



Inventions for a Sustainable Development of Agriculture



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Introduction

The Netherlands traditionally has a strong agro-food sector. The post-war development of knowledge was directed towards high-productivity agriculture. While this approach was very successful, it has now become apparent that there is a drawback to this success. Specialization not only leads to economic profit, but also to environmental pressures and encroachment on public spaces. The agro-food sector is running into ecological and social barriers. There is a clear need for a more sustainable development in the sector, that gives attention to not only 'prosperity', but also to 'planet' and 'people'.

TransForum was created to address this challenge. The needed development calls for innovations and new insights. Therefore, TransForum has a double goal: to demonstrate, together with entrepreneurs that there are viable new pathways, and to prove, together with knowledge institutions, that the needed knowledge can be delivered.

We try to deliver these results in a combination of a practice program and a scientific program. The programs are meant to deal with three main obstacles in a route towards sustainable development in agriculture. First, there is a tendency to only search for new potential within your own sector (in business) or discipline (in science). Second, there is a strong bias on the function of agriculture in relation to regional development, blocking new combinations of functions. Third, in almost all explorations the value added is supposed to be in the primary production of the chain. Possibilities further in the chain are overlooked, and 'knowledge about primary production' is not seen as an asset. We try to tackle these obstacles by creating consortia of people from business, knowledge institutions, (local) authorities and societal organizations.

The scientific program is meant to address knowledge questions that arise from the practice projects. To that end a division into five sub themes is developed that reflect different aspects of the innovation process. These themes are: (1) Images of sustainability, (2) Inventions for a sustainable agriculture (3) Organization of Innovation and Transition (4) Mobilization of Sustainable Consumption and (5) Design of an Innovation-Enhancing Environment.

This publication contains a number of commissioned position papers that were helpful to focus the scientific program. However, we feel that the content of these papers deserves broader attention. We hope that after reading them, you will agree.

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Inventions for a Sustainable Development of Agriculture

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These texts are focused on inventions for a sustainable development in agriculture and landscape. Inventions are defined as radical new ideas, perspectives, business models and technologies that hold the potential to trigger a step change in sustainable agricultural and regional development. However, they are initial ideas that may either require further elaboration, further development or further analysis to assess their true potential and before they can become the input around which innovation can be organized. Inventions have in common that they are radically new, that there is limited or no history and that, if successful, they hold the potential for a break through and step change in transition trajectories.

The Innovative Practice program is organized along three Innovation Strategies towards a more sustainable development of agriculture. The strategy Vital Clusters is oriented on new combinations of (parts of) economic activities in clusters thus reducing losses and creating new economic value. The strategy Regional Development is oriented on spatial aspects of intensive (agriculture without land), extensive (land without agriculture) or multifunctional systems. The strategy International Agro Food Networks is oriented on gaining a vital position in international chains. For the scientific theme 'Inventions for a sustainable development of agriculture' a rolling agenda will be developed, based on inventions or breakthroughs which are identified and needed in ongoing Innovative Practice projects underpinned with emerging insights from the external (scientific) world presented in Position Papers. Inventions can involve hardware (tools, products), software (organization models, protocols) as well as orgware (new legislations, and organisational infrastructure).

In order to give focus to this theme Inventions for a Sustainable Development of Agriculture, three Position Papers have been prepared focused on

1. The Potential of Plant Genomics in Breeding and Development of Sustainable Production Chains
2. Utilizing Intrinsic Robustness in Agricultural Production Systems
3. IT Innovatie en nieuwe organisatiestructuren in de Nederlandse bloemensector.

This scientific theme concentrates on the actual construction and development of new tools and products (inventions), directly implicated in sustainable innovation and transition trajectories (new genetic modification applications, new energy saving technologies, new more demand oriented products and production systems, innovative consumption contexts, new organisational models).

The Potential of Plant Genomics in Breeding and Development of Sustainable Production Chains

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1. Background

Dutch agriculture faces new challenges in the coming decade. With a successful history of developing into a significant economic sector with substantial growth in the second half of the twentieth century it has now reached its physical (in terms of the cultivation area), ecological and societal limits.

Its competitive strength diminishes and the strong scientific basis of agricultural research is presently more aimed at developing technological tools than at solving problems identified by the production chain. Transitions are crucial for the Dutch agriculture to remain at the forefront.

The goal of TransForum is to speed up the transition process and to initiate and consolidate a knowledge infrastructure directed more towards the implementation in agricultural and horticultural production chains of the advances and benefits of modern technology. The transition of Dutch agriculture towards a more sustainable agrosector will have to consider societal (people), ecological (planet) and economical (profit) aspects. The TransForum program has three central themes, 1) Vital clusters, 2) Development of rural areas and communities, 3) International networks in agrifood. The instruments of the TransForum program are Integrated Projects (IPs), in which strategies for innovation are to be explored and tested in a concrete practical setting. Their results will be used for deducing general principles for transition management and sustainability strategies. In addition to the IPs, Scientific Projects (WPs) will focus more on in-depth study on specific research questions derived from or linked to IPs. The position papers are meant to be at the intersection of IPs and WPs and will provide the framework for them in certain, well-defined areas.

This position paper on the potential of plant genomics in breeding and development of sustainable production chains will provide A) An inventory of the state-of-the-art in the relevant technologies and societal aspects, B) Potential areas for concrete cases and C) The research agenda giving some examples of ongoing IPs and how they link to other initiatives. The paper gives the framework for new IPs and WPs.

2. Inventory of Scientific Views; Molecular Technology, state-of-the-art

2.1. Forward genetics.

The traditional approach of genetics starts with a phenotype and aims by parent selection, crossing schemes and screening of progeny at unraveling the underlying gene(s) or mutation(s) causing or controlling that trait. Subsequently, the acquired knowledge can be used in the targeted production of desired phenotypes for plant breeding. After identification of the necessary and available genetic variation in a crop a collection of breeding or mutant lines or populations can be built. They represent the crucial basis for forward genetics.

