Protein biomarkers for the prediction of psychosis

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Psychotic disorders are a significant public health problem. Researchers in RCSI have identified a unique plasma proteomic signature in patients in a clinical high-risk group. This has resulted in the development of a blood-based biomarker test which can be used alone or in conjunction with clinical data and has shown excellent performance for predicting transition to first episode psychosis. This test has the potential to contribute to personalised prognosis and stratification strategies in individuals at risk of psychosis.

BACKGROUND

Psychotic disorders are a significant public health problem. The global anti-psychotic drug market is expected to reach $18.5 billion by 2025. Patients in a clinical high-risk (CHR) group typically transition to first episode psychosis (FEP) within 3 years in 16-35% of cases. The early identification of psychosis in such patient cohorts may allow for personalised prognoses, thus leading to improved clinical outcomes. The prediction of individual outcomes, however, is a significant challenge and the accuracy of predictive models based on clinical data alone have been shown to be limited. Although the accuracy of these models can be improved through the incorporation of neuroimaging and neurocognitive data, the development of a blood-based test for predicting psychosis would have the additional advantage of greater accessibility.

VALUE PROPOSITION

Researchers in the Royal College of Surgeons in Ireland have identified a unique plasma proteomic signature in CHR patients. This unique set of proteins can be harnessed as a diagnostic tool for predicting future psychotic disorders in subjects who present in the CHR group. This predictive model based on proteomic biomarkers has the potential to contribute to the personalised prognosis of individuals at risk of psychosis and lead to improved clinical outcomes. Furthermore, the test can be leveraged as a powerful tool in the stratification of patients undergoing clinical trials for new anti-psychotic drugs.

TECHNOLOGY

Using support vector machine learning algorithms, models based on baseline clinical and proteomic data have been developed. In an international study of 133 patients at CHR, this model demonstrated excellent performance for prediction of transition outcome, with the under the receiver operating characteristic curve area (AUC) calculated as 0.95, (Fig. 1). A parsimonious model based on the 10 most predictive proteins accurately predicted transition status in training (AUC, 0.99) and test (AUC, 0.92) data. Furthermore, in a study of 121 adolescents from a general population in the UK, a model using proteomic data at 12 years predicted psychotic experiences at 18 years with an AUC of 0.74.

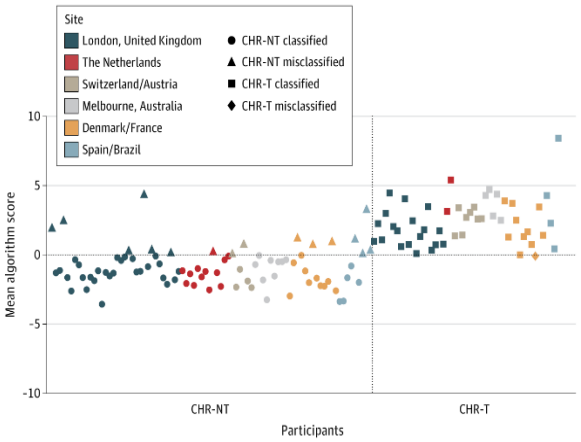

Fig 1. Model for the prediction of transition (T) or non-transition (NT) to psychosis. An algorithm score of greater than 0 is assigned as CHR-T and an algorithm score of less than 0 is assigned as CHR-NT. Note the excellent accuracy in predicting CHR patients that transition to psychosis (top right quadrant).

FEATURES	BENEFITS
Proteomic biomarkers	Can be used alone or in conjunction with clinical data
Excellent prediction for transition to FEP	Contribution to personalised prognoses and stratification strategies
Prediction of psychotic experiences	Predictive performance of adolescents in the general population

TECHNOLOGY READINESS LEVEL

- Patent application filed
- Evaluated in a diagnostic study involving 200+ patients

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