# Biomarkers for antidepressant treatment response

September 20 2012

(Medical Xpress)—Researchers from King's College London's Institute of Psychiatry (IoP) have identified new biomarkers for antidepressant treatment response, an important step towards developing personalised treatments for depression. The study, published today in *Neuropsychopharmacology*, is the first to identify blood biomarkers for antidepressant response in a clinical controlled study and is part of Genome-Based Therapeutic Drugs for Depression (GENDEP) project.

Professor Carmine Pariante, lead author of the study at the IoP at King's says: 'We've identified biomarkers in the blood which could help identify individuals less likely to respond to basic antidepressant treatment. This is a small study, but the findings are promising. Personalised treatments for depression could help us avoid the current 'trial and error' way of prescribing antidepressant medication.

'The study confirms previous evidence that increased inflammation is part of the mechanism leading to depression, especially to particular forms of depression that are less responsive to antidepressants. The study shows that we could use a blood-based "test" to personalise the treatment of depression. If a patient had high levels of inflammation, they could immediately begin with a more intensive treatment programme, such as combining antidepressants or stepping up the doses.'

Researchers aimed to identify two types of biomarkers: ones which could predict future response to antidepressant treatment (predictors), and others which are targeted by antidepressants and change over the course of treatment (targets).

Within human cells, information from genes is transcribed into m-RNA before the effect is visible as a physical or biochemical characteristic. Previous research has shown that depression interferes with three key biological systems: the glucocorticoid receptor (GR) complex, inflammation levels and neuroplasticity. The researchers therefore monitored how mRNA was produced for 15 specific genes linked to these three systems.

The study involved 74 depressed patients. Their levels of mRNA expression were tested before and after 8 weeks of treatment with either escitalopram (n=38) or nortriptyline (n=36). Escitalopram, a serotonin reuptake inhibitor and nortriptyline, a tricyclic antidepressant, are both commonly prescribed first line antidepressant treatments in the UK.

Individuals who did not respond well to treatment displayed significantly higher levels of three inflammation markers before treatment (IL-1B +33%; MIF +48% and TNF-a +39%), suggesting that these three biomarkers could be used to identify individuals who are least likely to respond to antidepressant treatment.

Individuals who underwent successful antidepressant treatment displayed reduced levels of inflammation (IL-6 -9%) and GR function (FKBP5 -11%) markers and higher levels of neuroplasticity markers (BNDF +48% and VGF +20%). These 'target' markers are different from the 'predictor' markers, suggesting that antidepressants do not adequately target the high levels of inflammation displayed in hard to treat individuals.

Professor Pariante adds: 'Additionally, these findings provide novel mechanistic insight into mRNA gene expression changes associated with antidepressant response which is likely to generate new ideas for novel and more effective antidepressants.'

**More information:** Cattaneo, A et al. 'Candidate gene expression profile associated with antidepressants response in the GENDEP study: differentiating between baseline "predictors" and longitudinal "targets"' *Neuropsychopharmacology* (19th September) doi: 10.1038/npp.2012.191

Provided by King's College London