In addition to the naturally occurring mutations, they can also be actively induced by treatment of e.g. seeds with chemical mutagens or radiation. The study of transposable elements (TEs), e.g. in maize) explained a part of the natural variation in some crops, but it also provided a tool to produce new mutations actively. Following the systematic analysis of transposition mechanisms, these natural insertional mutagens could be effectively employed to generate new mutant lines. Because active TEs do not occur in every plant species the deployment spectrum could not be enlarged until protocols for the transfer of genetic material had been developed. With the developments in genetic transformation methods, the maize transposable elements could be introduced in other species and used there for mutation induction or gene tagging by transposition. However, insertional mutagenesis could be done using Agrobacterium mediated transferred DNA (T-DNA), bearing a selectable marker for transformation. This method of T-DNA insertion mutagenesis became popular in Arabidopsis using a non tissue culture transformation approach to effectively generate a vast number of tagged mutant lines. Induced mutations are not only an instrument in forward genetics, where one can identify a visible or measurable phenotype or trait, but also in reverse genetics and functional analysis of sequences or genes.

2.2. Genome sequencing and analysis

Large genome sequencing initiatives have increased since the equipment has been available to handle large amount of DNA sequences with high throughput. The most well-known is the initiative to sequence the entire human genome. However, also in plants entire genomes have been sequenced e.g. from Arabidopsis thaliana, Oryza sativa and from Populus trichocarpa. The cheapest approach for this is whole-genome shotgun sequencing whereby the whole genome of an organism is randomly subcloned as 2-10 kb fragments and sequenced. The gener-

ated sequences are subsequently aligned with each other to generate the complete sequence. However, genome sequences generated in this way are often not complete. A more reliable but more expensive strategy involves the generation of a physical map of the genome prior to sequencing. For this, the genome is broken or digested into smaller parts and cloned into recipient cloning vehicles. Most appropriate for receiving large stretches of DNA are yeast artificial chromosomes (YACs) or bacterial artificial chromosomes (BACs). BAC libraries are the method of choice at the moment. The physical map is subsequently generated by fingerprinting the individual BAC clones, either through restriction enzyme digestion by screening with molecular markers like AFLP's, followed by the selection of BACs which form a minimal tiling path across the genome, i.e. align to form virtual chromosomes. In addition to BAC libraries containing random sequences of genomic DNA the expressed part of the genome can be taken for making a library. The genome contains a lot of non-transcribed DNA, i.e. not coding for any traits or phenotypes. When looking for specific genes, the mRNA population, derived from the actually expressed part of the genome, is a preferred starting point. Using reverse transcriptase cDNA can be prepared from the mRNA population which can be subsequently cloned into a recipient vector system, yielding cDNA libraries. Both types of libraries can be used in sequencing. Preferentially, smaller parts of the cDNA clones rather than the entire cDNAs are used for random cloning and sequencing. The sequence information from these smaller parts, so-called expressed sequence tags (EST), is used for further determination of putative functions. Bioinformatics methods can use the available DNA sequence information which can be analyzed with sophisticated computer software, and can identify open reading frames (ORFs) within the raw sequence data. This allows one to identify putative genes without having to have an idea of the function or role of that gene.

2.3. Reverse genetics

The availability of complete genome sequences and expressed sequence tags (ESTs) provide enormous numbers of genes whose exact functions are unknown but have potential for applications. Though bioinformatics tools can predict putative functions, for further utilization of this knowledge it is imperative to precisely determine the function of these genes using Reverse genetics strategies.

To analyze the expression pattern of a large number of genes together, genomic or cDNA sequences can be spotted in tiny droplets arrayed on glass slides and hybridized. These so-called DNA microarrays or DNA chips can handle thousands of clones in one go. When hybridization is done with two mRNA populations representing two opposing conditions, e.g. exposed and not-exposed to a pathogen, the array will provide information on which particular clones/genes are up- or down-regulated in each of the two situations. Hence, expression of genes is an important instrument in the efforts to isolate genes together with a putative function attributed to them. The analysis of the expression pattern of a gene by measuring mRNA levels

over time and place and comparing it to the variation in observed phenotype helps to confirm the gene function.

To provide a function of a gene based on phenotype mutant alleles of the gene of known sequence can be selected and analyzed. This can be done in a loss-of-function method using a knockout mutant of the particular gene under investigation, either by insertional mutagenesis of the gene, e.g. by T-DNA, or transposing insertion tags, or by silencing the expression in a posttranslational fashion through the generation of RNAi (interference) molecules. Both these methods use transformation to introduce the necessary DNA sequences. Methods for knocking out genes without the use of genetic transformation include the virus induced gene silencing technology (VIGS) or the induction of mutations chemically and using the known sequence information of the gene under investigation in a targeted search for lesions specifically present in the gene-of-interest. This latter method for Targeting Induced Local Lesions In Genomes is also known as TILLING or molecular mutation breeding.

A gain-of-function approach is to use over-expression of a gene, e.g. by introducing a construct into the gene under control of a strong or constitutive promoter to observe a gain in phenotype. Activation tagging is one method that uses an insertional mutagen with a strong enhancer or promoter that can activate the expression of adjacent genes in the genome and display a phenotype that can give a clue to a gene's function. Similarly, genetic transformation can be used to introduce a copy of a gene (natural form or over-expressed) into species or cultivars in which the desired phenotype is absent or present at very low levels. Subsequent production of the newly acquired phenotypes in the GMO is a validation of its function in the new plant that can be applied for plant breeding.

