Metabolic pathways of the diseased potato

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One of the greatest constraints on food production is the potential for crop losses through pests and diseases. Understanding molecular interactions in diseased cells has therefore provided opportunities not only for academic, curiosity driven research, but also new opportunities for manipulating disease resistance.

Most biologists are familiar with wall charts of metabolic pathways of healthy cells and, indeed, this information can now be accessed on the internet at a number of different locations (for example, http://expasy.hcuge.ch/cgi-bin/search-biochem-index and http:/www.genome.ad.jp/kegg/metabolism.html). The molecular complexity of the plant's response to

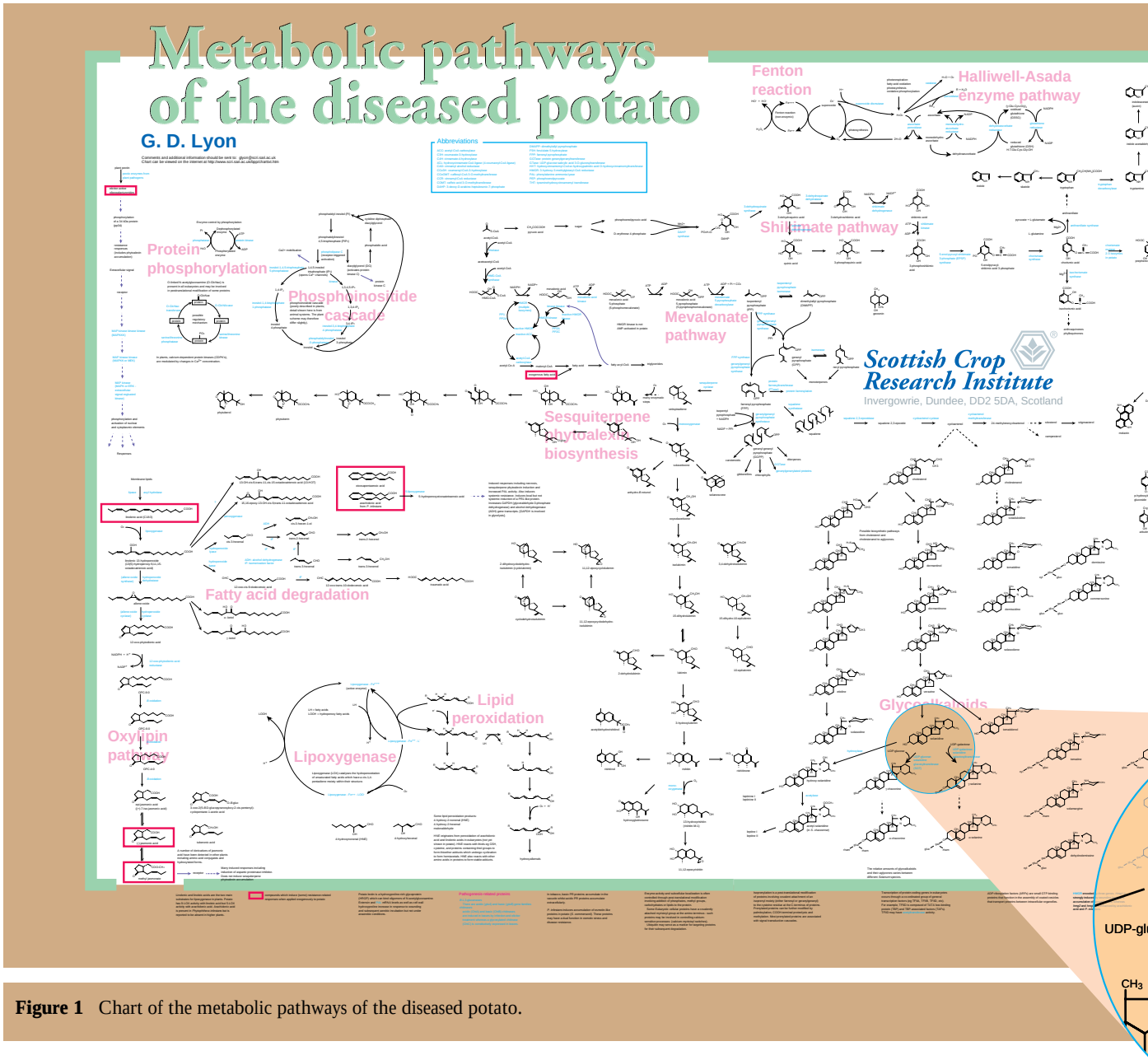
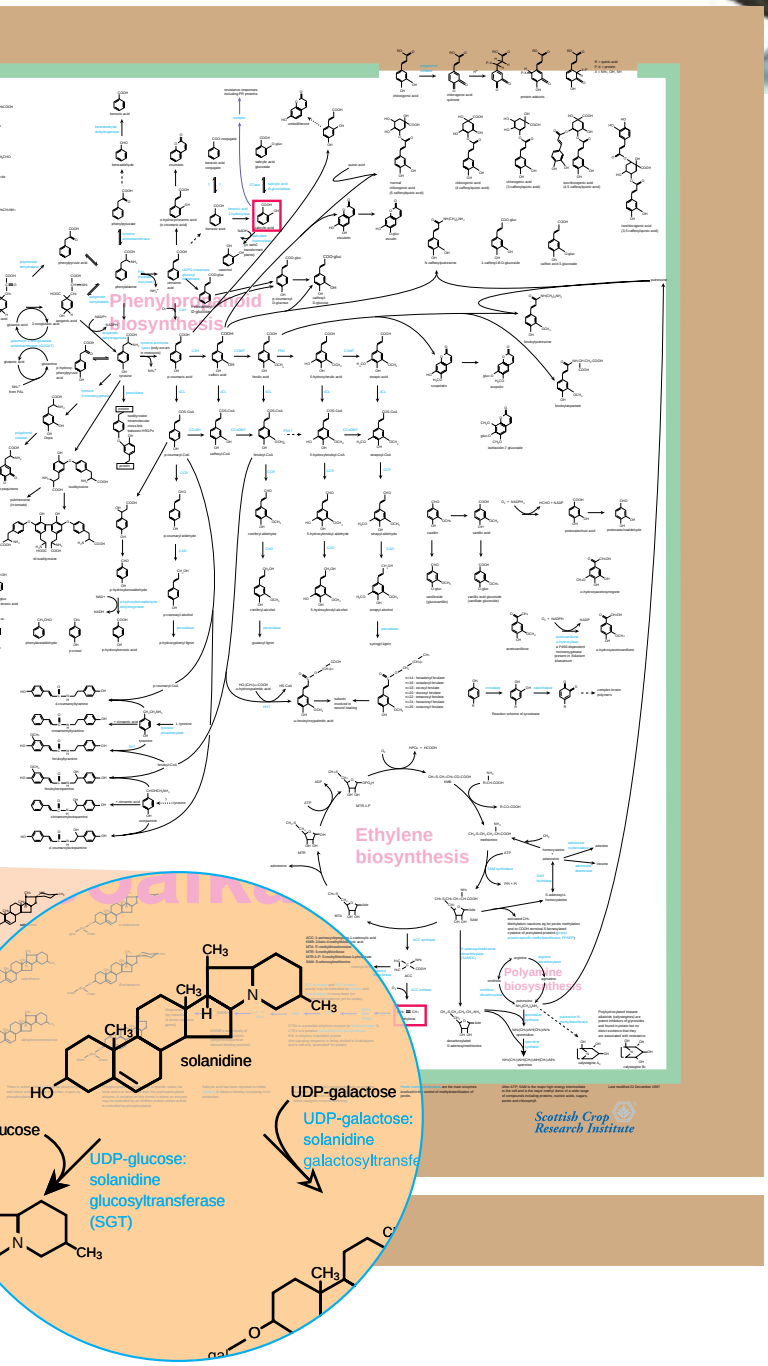


