Genetically Modified Crops and Soil

Introduction

Genetically modified (GM) crops pose a significant threat to the environment through pollution by GM pollen and the consequent flow of modified genes into the wider plant community. However, GM crops may also pose hazards to the ecology of soil. This briefing identifies four main areas of concern:

- changes in agrochemical usage on GM crops, with knock-on implications for soil microbes
- genetic contamination of the soil and associated micro-organisms as a result of horizontal gene transfer
- changes to the soil ecosystem through the changed characteristics of GM plants
- soil contamination through GM seeds remaining in the soil after harvest

It also highlights the current evidence that GM technology poses unacceptable risks to the health and fertility of the soil - one of our most precious natural resources.

About soil

Soil is often casually regarded as inert but in fact consists of a vast array of microscopic bacteria and fungi operating within a matrix of nutrients, minerals, plant material, water and air pockets. This living component is central to nutrient cycling and the health and fertility of the soil, protecting plants from disease and helping them to obtain nutrients. Scientists can only identify a fraction of soil organisms[i] and know even less about their life cycles or how this fits in to the total ecosystem.

Healthy and fertile soils will always be central to food production but we have not treated this vital resource with the respect it deserves. The health of the soil may be deteriorating in areas where intensive arable farming has been carried out over decades[ii]. And the implications for an unhealthy soil are significant; Dick Thompson of the Soil Survey and Land Research Centre at Silsoe Bedfordshire has said that: *"If you take the living component out of soil, it's a bit like switching the lights off in a factory. Everything comes to a grinding halt"*[iii].

Just as we are becoming aware of the damage intensive agriculture may be inflicting on soil ecosystems we have begun to toy with another potential danger. GM crops may pose many new threats to the living component of the soil and we are currently incapable of assessing or understanding the full magnitude of these impacts.

Changes in Agro-chemical Usage

The use of GM crops will mean new regimes of herbicide and pesticide usage and this could potentially impact on soil health. For example, the crops being used in the current farm-scale trials are resistant to the herbicide glufosinate but according to one report our knowledge of the effects of this product on soil microflora is "extremely limited"[iv].

The same research concluded that glufosinate was inhibitory to soil fungi and bacteria at realistic field rates of application. For agricultural soils, the chemical completely suppressed the activity of 40% of soil bacteria and 20% of soil fungi.

The current farm scale trials are not proposing to study the impacts of cultivating GM crops on soil microbes.

Horizontal Gene Transfer and Soil Contamination

GM crops may have major impacts on the genetic content of the soil. Through processes that are poorly understood, bacteria and fungi are capable of capturing and using genetic material from their surroundings (for example, from decaying plant matter or micro-organisms) or from other organisms. This is known as **horizontal gene transfer**.

Bacteria show a particular aptitude for horizontal gene transfer (which may be an important evolutionary mechanism) but, until quite recently, the probability of bacteria capturing genetic material from GM plants had been dismissed as negligible[v]. This inference was based on a small number of experimental studies[vi], and is reflected in the current risk assessments of horizontal gene transfer from GM crops.

This lack of information on the behaviour of soil micro-organisms means that the extent and significance of horizontal gene transfer from plants to bacteria[vii] in the field is difficult to assess. Successful horizontal gene transfer is also likely to be highly dependent on environmental conditions[viii] that vary widely in the field. The usefulness of the novel DNA to microbes will also depend on selection pressures within the soil ecosystem which are poorly understood.

Significant proportions of genetically engineered material from decaying GM plants have been shown to persist in the field for several months[ix]. Recently published material reports that isolated genetic material from GM sugar beet has been detected in soil samples for up to six months, and in one sample for up to two years under field conditions[x]. Naked DNA may be protected from degradation by adsorption to soil particles[xi xii] and this would enable bacteria to then take up the DNA[xiii xiv]. The ability of soil micro-organisms to use this genetic material and pass on GM traits to the wider microbial population is worrying because no-one can predict the long term impacts on poorly understood (yet vitally important) ecosystems.

Direct verification that GM DNA can be taken up by soil bacteria has become available recently[xv]. A gene conferring resistance to several antibiotics, including kanamycin, was genetically engineered into sugar beet. It was found that soil bacteria were able to take up the gene from purified sugar beet DNA as well as from liquefied samples of whole sugar beet. These bacteria became resistant to kanamycin, confirming that there had been integration and utilisation of the engineered gene by the bacteria. However, there appears to be a need for some similarity between the DNA taken up and that of the host organism for this to occur. Some of the bacteria also took up additional sugarbeet DNA (i.e. DNA that was not part of the antibiotic resistance gene).

Other researchers have shown that bacteria carrying a defective gene for kanamycin resistance can replace the defective portion of the gene by acquiring genetically engineered material from potato, sugar beet, tobacco and oilseed rape[xvi]. Horizontal gene transfer has also been reported in plant-associated fungi[xvii xviii xix].