2.4 Molecular Markers

The desire to have genetic markers originates from forward genetics where maps of known and unknown mutants of genes are integrated on a chromosome. However, certain specific traits or phenotypes can only be seen in a relatively late stage of development or cultivation, or only with great difficulty or labour input, or only after exposure to specific (a)biotic stresses. At first, isozymes were used to serve as markers linked to traits; these markers could be used to predict the presence of the desired trait prior to visualization of the actual phenotype. The biochemical markers have now given way to molecular (DNA) markers. It started with Restriction Fragment Length Polymorphisms (RFLPs) to demonstrate genome variation, but at present a large number of molecular marker types are available. After being solely based on restriction enzymes, the development of the polymerase chain reaction (PCR) and DNA microarray technologies expanded their number and type. These marker types include Random Amplified Polymorphic DNA (RAPDs), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeat DNA length polymorphisms (SSRs), Single Nucleotide Polymorphisms (SNPs), Diversity Array Technology (DarT), Expressed Sequence Tag Polymorphisms (ESTPs), Conserved

Orthologue Set (COS), Amplified Consensus Genetic Markers (ACGMs), Gene Specific Tags (GSTs), Resistance Gene Analogs (RGAs), Exon-Retrotransposon Amplification Polymorphisms (ERAPs) etc. The different technologies differ amongst others in ease-of-handling, codominance, number of markers generated on a chromosome (density), and being linked to or actually inside a gene. Saturated maps of the individual chromosomes of a species are of great help in breeding, especially when molecular markers can be linked to traits of agronomical importance. The more dense the map, the more reliable are the markers. The chances of recombination occurring between the marker location and the trait (gene) become less in case of a high density map and the marker can be used in marker-assisted selection (MAS) with high fidelity. The genomic maps provide insight in the organization of the genomes of species. They showed that the organization of genes and markers across chromosomes can be quite similar among species. This is called synteny. Synteny can be found even among distantly related species such as rice and Arabidopsis, but can be much higher among more closely related species, e.g. rice and grasses or Arabidopsis and Brassica. This phenomenon can be used in positional cloning and comparative genomics. When in species 1 the organization (location) of markers and a trait/gene is known, synteny enables one to look in the homogenous chromosome in species 2 for a similar organization of markers. By cloning the appropriate region one can look for the presence of the desired trait in species 2.

Although linked markers can be very useful, markers in the genes themselves are considered more valuable because of the absence of recombination and the highest reliability. However, when a map is covered densely enough with molecular markers, genome walking can be performed to go to the gene itself. Ultimately, the causal relationship between the gene and the trait needs to be established and confirmed (see 1.A.3).

Techniques such as pyro-sequencing can be used to identify single nucleotide polymorphisms (SNPs) and through this to identify individual alleles including conditional ones. Allele mining and the development of molecular markers for all the existing alleles of a gene will be a powerful tool in molecular breeding.

2.5. Applications

All of the above-mentioned approaches use functional genomics to aim at revealing the functions of the identified gene sequences. Based on the information available from microorganisms such as yeasts or bacteria and from mutant lines that were available in some plant species, genes and sequence data can be linked and the function of specific genes deduced or established. This information on functions is entered in data-bases and can be used with new crops in two ways. When you are looking for a specific function in species 1 and a gene sequence coding for this trait is available in the data-base from species 2, the latter sequence can be used to design primers to use in PCR for the isolation of the homologous gene from genomic DNA of species 1. Another way is to use PCR to prepare a probe that can be used to identify within a

genomic or cDNA library of species 1 the clone carrying the homologous gene. This represents comparative genomics by sequence similarity, the candidate gene approach. This approach is largely used to isolate genes with a specific function from the desired species itself, orthologs. In the end, the causal relationship between the gene and the trait needs to be established and confirmed (see 2.3).

Knowledge on individual genes and the phenotype or trait for which they encode can be put to use in three areas. First, the genes can be used to consciously introduce a new, well characterized and desired trait into a crop by genetic modification. The cultivation of GM crops for more than 10 years without negative effects on man or environment has proven to be safe. A new generation of GM crops can be made without the presence in the end-product of DNA sequences that are no longer required or desired. They are called 'marker-free' because of the absence of selectable markers needed for the preferred growth of cells and plants carrying the new genes. The selectable markers used are mostly based on resistance to antibiotics or herbicides. As said previously, they can be removed or absent in the final products. Because of the efforts in plant genomics more and more plant-derived genes are becoming available for use in preparing the latest series of GM crops. Species-own genes, i.e. genes present in lines or cultivars within the species, can be used for rapid and efficient transfer from one line to the other. Existing varieties are the result of a long and meticulous conventional breeding and selection process and are preferred by growers, retailers and consumers for many aspects. However, in many instances they are still lacking a few important characteristics, e.g. disease resistance, prolonged shelf-life or growth under marginal conditions (drought or salt stress). These varieties can be equipped with the desired extra traits through genetic modification in a much more rapid fashion without having to introgress these traits from (wild) relatives by crossing. The latter process usually results in loss of a few of the established and appreciated traits and gain of some less favorable traits of the (wild) relative through linkage drag. Marker-free GM crops solely carrying gene and promoter sequences derived from the species itself can be called cisgenic crops and could be considered so similar to crops derived from conventional breeding that a relaxation in the implementation of the EU rules according to Directive 2001/18/EC might be in order.

Secondly, the well-identified genes and alleles can be used as true functional molecular markers for specific phenotypes in marker-assisted-selection (MAS). Quantitative trait loci (QTLs) can be linked to specific genes and the role of that particular gene, as the mechanism responsible for its contribution to the final trait, can be visualized. The breeding process can be speeded up and become even more efficient and reliable with these functional markers associated with a trait and located in the gene itself. Preferred genotypes in which specific desired alleles are combined can be easily identified in an early stage.

Thirdly, the molecular information on specific genes and allocated functions can be put to use in diagnostics. Identification of the genetic or allelic constitution of a plant can be linked to predictions on specific phenotypes.