Figure 1 Chart of the metabolic pathways of the diseased potato.

infection has long been known by pathologists working on resistance. The problem for plant pathologists is that the widely published charts on metabolic pathways only refer to healthy cells and do not include secondary metabolic events associated with resistance responses. There is a further complication: whilst some processes of resistance are common between plants belonging to different families, the chemistry of those induced responses varies and therefore it is not possible to provide a single unifying metabolic chart.



However, it is possible to present information on secondary metabolism for a single plant species. Information on secondary metabolism in the diseased potato has been published over many years, most of it associated with infection by *Phytophthora infestans* or *Erwinia carotovora*, or the application of resistance elicitors. Combining information in the format of a metabolic pathways chart[1] has a number of advantages. Not only does it draw attention to the complexity of the plant's response to infection, but it shows some of the responses which may not be so obvious when reading primary publications. It can act as a focus for designing new experiments and clearly highlights those areas where information is lacking. For example, enzymes involved in the biosynthesis of the sesquiterpene phytoalexins have not yet been purified or characterised. This contrasts with the greater knowledge about phenylpropanoid metabolism, although even this is still incomplete. Importantly, there is little firm data on signal transduction pathways in plants in general, even in healthy cells, and hence the chart includes some generalisations about potential signal induction cascades. For example, the MAP kinases and phosphoinositide signalling pathways have been poorly described in plants but are much better described in animal systems.

