

Poor diagnosis and access to health facilities still hamper progress in this field in Zimbabwe as victims of mental illness are neglected and/or stigmatised by communities. There is therefore need to make communities aware of the disease and to instil healthcare seeking behaviour in patients and relatives of affected individuals.

Research to find if there are any predictive genetic markers for risk of mental illness have been going on for many years. Genome Wide Association studies (GWAS) have now shown a significant heritability and coheritabilities of mental illnesses (Fig 2, Cross-Disorder Group of the Psychiatric Genomics Consortium, 2013). Whilst the heritability has been associated with numerous genes, hence polygenetic (U Demkow and T Wolańczyk.2017), some genetic markers have shown both strong association and prediction of several mental illnesses. The rs2535629 is one such SNP and is located in an intron of *ITIH3*, a domain of a protease inhibitor. The rs2535629 was recently shown to be significantly associated with multiple mental disorders: autism-spectrum disorders, attention deficit hyperactivity disorder, bipolar disorder, depression, schizophrenia, where A is the risk allele. However, the causative gene has not yet been determined since the SNP is in linkage disequilibrium with more than 30 genes in the surrounding 1Mb region (<https://www.snpedia.com/index.php/>).

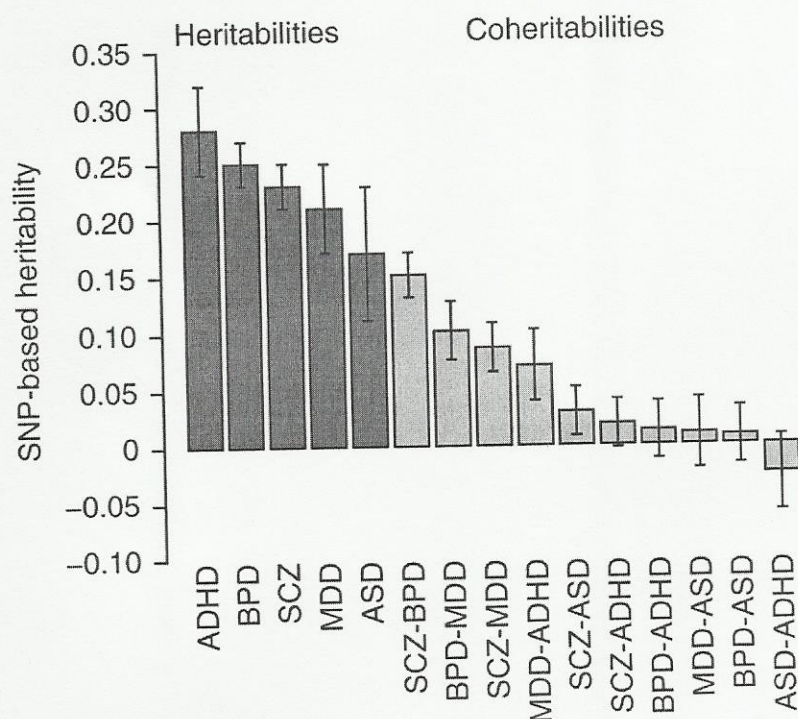


Fig 2: Evidence for genome-wide pleiotropy between psychiatric disorders. Proportion of variance in liability (SNP-based heritability) and proportion of covariance in liability between disorder (SNP-based coheritability) for five major psychiatric disorders. The 95% error bars represent the estimates  $\pm 1.96$  s.e. SCZ, schizophrenia; MDD, major depressive disorder; BPD, bipolar disorder.

A preliminary survey by the St Faith Science team on the burden of mental health in the Madetere community in Rusape found that over 50 cases of potential victims of various form of mental health. The survey also identified two family with 4 and 5 members respectively afflicted by mental health.

This study therefore aims to systematically evaluate the burden of. Mental health in the Madetere family and evaluate the possible role of genetic factors in risk for the diseases at population level and in the two identified families.