3. Inventory of Scientific Views; The role of bioinformatics

3.1. Introduction

Bioinformatics involves the development and application of computational resources in biological research. The discipline started to take shape in the early eighties in response to a need for computational tools with which the growing amount of bio-molecular sequence data could be better managed and analyzed. Among the early achievements of what would nowadays be called 'bioinformatics' were, for instance, the establishment of the first molecular sequence database in 1982, the EMBL Nucleotide Sequence Data Library, and the development of tools for the alignment and database comparison of DNA and protein sequences, such as the Smith-Waterman algorithm (Smith and Waterman, 1981) and the FASTA package (Pearson, WR, Lipman, 1988), respectively. In the past ten years, bioinformatics has undergone a spectacular growth and has evolved, from a somewhat arcane intersection of molecular biology, computer science, mathematics and statistics, into a mature scientific discipline. An illustration of this growth is given by the number of PubMed abstracts containing the keyword bioinformatics (Figure 1). Without bioinformatics, the practice of modern, large-scale biology has become unthinkable.

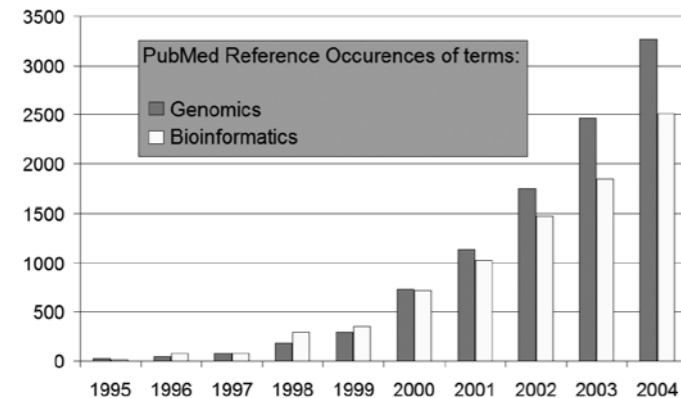


Figure 1. Growth in the number of PubMed records in the past decade, containing the keywords "bioinformatics" or "genomics".

Two technological developments have been instrumental for the advancement of the field. Firstly, the advent of high-throughput technologies in the late nineties changed the face of experimental biological research. Within a short time-span, beginning with the introduction of capillary DNA sequencers and DNA microarray technology, laboratories all over the world acquired the means to rapidly generate large amounts of bio-molecular and genetic data. The management, processing and analysis of these datasets soon called for novel, dedicated and user-friendly software, enabling bench-top biologists to fully exploit the results of their experiments. Secondly, the early internet, that had hitherto functioned as an information and communication network mainly operated by expert users and computer scientists, saw the introduction of its first, user-friendly interface in the early nineties. Since then, the internet has grown explosively and unleashed its enormous potential as an information resource and application environment to the life sciences community. With current hardware technologies, including high-speed internet connections, the immense amount of data and information stored in databases worldwide is at everyone's fingertips and its use has become every-day practice in biological research.

To date, a diverse array of powerful, high-throughput technologies has made its way into almost every area of molecular and genetic research. It ushered in a shift in research methodology, from hypothesis-driven, mostly gene-centric investigation to data-driven, exploratory investigation of biological systems. In the latter, the network of interactions among cellular components has become the focus of attention. In practical terms, this meant that, in contrast to a mere ten years ago, when genes, transcripts, proteins, and metabolites were analyzed basically on a one-by-one basis, an experimentalist today typically will study a large or complete complement of these biomolecules in response to environmental or genetic alterations to the system under investigation. The terms genomics, transcriptomics, proteomics, and metabolomics are commonly used to refer to these system-wide explorations of molecular components.

Bioinformatics facilitates many stages of this new way of experimentation, from the initial experimental design to the final steps of analysis and integration of results with information available from public databases via the internet. In the previous section we have reviewed modern molecular technologies used in research for breeding, crop improvement and development of sustainable product chains. Among these were several of the aforementioned high-throughput technologies. In this section we will give an overview of the bioinformatics resources that are being used in concert with such technologies.

3.2. Bioinformatics resources for plant breeding research

In many areas of biology, we want to come as efficiently as possible from the phenotype to the genotype. In breeding and breeding research the challenge lies in translating key-agricultural traits of crops (relating to yield, quality, resistance to disease and sustainability) in molecular

terms and so making these amenable to genomic analysis and faster breeding.

There are several areas of development within bioinformatics that are of major relevance to current plant breeding research:

1. Genome annotation
2. Statistical genetics
3. Comparative genomics
4. Metabolite identification and metabolic pathway elucidation
5. Biomolecular data management, integration, and mining

We will discuss these hereafter with reference to the technologies discussed in the previous section.

3.2.1. Genome annotation

Once the genome sequence of an organism has been determined, using the strategies outlined in 1.A.2., a process of analysis starts that aims to extract biological meaning from the raw DNA sequence. Results from these analyses are commonly stored in a relational database that provides useful connections between the bits of information inside the database as well as outlinks to information in other databases around the world. Most genome databases are made accessible to the research community through the internet and use rich interfaces and genome browsers that enable interactive, graphical exploration of the data. This entire process of extraction, storage, and representation of information is referred to as genome annotation.

The initial steps of annotation are “structural annotations” and start with the identification or prediction of physical attributes of the sequence and anchors these on to it. The attributes include protein- and RNA encoding genes, regulatory signals, ESTs, repetitive elements and segmental duplications, physical and genetical markers, SNPs, etc. The key activity in structural annotation is gene-finding. In eukaryotes, the coding content of the genome is usually very low (<10%) and identifying the genes and correctly predicting their intron-exon structure is not a trivial task. A wide array of gene prediction algorithms and tools has been devised in the past ten years. Many of these work by analyzing motifs and statistical properties of putative genes and often require a considerably sized set (>200) of reliable gene structures as models to train the software in preparation of the prediction step. Such models can be built by alignment of EST and cDNA datasets to the genomic sequence. This is also one of the many reasons why the availability of large expressed sequence datasets for a species is so important.