The risk of horizontal gene transfer is of particular concern at the laboratory plant-transformation stage itself. Research from the Scottish Crop Research Institute has shown that the vector *Agrobacterium tumefaciens* used to convey the novel gene into a target species is not destroyed by standard laboratory treatments of the GM plant tissues with antibiotics. In fact, the remaining viable GM bacterial populations within cultures and shoot material have been shown to remain capable of further transformation for at least five months after the laboratory transformation of plant tissues.[xx] The implication of this is that there is serious potential for these GM bacteria to transform other organisms present in soil either within the laboratory environment or following the GM plants' release into another environment such as a greenhouse or field. The specific concern in this instance is not therefore the escape of pollen, but of contamination of soil and the risk of transformation of non-target bacterial and plant species.

There are no procedures for recalling genetic material back from the soil once it is introduced and no techniques for predicting likely impacts. As Professor Steve Jones, a geneticist at the University of London, puts it: *"Exposing genes to nature is to expose them to evolution and evolution has no designer. It is impossible to know what it is going to do next"*[xxi].

It could be argued that the GM crops are often only using genes derived from soil bacteria in the first place, so that the genes are 'going home'. But this ignores our very limited knowledge of evolutionary pathways and whether the prospect of horizontal gene transfer from plant DNA gets round existing barriers to gene movement. As the UK Advisory Committee on Novel Foods and Processes (commenting on a Monsanto application for marketing consent for GM crops containing antibiotic resistance genes) said:

"In the production of novel foods or the exploitation of novel processes, we open opportunities for microbial evolution that would not otherwise exist. The production of large numbers of crop plants increases enormously the biomass of resistance genes. We cannot predict what the effect of such amplification will be....It is considered that the growth and use of transgenic plants [containing a particular gene] will increase significantly the number of resistance genes in the environment and could create new opportunities for this gene to spread to microbes that would not normally encounter this [gene]"[xxii]

It has also been reported that genetically engineered micro-organisms can cause a variety of changes in different soil habitats including increased enzymatic activity, increased culture respiration rates and, in some cases, the loss of a fungal component from the soil[xxiii].

Direct impacts of GM plants on soil

GM crops can have a direct impact on the soil in addition to genetic contamination through horizontal gene transfer. Alterations in the rates or processes of decay of plant material could have a tremendous impact on the proper functioning of nutrient recycling, and thus on the soil ecosystem as a whole. Evidence for this concern exists: leaves from cotton genetically engineered to produce Bt-toxin have been found to decompose more rapidly, releasing nutrients to soil micro-organisms more quickly than ordinary leaves[xxiv]. Control experiments showed that it was not the presence of the Bt toxin that made the difference, but an unexpected side effect of the genetic modification itself.

Recent studies of bacterial communities associated with plant root systems have found consistent differences in the types of bacteria associated with GM plants compared to the untransformed parent plants and the changes appear dependent on the nature of the genetic modification[xxv].

A report published in *Nature* has found that some GM Bt maize varieties can release the activated GM Bt toxin through their roots where it binds with soil particles and persists in the soil. The GM Bt toxin remains toxic to some soil insects for very long periods.[xxvi]

The implications of these findings are largely unknown but could be enormous. Bt comes from a common soil bacterium. GM Bt crops significantly enhance the quantity of a particular toxin in soil. The impact of this increase on soil microbial diversity and activity is completely unknown. Further, the GM Bt toxin produced by the plant is not identical to the naturally occurring Bt. What the impacts on other soil micro-organisms and soil microbial communities are, or how in turn that impact affects nutrient cycling and uptake or microbial biocontrol of soil pathogens, is simply not known.

Contamination through seeds

Seeds from GM crops can cause contamination simply through their persistence in the general store of ungerminated seeds that every soil contains (known as the 'seed bank'). Seeds from previous GM crops can lie dormant in the soil for many years only to re-emerge as so-called 'volunteers' in another growing season. Examples already exist of GM volunteers appearing on sites where trials have been held: potato volunteers following a UK GM crop trial were reported in the newsletter of the Advisory Committee on Releases to the Environment[xxvii].

Seed characteristics are often complex combinations of genetic and environmental influences. Genetic modifications to seed-oil properties may have significant effects on the balance of crop and wild plants in the soil because they change the composition of the energy and carbon stores used during dormancy and early seedling growth[xxviii].

Experiments have been carried out to determine whether GM oilseed rape (high-stearate and high-laurate canola) and a hybrid of the high-laurate canola with Brassica rapa (a wild relative) have altered seed dormancy and germination characteristics. The results showed that seed dormancy and germination were unpredictable and that the GM line would be more capable of forming a larger and more persistent seed bank than the non-GM parent despite earlier studies suggesting a lower risk of this. The germination characteristics allowed for a greater risk of gene flow to wild relatives. Several high-stearate and high-laurate GM oilseed rape lines have been released in a number of field trials in the UK[xxix], prior to the publication of this research in 1998.

