The problem with the genetics of psychosis at the present time as everyone recognizes is that there are many false positives in the literature, and no criteria for distinguishing a true positives from the background of noise. It may be as many believe that there are multiple genes of small effect. If so it is surely now apparent that they must be very small and very many if, and this is the crucial assumption, the relevant variation is in the DNA sequence. But there is an alternative, and that is that the genetic variation is either in part or even in toto epigenetic. In that case a major genetic defect might have escaped the systematic genome scan that have been conducted, and now the association studies.

This paper is significant because it reports a negative finding, but also because it illustrates the way in which systematic and careful epigenetic investigations can be conducted. The authors started from a plausible hypothesis, and have effectively eliminated it. In the course of doing this they have spelt out a paradigm that can be applied to other candidate genes and other epigenetic mechanisms. That is progress.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

none.