In a second phase, functional information is added to the primary sequence attributes (functional annotation), most importantly to the predicted genes. Although experimentation using biochemical assays or reverse genetics still is the golden standard for establishing gene function, computational prediction of function, the holy grail of bioinformatics, is gaining power and accuracy. This is largely due to the modern practice of massively storing results from both laboratory research and in silico analyses in databases and making these accessible to the wider

research community.

The evidence coming from this body of genomics and functional genomics information can be mined with automated computational procedures for gene function prediction, by exploring the diverse kinds of associations among genes in these datasets. There are three levels at which such associations can be found. At an operational level, a gene may be associated in terms of its expression with other genes of known function or with specific biochemical, cellular, physiological or developmental processes. At a structural level, a gene can be linked with other genes through genomic neighborhood or through sharing of similar regulatory signals, while the gene product may be associated with protein structures of known function, with protein complexes of known function, or with particular subcellular localizations. At an evolutionary level, a gene is related in terms of its nucleotide sequence to other genes within its own genome or within the genome of other species. Evolutionary associations form the basis of most classical function assignments in computational gene annotation. This method is commonly known as homology-based function prediction. It relies on the assumption that homologous proteins in different species perform similar functions and that experimentally gained knowledge obtained in one species can therefore be transferred to its homologue in another species.

When available, each of the above types of association will contribute to the global probability that a particular gene is involved in a particular biological process and can thus be assigned a particular function.

Computationally, homology-based function prediction starts with subjecting a gene from a newly sequenced genome to a database homology search with a program such as BLAST (Altschul et al., 1990). One can choose from a large collection of databases available for this purpose, among which the manually curated SWISS-PROT database stands out for the reliability of its annotations. BLAST will return a ranked list of genes from other species held in the database to which the query sequence is most similar. Annotations from these “database hits” can then, in a fully automated way, be parsed from the BLAST output, attached as a functional annotation to the query gene, and be stored in the annotation database of the new genome.

Although annotation transfer by homology is powerful, it is also fraught with several difficulties. Obviously, the gene may be short of clear homologues in the sequence databases or it may be homologous to other genes of unknown function. In addition, homologues not necessarily need to perform the same function, in particular when gene duplication is involved in their evolutionary origin. Such genes, known as paralogues, therefore have to be distinguished from true orthologues, i.e. homologous genes derived from a single ancestral gene through speciation only. Accurate orthology prediction is difficult, particularly when one is dealing with genes from large gene families, and may often require a considerable computational effort.

In addition to BLAST, more sensitive analyses and sequence comparisons can be performed to assign putative functions, in particular when plain sequence divergence obscures homology relationships. One approach is to compare the protein sequence of a newly sequenced gene against the various databases of protein functional domains and motifs, including PFAM,

PRINTS, PROSITE, ProDom, SMART, BLOCKS. An extremely useful addition to these databases has been the recent development of InterPro (Apweiler et al., 2001), a system that unifies all of these overlapping resources and allows them to be searched in a single run, returning a single integrated output.

Further functional information that can be attached to predicted genes include alignments of available EST and cDNA sequences, gene expression data, protein structure, interaction and localization data, classification data, e.g. using the gene-ontology scheme, and cross-references to databases that hold further information on homologous sequences such as metabolic and regulatory pathway databases, structural databases, etc. Another level of information with which genome annotations can be enriched involves structural similarities to other genomes. Such similarities are found through gene order comparisons and whole genome alignments and will be discussed hereafter in the context of comparative genomics methodology.

Genome annotation is a complex and multi-step process in which many databases are used and a broad range of computational tools is employed in both parallel and sequential fashion. To this end, the in- and outputs from different analysis have to be interconnected, jobs have to be computationally managed in a robust way and results have to be integrated for representation. Not only is the automation of this entire process important in order to match the increasing pace with which the raw sequence data are being produced. It is also critical for the organization and visualization of the extracted information with which we are to build our understanding of the primary sequence. These requirements have made the operation, accuracy, and flexibility of automated annotation systems a prime challenge in the field of genomics and, with respect to genomes of agricultural crops and their model species, one of utmost importance to breeding research. The relevance of having high-quality genome annotations of crop and model species available and accessible in an easy and seamless way becomes apparent, for example, when through breeding research a QTL or candidate gene region has been localized on the genome. Subsequently, the researcher will want to explore the genome annotation to find out what genes or regulatory elements map to this specific region. Examining the annotated gene functions may then provide clues as to which genes are most likely to be involved in the trait under investigation.

3.2.2. Statistical genetics

Plant breeding relies on the selection of favorable genetic variation that corresponds to phenotypic variation of agricultural traits of interest. The goal of statistical genetics is to localize regions in the genome that influence these traits and to dissect their underlying molecular and environmental components. The field traditionally has had close ties to forward genetics technology, outlined in the previous section, and to the practice of marker-assisted breeding and crop improvement.

Statistical genetics develops methodology and computational tools for genetical linkage map-

ping and the analysis of quantitative trait loci. The identification of single-gene traits with qualitative variation through the construction of high-density genetic maps has been extremely successful, both in plant and animal species. In contrast, unraveling the molecular basis of more complex, quantitative traits by QTL analysis has proved to be far more difficult. Yet, the availability of complete genome sequences and their rich and accurate annotation has opened up faster routes for the identification of candidate genes in QTL. An example of the dissection of a major fruit weight QTL in tomato (Alpert KB, Tanksley SD, 1996) may illustrate the application and value of bioinformatical analysis of QTL and candidate gene regions. Using high-resolution physical and genetic mapping, the localization of the fruit weight QTL could be narrowed down to a region of less than 150 kb. The QTL was deduced to be a single gene with a large effect (30% of the variation) and could be further isolated by positional cloning. Had the complete genome sequence of tomato been available at that time, however, the investigators could have moved on directly to an analysis of the annotation of the respective region in an attempt to identify or delineate the number of candidate genes or regulatory sequences and their variants responsible for the trait.

