

SIXTH FRAMEWORK PROGRAMME
THEMATIC PRIORITY 5
FOOD QUALITY AND SAFETY



ResistVir

Co-ordination of Research on genetic resistance to plant Pathogenic Virus,
and their Vectors in European Crops

Project number: FOOD-CT-2005-006961

Co-ordination Action

***Deliverable 2: Report of activities of ResistVir partners based
on the first co-ordination event.***

Due date of deliverable: **M1**

Actual submission date: **M7**

Start date of the project: **February 1st, 2005**

Duration: **48 months**

Organisation name of lead contractor: **JIC**

Project co-funded by the European Commission within the sixth Framework programme (2002-2006)	
Dissemination Level	
PU public	PU
PP Restricted to other programme participants (including the Commission Services)	
RE Restricted to a group specified by the consortium (including the Commission services)	
CO Confidential, only for members of the consortium (including the Commission services)	

Background

In the field, virus infection of crops is the sum outcome of a series of biological processes that involve three-way interactions between the virus, its transmission vector and the host plant. All of these in turn will be influenced by their respective population structures and environmental factors. Each of these interactions provides potential target points for intervention to achieve resistance to virus infection. Within the Co-ordinated Action programme, ResistVir, greatest attention is given to researching the nature and development of virus resistance in the plant, although there are also important contributions relating to the changing of vector (mostly aphid and whitefly) feeding behaviour and the nature of the insect-virus relationship. Within host plants, two classes of resistance may be effective, innate (or constitutive) resistance and induced resistance. Within the former class the fundamental and universal process of RNA silencing is active, whereby viral RNAs are targeted by a sequence homology-dependent RNA degradation mechanism. However, a second form of innate resistance lies in the recent identification of host factors necessary for virus replication and the potential for these to exist as allelic variants that fail to support infection. Induced resistance depends upon the molecular recognition of a virus-specific product (usually protein) and the activation of a signal transduction pathway that leads to the restriction of virus spread in the plant. This form of resistance is usually, but not always, accompanied by the death of host cells, the so called 'hypersensitive response' or 'HR'. Deeper understanding of all these resistance processes offers the opportunity to harness their potential for improvement and predictive deployment to tackle significant virus problems in crop plants.

Targets for new understanding

The three-way virus-vector-host interactions are being studied with respect to virus epidemiology (1), and virus evolution, including studies of the structure of virus populations (2). These studies are important in determining the nature of the pathogenic threat to crop plants and the durability of existing and novel resistances that are to be deployed. These studies are supported within the Resistvir consortium by the extensive and widespread expertise in virus detection and diagnosis.

RNA silencing is an extremely powerful innate antiviral mechanism. Within ResistVir, a number of groups are attempting to dissect the underlying molecular processes (3) by studying the role of RNA silencing within uninfected plants and by studying the way viruses have evolved to minimise the consequences of this antiviral process (4). The potential of this knowledge has already been realised in the development of transgenic strategies for overcoming virus infection (see below) but refinement and optimisation will lead to second and third generation improvements.

The importance of compatibility factors as potential sources of resistances has recently been realised through the characterisation of natural recessive resistance genes (5). Curiously,

these have universally identified translation initiation factors (e.g. *eIF4E*) as genes that can exist as mutant alleles incapable of supporting infection, although additional genetic determinants will doubtlessly be identified in the future. Detailed knowledge of the molecular basis of the molecular interactions between these host gene products and virus-specific components will allow this knowledge to be converted into predictive strategies (see below).

Induced resistance (e.g. the HR) against viruses relies upon genetic and molecular signalling pathways similar to, but not identical to, those effective against bacteria and fungi. These resistances, typically the function of dominant resistance genes, are being studied with respect to the nature of the signalling pathways (6) and the ways in which they may be specifically and generically developed to provide pathogen resistance.

Collectively, these fundamental studies are providing the foundations for the development of crops with improved virus resistance. Much of the work is carried out with model plant species (e.g. *Arabidopsis*) that builds upon genomic and genetic resources available to the global scientific community. This establishes the scientific principles for translation into crop species to tackle virus disease problems.

Targets for intervention and resistance delivery

Current activities within ResistVir cover many of the major virus diseases affecting EU crop species. Those mentioned within the posters and literature available for the ResistVir kick-off meeting include:

- **Cereals and grasses** variously infected by *Barley yellow dwarf virus*, *Barley mild mosaic virus*, *Barley yellow mosaic virus*, *Soilborne wheat mosaic virus*, *Wheat spindle streak mosaic virus*, *Wheat dwarf virus*, *Cocksfoot streak virus*, *Ryegrass mosaic virus* and *Festuca necrosis virus* (7).
- **Solanaceous crops** (tomato, potato, pepper, tobacco) are studied widely, with members investigating *Tobacco ringspot virus*, *Tobacco rattle virus*, *Tomato spotted wilt virus* (TSWV), *Cucumber mosaic virus* (CMV), *Tobacco necrosis virus*, *Tomato mosaic virus*, *Tobacco mosaic virus*, *Tomato yellow leaf curl virus*, *Tomato yellow leaf curl severe virus*, *Potato leaf roll virus*, *Potato virus Y* and *Potato virus X* infections (8).
- **Cucurbit** susceptibility to CMV, *Melon necrotic spot virus* and *Zucchini yellow mosaic virus* is being researched (9).
- **Sugar beet** viruses under study include *Beet necrotic yellow vein virus*, *Beet mild yellowing virus* and *Beet yellows virus* (10)
- For **ornamentals**, the major infection under investigation by members of the consortium is TSWV (11)
- **Grapevines** suffer mainly from *Grapevine fanleaf virus* and several institutes consider the approaches appropriate for protection against this disease (12)
- **Fruit** viruses are studied by many of the consortium members. The varied distribution of the crops determines the hosts and viruses studied:

