels differ among the three diagnostic groups and correlate with age of the participants in each group. These data do not support the previously observed distinct expression in plasma or CSF G72 protein levels in schizophrenia. On the other hand, we found a significant positive correlation between plasma G72 protein levels and the positive score (r=0.275, p=0.043) of the Positive and Negative Syndrome Scale (PANSS), but not the PANSS negative, general psychopathology or total scores, in the patients with schizophrenia. The CSF G72 protein levels did not significantly correlate with each of the four PANSS scores. In MDD, there was no significant association of either of plasma or CSF G72 levels with depression severity scores. To obtain an insight into the significance of the above correlation in schizophrenia, further studies to clarify the molecular and cellular mechanisms and extrinsic factors of the control of G72 expression are required.

PM540
Differential changes on the white matter brain network in ultra-high risk for psychosis and first-episode psychosis
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Abstract
Background: Developmental process of dysconnectivity during transition into psychosis could appropriately be explored at the network level. However, no study has concurrently explored alterations in the white matter (WM) network of the brain among first-episode psychosis (FEP) and its prodromal stage.

Methods: Thirty-seven subjects with ultra-high risk for behavior and neural activity that are testable in humans or animal models to study how neural activity and cognitive behaviors are impacted by disease-related synaptic perturbations.

PM543
Disruption of the balance between excitation and inhibition (E/I balance) is a leading hypothesis for pathophysiologies of neuropsychiatric disorders, e.g. schizophrenia. However, it is poorly understood how synaptic-level E/I disruptions propagate upward to induce behavioral-level cognitive deficits. To link these levels, we have developed a framework for Computational Psychiatry using biophysically-based models of neural circuits to study how neural activity and cognitive behaviors are impacted by disease-related synaptic perturbations.

PM541
Computational modeling of cognitive deficits from cortical circuit dysfunction associated with schizophrenia
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Abstract
Disruption of the balance between excitation and inhibition (E/I balance) is a leading hypothesis for pathophysiologies of neuropsychiatric disorders, e.g. schizophrenia. However, it is poorly understood how synaptic-level E/I disruptions propagate upward to induce behavioral-level cognitive deficits. To link these levels, we have developed a framework for Computational Psychiatry using biophysically-based models of neural circuits to study how neural activity and cognitive behaviors are impacted by disease-related synaptic perturbations.

PM542
Cognitive control deficits in patients with schizophrenia, bipolar I disorder and unaffected first-degree relatives
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Abstract

Objectives: Cognitive control is an adaptive action in a constantly changing environment required the ability to maintain intentions and goals over time and to flexibly switch between these goals in response to significant changes. This study aimed to identify the differences and the profiles of cognitive control deficits and possible candidates as endophenotypes of schizophrenia and bipolar I disorder.

Methods: Five groups were included in this study: remitted patients with schizophrenia (n=42), patients in euthymic states of bipolar I disorder (n=37), unaffected first-degree relatives of probands with schizophrenia (n=35), those with bipolar I disorder (n=29), and healthy controls (n=38) who were matched on age, sex, years of education. A version of the AX-CPT paradigm was used to examine cognitive control. Psychopathology, intelligence, and psychomotor speed were also assessed.

Results: Both patient groups performed worse in BX trial than the other groups (p<0.01). Patients with schizophrenia also showed higher mean error rates in AX trial (p<0.01), and delayed response in all CPT trials than the rest (p<0.01). However, first-degree relatives of both probands did not showed deficits for the accuracy and response time in all trials.

Conclusion: These findings suggest that cognitive control is impaired in schizophrenia and bipolar I disorder with poorer ability of schizophrenia, and the impairments in cognitive control seems less likely to be a possible endophenotype shared both mental disorders.

PM543
A Data Mining Algorithm for Personalized Medicine in Schizophrenia

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Abstract

Background: Despite opportunities provided by genome-wide association studies (GWAS) for personalized medicine, there exists no known method to predict who will or will not benefit from a specific antipsychotic drug. While conventional methods seek to identify significant genes or factors for prediction, this study proposes a data mining algorithm that integrates multiple genes and baseline profiles simultaneously, resulting in a mechanism to directly identify individuals who will response to a specific type of antipsychotic medication.

Methods: The approach included revision of Latent Group Effectiveness Modeling (LGEM). The revised algorithm was applied to the data obtained from the CATIE study. The predictors were either (1) 13 single-nucleotide polymorphisms (SNPs) and 53 baseline variables or (2) 25 SNPs and the same 53 baseline variables, depending on the previous GWAS findings and data availability. The outcome variables were either (1) improvement in the Positive and Negative Syndrome Scale (PANSS) (Yes/No) or (2) completion of phase 1/1A (Yes/No). Each of those four predictor-outcome combinations was tried for each of the five antipsychotic drugs (Perphenazine, Olanzapine, Quetiapine, Risperidone, and Ziprasidone), leading to 20 prediction scenarios in total.

Results: For 18 out of 20 prediction scenarios, all three performance measures were greater than .50 (sensitivity .51–.79, specificity .52–.79, accuracy .52–.74). Notably among several relevant predictions, the model provided a promising prediction for Ziprasidone for the case involving completion of phase 1/1A (Yes/No) predicted by 13 SNPs and 53 baseline variables (sensitivity .75, specificity .74, accuracy .74).

Conclusion: The proposed algorithm simultaneously used both genetic information and baseline profiles to identify which individual person will benefit from a specific antipsychotic drug among the patients with schizophrenia. As this method employs a general algorithm applicable to a variety of diseases and medications, it can be easily adopted in many other clinical practices for personalized medicine.