One step further is that genome annotation would include an analysis aimed at predicting what sequence variation in genes, proteins and regulatory elements might have functional effect. It will be extremely difficult to achieve acceptable sensitivity and specificity with such computational predictions in the near future. However, the ongoing accumulation of genome sequence data and the insights we are gaining from their comparative analysis in terms of conservation of functional and regulatory sites, can be expected to improve the results of such predictions of functional effect.

From a rather different angle, another important proposal to bring statistical genetics and genomics together has recently been put forward. Jansen and Nap (2001) suggested both fields to be merged in an approach of sampling variation in gene, protein or metabolite expression and molecular markers in parallel in a segregating population. They dubbed the field "genetical genomics". The innovative idea was to treat expression as a quantitative phenotypic trait, which, in conjunction with molecular marker analysis, makes these data amenable to QTL analysis. This provides an entirely novel route to the dissection and identification of factors that influence the expression of a gene. Genetical genomics is starting to fulfill its promises, witness a recent flow of publications that apply the approach to gene expression studies (see Editorial in Nature Genetics, March 2005).

3.2.3. Comparative genomics

The same evolutionary principle that underlies the method of homology-based gene function prediction outlined above, underlies the field of comparative genomics as a whole. Genomes are compared to each other in light of their common ancestry and the inferences and predictions made from such analyses are rooted in evolutionary reasoning. The basic premise is that

conserved segments between different genomes are constrained by selection and are therefore most likely to be functional. Without selection, random mutations will wear away similarities over time. Discovering all the functional parts and the details of their structure in a newly sequenced genome can thus be greatly enhanced through comparative genomics.

Powerful alignment algorithms have been developed to perform cross-species comparisons of genomic sequences, including AVID, BLASTZ, MUMmer, MLAGAN, WABA, and many others (Ureta-Vidal et al., 2003), and comparative genomics repositories are being established that hold precomputed alignments (e.g. www.tigr.org) which can be explored by researchers for regions of their specific interest. The global alignments between two or more species can be used directly to delineate conserved regions and provide important information on: 1) the extent of colinearity or synteny among the genomes, that is, regions of the genome in which the gene order is similar; 2) colinearity of physical and genetic maps between closely related species; 3) the location of genes, which are more conserved sequence regions than non-functional ones; 4) the detailed intron-exon structure of genes, and; 5) the location of conserved non-coding sequences, mostly regulatory elements. Alignment strategies that focus on the latter type of information are also known as phylogenetic footprinting and phylogenetic shadowing. In phylogenetic footprinting, regulatory elements are identified as stringently conserved sequences by comparing species over large evolutionary distances. In phylogenetic shadowing, known relationships among more closely related species are used and in the context of a model of sequence divergence for the same purpose. Again, these methods are extremely valuable for exploring candidate gene regions and QTL to narrow down the segments with the highest probability of being involved in expression of the trait under investigation.

Comparative genomics further provides a very direct way to identify species-specific genes and other genetic elements among closely related species that differentiate them phenotypically. A gripping example is the comparison of human and chimpanzee genomes. Their genomes are extremely close, showing over 98% similarity at the nucleotide sequence level, yet at the same time they represent two species that show a number of profound phenotypic differences. Comparison of their gene complements and regulatory mechanisms of gene expression will thus enable faster delineation of candidate genes and regions involved in these differences.

In the context of breeding research and crop improvement, comparative genomics provides the conceptual framework and the necessary tools for the transfer of genomic information from model species to related crop species.

3.2.4. Metabolites and metabolic pathway elucidation

Plants contain a bewildering array of metabolites. Many of these compounds stem from secondary pathways that uniquely evolved in plants. They include constituents essential for a healthy human diet, human dietary supplements with health-promoting properties, important nutrients for farm animals, compounds that determine food flavor and taste, and, not in the

least, a large number of compounds used either directly or indirectly as pharmaceuticals. Knowledge of the biochemical pathways that underlie the synthesis of these metabolites by plants is essential for their engineering and optimization in existing crops and possible transfer to novel crops.

Metabolomics is a relatively recent development in plant functional genomics as well as within the 'omics' family of high-throughput technologies. The aim of the field is the discovery and identification of the complement of metabolites present in plants and the elucidation of the pathway structure and dynamics that lead to their synthesis. Bioinformatics plays a key role in the development of metabolomics. At present, the mass spectrometry technologies that drive the field evolve faster than the computational means with which the data can be processed, interpreted and integrated with other types of molecular data. The most significant limitation is our current inability to automatically translate mass spectral data into molecular data on compounds and thus biochemically identify the metabolites. For some technologies, commercially-available reference databases can be used to this end, but for others, in particular those commonly employed for the analysis of plant secondary metabolites, no such standard reference systems are available. The latter identification strategies are therefore based on manually combining accurate mass information with additional, complementary information from other sources. This creates a serious bottleneck that hampers the further development of metabolomics as a tool to comprehensively study pathways, not only qualitatively but also quantitatively. Novel bioinformatics strategies that allow for faster and more accurate metabolite identification are therefore urgently needed.

Breeding research is expected to benefit in particular from improved metabolite and pathway identification in combination with the genetical genomics approach of quantitative genetic analysis of metabolite expression levels.

3.2.5. Biomolecular data management, integration, and mining

Critical for opening up genomic information for breeding research is the integration of the heterogeneous molecular, genetical and phenotypic data repositories. It enables researchers to direct their questions simultaneously at multiple levels of organization and derive answers that reveal associations among them. There are many factors that hamper this system-level type of data integration. Apart from sociological and commercial reasons, which may force laboratories not to (fully) disclose their data, most factors are of a technical nature. To overcome these, not only computational solutions are needed, but also development and broad acceptance in the research community of standardization of data models and data exchange formats.