Conclusion

The effects of GM crops on soil functioning are poorly studied yet the implications for soil health and fertility may be enormous. GM technology may substantially alter the genetic make-up of soil micro-organisms and will have impacts on the delicate balance of soil ecology. The long term implications for farmers wishing to stay GM-free, and indeed on food production as a whole, are unknowable. Greenpeace believes that given the high level of potential risk associated with GM technology there should be no environmental releases and that any sites previously used to grow GM crops should be logged on a register of contaminated land to avoid accidental contamination in the future.

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[i] Pace, N.R. (1997). A molecular view of microbial diversity and the biosphere. Science 276, 734-740; Hugenholtz, P. and Pace N.R. (1996). Identifying microbial diversity in the natural environment: a molecular phylogenetic approach. Trends Biotechnol. 14, 190-197.
[ii] BBC Online news (2000). Soil problems prompt farming ban call, 10 January, 2000. http:\\news2.thls.bbc.co.uk/hi/english/sci/tech/newsid%5F594000/594695.stm
[iii] BBC Online news, ibid
[iv] I.Ahmad and D. Malloch (1995). Interaction of soil microflora with the bioherbicide phosphinothricin. Agriculture, Ecosystems and Environment 54 pp 165-174. Elsevier Science.
[v] See for example, OECD (1992) Safety Considerations for Biotechnology, Organisation for Economic Cooperation and Development, Paris.
[vi] Nielsen K.M., Bones, A.M., Smalla, K., and van Elsas, J.D. (1998) FEMS Microbiology Reviews 22:79-103
[vii] Gebhard F. and Smalla,K., (1999) FEMS Microbiology Ecology 28:261-272
[viii] See for example Sikorski, J., Graupner, S., Lorentz, M.G. and Wackernagel, W. (1998) Microbiology 144, p.569-576
[ix] Widmer, F, Seidler, R.J., Donegan, K.K. and Reed, G.L. (1997) Molecular Ecology,6(1):1-7
[x] Gebhard, F. and Smalla,K. (1999) FEMS Microbiology Ecology 28:261-272
[xi] Paget, E. and Simonet P., (1994) FEMS Microbial Ecology 15, p.109-118
[xii] For example: Widmer, F., Seidler, R.J., and Watrud L.S. (1996) Molecular Ecology 5(5):603-613
[xiii] Gallori, E., Bazzicalupo, Dal Canto, L., Fani, R., Nannipieri, P., Vettori, C. and Stotzky G. (1994) Microbiology Ecology, 15, p.119-126
[xiv] Sikorski et al, (1998) ibid
[xv] Gebhard and Smalla ,K. (1998) Applied. & Environmental Microbiology 64(4):1550-1554
[xvi] de Vries, J. and Wackernagel, W. (1998) Molecular and General Genetics 257:606-613
[xvii] Bryngelsson,T., (1988) Physiology and Molecular Plant Pathology 33:163-171
[xviii] Buhariwalla,H., (1995) Physiology and Molecular Plant Pathology 47:95-101
[xix] Hoffmann T., (1994) Current Genetics 27:70-76
[xx] Barrett, Carol et al (1997) 'A risk assessment study of plant genetic transformation using *Agrobacterium* and implications for analysis of transgenic plants' *Plant Cell, Tissue and Organ Culture* 47: 135-144
[xxi] As quoted on BBC2 'Leviathan' programme, April 1999
[xxii] Advisory Committee on Novel Foods and Processes, 1999. Opinion on use of aad gene in Monsanto sugar beet. ACNFP, February 1999 [cite web address]
[xxiii] Reviewed in: Doyle,JD., et al, (1995) Advances in Applied Microbiology vol 40, Academic Press, San Diego CA. 237-287
[xxiv] Donegan K.K., Palm, C.J., Fieland, V.J., Porteous L.A., Giano, L.M., Schaller, D.L., Bucao, L.Q. and Seidler, R.J. (1995), Appl. Soil Ecol. 2:111-124
[xxv] DiGiovanni, G.D., Watrud, L.S., Seidler, R.J., Widmer, F. (1999) Microbial Ecology 37(2) p.129-139
[xxvi] Saxena, Flores and Stotsky (1999) 'Insecticidal toxin in root exudates from Bt corn' *Nature* 02.12.99 http://www.nature.com/server-java/Propub/nature/402480A Analysis of implications taken from e-mail from Charles Benbrook.
[xxvii] Advisory Committee on Releases to the Environment Newsletter. December 1997. Issue 8. p3
[xxviii] Randal,L., (1998) Ecological Applications 8(4) p.1180-1195
[xxix] for example: DETR register numbers 95/R2/6, 96/R14/5, 97/R28/3