The chart also emphasises the importance of post-translational modification of proteins through addition of phosphates, methyl groups, carbohydrates or lipids. For example, isoprenylation is a post-translational modification of proteins involving covalent attachment of an isoprenyl moiety (either farnesyl or geranylgeranyl) to the cysteine residue at the C-terminus of proteins. Prenylated proteins can be further

modified by palmitoylation, COOH terminal proteolysis and methylation. Most prenylated proteins are associated with signal transduction cascades. To understand 'resistance' it is therefore not sufficient to just isolate and sequence genes but a knowledge of all the processes in 'cell biology' and how protein function is regulated, is necessary.

There may be some common elements in the manner in which a plant responds to infection but this varies between plant pathogens, suggesting that plant signals can discriminate between different pathogens e.g. not only between fungi and viruses but between biotrophs and necrotrophs, etc. The metabolic pathways chart should therefore be viewed as a potential response to infection; it does not imply that all such processes are, or can be, activated by every pathogen. In addition, not all of the pathways shown will be up-regulated after infection. For example, after infection, glycoalkaloid accumulation is suppressed in favour of sesquiterpene accumulation. Importantly, many enzymes exist as isozymes which may have different intracellular locations and hence may be differentially regulated. For instance, 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR) involved in the mevalonate pathway is encoded by three genes. *Hmg1* is strongly induced by wounding, leading to the accumulation of glycoalkaloids, whereas *hmg2* and *hmg3* are up-regulated by arachidonic acid and *P. infestans*. Such compartmentalisation plays a crucial rôle in enabling the plant to differentially up-regulate gene products to give a different wound- or pathogen-induced response. The sequential expression of ACC synthase genes suggests that they may be controlled by different signal transduction and gene regulatory mechanisms.

With recent work at SCRI on identifying and sequencing resistance-related genes in potatoes[2], and, in consequence, the potential to analyse the signal transduction pathway leading to induced resistance, the production of this metabolic chart is timely. Clearly, the molecular interactions and intracellular signalling responses in animal cells have their analogues in plant cells. With the isolation of signalling genes, there will be increased potential to engineer resistance cascades in order to modify resistance responses. This can only be carried out effectively if the complexity of the plant's responses is understood and the resistance-related pathways integrated into a unified structure. It is clear that plants possess a lot of plasticity in the way that they can react to stress and the environment. Genetic manipulation of response genes has a number of important considerations, not only the primary one in relation to disease resistance, but also the toxicological implications and whether such manipulation can alter the nutritional status of the plant. For example, Laurila *et al*.[3] showed that new glycoalkaloids are present in potatoes derived from a cross between *S. tuberosum* and *S. brevidens* which are not present in either parent. Concepts on plant transformation over the last few years have, of necessity (given the paucity of information available), been on a simplistic basis, suggesting that dramatic changes in resistance can be achieved by insertion (haphazardly within the genome) of a single gene producing greater amounts of an antifungal protein. Once the signalling cascades activated in a resistant plant have been better characterised, we should expect to see much more subtle concepts being considered for engineering increased levels of resistance. Future transformations will therefore involve manipulation of genes involved in signalling, rather than genes associated with the synthesis of antimicrobial proteins.

The chart[1] summarising the metabolic pathways of the diseased potato is nowhere near a complete and full description of the potato's response to infection but it does include much of the information currently available. As we progress from sequencing plant genomes, a knowledge of non-intermediary metabolism will become increasingly important in assigning functionality to genes. Metabolic databases will become important in maximising the impact of genome sequencing projects.

The chart is accessible on the Internet as a Portable Document Format file which can be read using Adobe Acrobat Reader 3.0 and a wall chart printed if access to a large format (e.g. A0) printer is available. Acrobat Reader can be down-loaded free from the Internet. The chart will be up-dated as new information becomes available.

References

[1] Lyon, G.D. (1997). Metabolic pathways of the diseased potato. *http://www.scri.sari.ac.uk/bpp/charttxt.htm*

[2] Avrova, A.O., Birch, P.R.J., Toth, R., Lyon, G.D., Duncan, J.M. (1998). *Proceedings 7th International Congress of Plant Pathology (ICPP98).* (Abstract in press).

[3] Laurila, J., Laakso, I., Valkonen, J.P.T., Hiltunen, R., Pehu, E. (1996). *Plant Science* 118, 145-155.