Different approaches are being followed to solve the data integration problem, the most successful among which include 1) link integration, in which data sources are linked to each other through hypertext links; 2) data warehousing, in which basically all data relevant for the pur-

pose of a specific biological database are modeled coherently and brought together under a single roof, and; 3) web services (Stein, 2003). In the last approach, similar to link integration, data are left residing in their original repository, with their specific domains of biological information remaining intact, but a special software layer is developed for standardized access and data exchange among databases. This allows the user to automatically retrieve all relevant information on a biological question using just a single query. Furthermore, the technology allows not only the integration of datasets but also of bioinformatics analysis tools. The emerging web service technologies now appear very promising in overcoming important hurdles in data integration and are currently being developed in the BioMoby and MyGrid projects.

A different aspect to the data integration problem is a semantic one and involves the need to use common, standardized vocabularies to describe information within a certain biological knowledge domain. Such vocabularies are called ontologies, which, more specifically, provide a formal system for describing objects, concepts, and other entities in a knowledge domain, as well as the hierarchical relationships that exist among them. A number of international initiatives have been taken in the past five years to develop biological ontologies. The most successful among these is the Gene Ontology, which describes the gene product attributes of function and cellular location. Particularly relevant for the integration of plant genomic and phenotypic information is the Plant Ontology initiative, which has started to develop ontologies describing anatomy, morphology and development for a number of plant model species. This ontology will greatly improve our means to compare phenotypes among species and associate these with the various types of genomic information.

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4. Inventory of Scientific Views; Plant genomics and consumers in a sustainable food chain

4.1. Introduction

All the activities in the area of plant genomics research may lead to the development of interesting future products and the potential implications are likely to be wide and may affect many consumers. Various consumer issues may occur in the areas of People, Planet, and Profit which are important in the context of an appropriate societal embedding of genomics as a scientific field. Somehow these consumer issues need to be described, addressed and managed appropriately to realize the potential of plant genomics. This is rather difficult because consumers are still unaware of plant genomics, and also because at present, no plant genomics enabled or enhanced products can be found in the market.

4.2. Consumer issues in the food chain

Improved disease resistance qualifies best for application of genomics, also abiotic stress and health promoting characters are appealing applications. Plant genomics could focus on the 'difficult' traits, but most important is that products appeal to markets and consumers. Markers have been the first product of potato genomics, in addition to increased knowledge. Such markers may be used for diagnostics. However, the real product of plant genomics will be a new cultivar. That may take another 4 to 15 years. In the process of cultivar making, genomics (markers) will facilitate the selection process, but not necessarily speed it up. This production process requires the coordinated activities of the various branches of the food chain in order to provide convenient, wholesome, tasty, safe and affordable foods. Also, the size and complexity of the food sector ensures that no single player can control a single process from seed production, through farming and processing to a final product marketed in a retail outlet. Furthermore, the scientific advances in genome research and their exploitation via biotechnology is leading to a technology driven revolution that will have advantages for the consumer and food industry alike.

Currently the most general issue is that society will not accept agricultural genomics because it will consider 'genomics' synonymous with 'genetic engineering'. Given public fears with respect to genetic engineering, this would imply a rejection of genomics. Apart from the benefits missed, an issue to consider as well is that such a rejection would also deny experts to do the type of work they know and like best. The 'genomics equals genetic engineering scenario' is far from hypothetical. Both genomics and genetic engineering deal with genes, genetic material and improvements of plants. The distinction is a subtle one at most, which is easily forgotten.

The term 'genomics' may turn out to be a poor one.

Agricultural genomics may already have image problems in relation to genetic engineering. Worldwide, most prominent proponents of agricultural genomics were previously proponents of genetic engineering. This is also the case in the Netherlands. Moreover, the promises of agricultural genomics are not very different from the earlier promises of plant genetic engineering, nor are the research topics.

Another issue may be certain aspects of (over?)regulation. The level of regulatory scrutiny currently imposed on a genetically engineered crop is high and unprecedented for any product of plant breeding. Development and costs of such regulatory requirements may have significantly negative impacts on agricultural genomics.

In the development of agricultural biotechnology, private funds have slowly taken over public funds in size and impact. This development is continuing in the development of agricultural genomics. Agricultural genomics is a costly enterprise. High throughput technologies may make a single data point relatively cheap; total costs are considerable, due to the sheer numbers involved. Private investments far outweigh public funds, supported by mergers and continuous scale-up of life science companies. This implies that a few companies may decide over genomics research targets and applications. The corporate control of biotechnology in general, and future agricultural genomics in particular, are likely to generate considerable social concern. Despite all the promises, agenda setting in genomics seems still focused on short-term goals. These relate to conventional, high-yield industrial agriculture aimed at profit. Publicly funded programs such as TransForum may help to rebalance the control and agenda setting power of the private companies.

Consumer issues about corporate control are immediately related to issues of ownership and intellectual property (IP). Different from plant breeding, ownership in agricultural genomics is based on patenting and patent protection. Genomics research is seen as economic investment that requires return. The patenting frenzy of agricultural biotechnology will continue in plant genomics. This will raise questions about the equity, accessibility and desirability of plant genomics and its applications. Also in this case a program such as TransForum may enhance the possibility for the public to gain access to genomics information. When plant genomics is seen as a high-input, high-cost, high-protected enterprise, a related legitimate issue is about the benefits of such genomics for the developing world. The developing world will face most serious problems with food supply. This issue is known as 'the genomics divide'. In the current settings of genomics, it is unclear whether these problems will truly affect the genomics research agenda. Not everybody in society is likely to consider plant genomics into the quality of potato for baking french fries a priority target for research. Plant genomics could be seen as again a technological solution for problems that may have at least as many negative impacts as it presents solutions. It can be perceived to contribute to a further industrialization, economization and mechanization of agricultural production that is seen as undesired. In probably small parts of society, this will be related to difficult concepts as 'the integrity of life'. Particular

schools in plant breeding are still debating the acceptability of markers and similar discussions can be expected on the large-scale approaches of agricultural genomics. Moreover, any impact of plant genomics on a further industrialization of food production may trigger uncertainties about the safety of genomics products.