Citrus fruits are mainly affected by *Citrus tristeza virus* (13) whilst for the soft fruits (e.g. raspberries, cherries and blackcurrants) *Raspberry bushy dwarf virus*, *Prunus necrotic ringspot virus* (PNRV), *Prune dwarf virus* (PDV), *Blackcurrant reversion virus* and the phytoplasma causing full blossom disease are noted as particularly important (14). For the pome fruits, *Apple stem pitting virus* and *Apple chlorotic leaf spot virus* are studied (15). The large number of laboratories involved in the production of plants resistant to *Plum pox virus* reflects its importance to the plum industry although PNRV, PDV and *Apple mosaic virus* are also under study (16). Of the other stonefruits studied (peach, apricot and nectarines), only a viroid (*Peach latent mosaic viroid*) is reported as being under study (17).

Despite the Europe-wide cultivation of rape (*Brassica napus*) only three groups were mentioned as investigating its infection by a number of viruses (*Turnip yellows virus*, *Turnip mosaic virus*, *Cauliflower mosaic virus* and *Beet western yellows virus*) (18).

Many of these targets have been identified as current problems by EU industries. However, it is important to recognise that international movement of agricultural products, changes in agricultural practice and the impact of climate change will create new challenges for which the science base should be prepared.

The current uncertainty and concern over the acceptability of transgene technology for the European food market has led to the assessment of the risk involved in deploying these crops (19). In the longer term, the strategy of choice for the delivery of new genetic resistance would be the breeding of natural resistance genes into commercial crops. However, in some cases no naturally resistant lines exist with the available germplasm and in many cases introgression of new genes from outcrossed parents is slow to deliver a commercial product. This is especially notable for woody species. In such cases, the options are limited to a continuation of control through agricultural management practices or to a change of view on the acceptability of modern transgenic technologies to achieve sustainable control of virus diseases. Our expanding knowledge of the principles of RNA silencing is opening new doors on the development of transgenic resistance that could be both rapid and effective in combating either single or multiple virus pathogens with a single transgene. For this reason, significant effort within ResistVir is devoted to the development of strategies for deploying of RNA silencing-based resistance (20). This is complemented by an advancing capability in tissue culture technologies underpinning genetic transformation (21). Notwithstanding these factors, natural resistance remains a central component with the ResistVir activities. In cases where the precise genetic basis of resistance is not known, a key output from this effort is the identification of new resistant germplasm and the identification of linked markers (22). These constitute short-term deliverables to the industry. The natural resistance may relate to resistance to virus replication (23) or resistance to the fungal- or insect-vector (24). The latter supplements a growing understanding of the chemical basis of insect attraction and repulsion to plant hosts (25).

Concluding comments

Clearly from the limited data available at the kick-off meeting it has been possible only to provide a snapshot of the studies being undertaken by consortium members. However, in this report we have identified technological, scientific and discipline-based groupings that should stimulate a sharing of ideas, concepts, techniques and materials within ResistVir. To establish a significant and co-ordinated core competence in the delivery of virus resistance to EU agriculture, it will be necessary to convert our understanding of molecular and genetic mechanisms to operational processes, and to translate principles established in model plant systems to crop improvement. It will also be necessary to identify the limitations for the deployment of natural virus resistance and to seek political, legislative and public understanding and approval for the benefits of virus resistant transgenic plants.

Partners involved in the referenced activities mentioned in the text (based on abstracts submitted in the 1st co-ordination event and on institute profiles in Annex1):

Reference	Partners
1.	3, 4, 11, 13, 17, 18, 19, 29, 30, 35, 41, 42, 44, 45
2.	17, 44, 45, 49
3.	10, 21, 27, 37, 38, 40, 42, 43, 45, 46, 47, 48
4.	10, 11, 37, 40, 43, 45
5.	36, 39a,b, 40
6.	31, 47
7.	3, 22, 26, 32, 40, 42
8.	2, 3, 13, 15, 16, 18, 22, 26, 31, 33, 34, 35, 39, 40, 42, 46, 47
9.	32, 35, 36
10.	24, 26, 29
11.	3, 16
12.	9, 25, 34
13.	2, 18
14.	3, 17, 42
15.	8
16.	3, 13, 17, 32, 33, 34, 35
17.	17, 27
18.	22, 26, 33
19.	42, 44, 47, 49
20.	10, 22, 30, 37, 38, 42, 45, 46, 47, 48
21.	8, 9, 11, 13, 24, 25, 27, 34, 40, 42, 43, 45, 46, 47, 48
22.	15, 21, 24, 25, 26, 32, 38, 39, 40, 42, 47
23.	35, 39, 40, 41
24.	26, 28, 29, 35, 42,
25.	2, 28