ADVISORY COMMITTEE ON RELEASES TO THE ENVIRONMENT

Advice on the implications of results in a Defra-funded project: 'non-target effects of transgenic crop plants resistant to virus diseases'

17th December, 2005

Background:

This research project considered the effects of cauliflower mosaic virus (CaMV) and turnip mosaic virus (TuMV) infection (singly and in combination) on transgene expression, viral titer and disease symptoms in oilseed rape (*Brassica napus*) and pakchoi (*Brassica rapa*). Some of the transgene DNA (genes and elements regulating their expression) inserted into these GM lines was derived from TuMV and CaMV (i.e. there was 'homology' between the transgene and the genetic material in the infecting virus), whilst other genes and regulatory elements were isolated from organisms other than TuMV and CaMV. The transgenes in these GM pakchoi and oilseed rape plants did not confer resistance to CaMV or TuMV infection.

The researchers reported finding increases as well as decreases in the expression of transgenes as a result of virus infection. In some cases, this was attributed to homology between genetic material transformed into the GM plants and the infecting virus. In other cases (that resulted in increases in transgene expression), there was no homology between the virus and the genetic material inserted into the plants.

ACRE was asked to advise on whether the results of this project add to or alter the current understanding of the effects of virus infection on transgene expression in GM crops, and whether there are any implications for environmental risk assessments.

Advice:

We advise that this research does not alter or add to current understanding of changes in transgene expression as a result of virus infection. Gene expression varies temporally and spatially in plant tissues according to environmental conditions (including environmental stresses such as virus infections) and on the developmental state of the plant. This is typical of plant genes in general, it is not unique to transgenes. The study illustrates this by showing that the expression levels of two native plant genes (which had been included in the study for control purposes) were altered in response to virus infection.

Suppression/silencing of gene expression as a consequence of homology between the genetic information within and between genomes (in this case, between the genome of the infecting virus and transgenes in the GM plants) is well documented. The results of this research do not add to the understanding of this phenomenon.

ACRE applies the knowledge that transgene expression can increase or decrease in response to changing conditions on a case by case basis. In assessing the potential risk posed by a GMO, we routinely consider whether altered expression of a particular transgene or changes in the amount of protein that it encodes, could have implications for the safety of the GMO.