Overall, there seems place and need for substantial research into the mechanisms of agenda setting in plant genomics research, the extent of corporate control and the diversity of society's evaluation of such issues. Policy makers and genomics researchers seem aware of the need to include society and the need to deserve a 'license to produce' and 'a license to sell', rather than to exclude society and go on. How this awareness works out in day-to-day management decisions is yet unclear and requires more analyses and possibly new approaches.

4.3. Sustainability

Literally, sustainability means 'the ability to sustain'. This implies either to maintain something or keep it going for a period of time, or something that is supported by giving help, encouragement or support. Over the last decades the best-known, widely adopted, and now almost 'traditional', definition of sustainable development was given in the Brundtland report (1989). Sustainable development is here defined as "development that meets the needs of the present without compromising the ability of future generations to meet their own needs". However, there are many different interpretations, modifications and reformulation of what is sustainability. A World-bank inventory listed no less than 190 different attempts. Sustainability has become linked to a large variety of human activities, concepts and issues, such as biodiversity preservation, and corporate social responsibility. Meanwhile, sustainability has become a priority for the world's policy makers. The concept is now at the core of laws in many countries around the world and has become a societal norm. Generally, people will do what they believe is 'right', i.e., whatever is consistent with their personal beliefs and/or the norms of the society they live in.

In the view of many, somewhere along the course of time, mainstream agriculture has lost its roots of sustainability. The development of increasingly intensive and specialized forms of agriculture has culminated in what some refer to as 'industrial agriculture' or 'chemical farming systems'. The farm is viewed as a factory with inputs and outputs, aiming at increased yields with reduced costs, often by exploiting the economy of scale. It is accompanied by use of and reliance on agrochemicals, large-scale mono-cropping, mechanization and energy consumption. Such agriculture sees as its primary objective to produce as much food and fiber as possible for the least cost. According to Lyson (2001), current conventional agriculture is anchored to the scientific paradigm of reductionist experimental biology, in combination with the reductionism of neoclassical economics, driven by a continued (desire for) industrialization.

Although successful in the past, virtually every aspect of this conventional agriculture has become problematic. The problems center on both the environmental aspects and on the social

and community aspects of agriculture. There are problems with the supply and quality of water, erosion, soils that become unfertile, contamination by pesticides, use of manure, and various levels of pollution of groundwater, soils and atmosphere. This makes agriculture a major cause of damage to the earth's ecosystem at large.

Combining sustainability and plant genomics is the combination of a difficult, multidimensional concept with a complex technology. To do so, plant genomics researchers have to translate their research activities into sustainability. Such a translation will mainly focus on the applications or applied aspects of genomics research. Having shown above that sustainability in general is seen as very positive in current society, genomics could try to become associated with this norm. Such an association may be used to translate scientific approval in societal approval, or to counterbalance societal concerns.

Sustainability in its most broad connotation has to do with (natural) resources (see above). Genomics can for example help replacing petroleum with biomass derived mostly from plants. Such a biomass is or could be a renewable natural resource, hence more sustainable. Actually, many of the goals of agricultural genomics as summarized above seem to reflect the need and desire for increased sustainability in the sense of renewable resource use and a significantly reduced environmental burden of agrochemicals. In this context, the issue is whether sustainability is used to legitimize agricultural genomics, or, vice versa, whether this genomics research and results will effect or change the norm sustainability of society. Moreover, if so, how that may happen. This relationship between legitimization, research and sustainability in relation to genomics is an issue that merits more analysis.

Depending on its research agenda and achievements, agricultural genomics may change its perspective with sustainability and ecological agriculture in society. For the future of genomics, its relationship with sustainability should therefore become better defined and clearer in society. Initially, this could be attempted on a case-by-case basis and may be used for generalizations in the future. Unless the public comes to agree that the benefits of agricultural genomics are equivalent to a sustainable, desirable and acceptable agricultural practice, society is likely to fail to recognize and realize much of the potential benefits of agricultural genomics.

4.4. Conclusion

Plant genomics, especially when presented as a 'new' technology, will have to face all the suspicions any new technology is usually confronted with. Plant genomics can be considered a next step in the process of agricultural biotechnology that started with the discovery of the Laws of Genetics by Mendel and the double helix structure of DNA by Watson and Crick. Plant genomics will have to face all the ethical, moral, social and technical issues associated with agricultural biotechnology in general. These are issues about corporate control, ownership, distribution of profit and benefits, overall approach as well as safety.

Also, the distinguishing characteristics between plant genomics, plant breeding and plant bio-

technology could be clarified better. A truly hot potato is the relationship between genomics and genetic engineering, in terms of both scientific activities and image of genomics. It would seem a valuable exercise to analyze in detail which societal groups are using what terminology of 'genomics' in what context and with what agenda. Whereas the stakeholders tend to stress the differences between genomics as a research activity and genetic engineering as a potential (but not automatic) application of that research, the public at large seems already in the process of confusing the two. Policy makers often attribute this reaction of the consumers to a lack of knowledge and to ethical and emotional concerns. (e.g. Marris et al., 2002). However, these rational policies are likely to enhance the ethical and emotional concerns of consumer and leave little room for the every day experiences of consumers. Communication and information about risk did not take into account the actual issues of consumers, but instead the knowledge of experts about risk assessments was communicated. Hilgartner (1990) has described this as the "deficit model". Particularly the government and groups of experts assumed that the public is in some way deficient in their understanding of risk. Also, not all risks are evenly important. According to Miles and Frewer (2001) people perceive risks as higher when they experience a lack of control over their exposure to potential hazards. So, trust in risk assessment and risk management is likely to be a particularly important determinant of public confidence in food safety in cases where there is a lack of trust. Miles and Frewer (2001) consider genetically modified foods, where consumer concern did not focus primarily on risk per se, but rather on the lack of personal control on the part of the consumer over consumption, as an example.

Plant genomics research and applications may effect or change the societal norm sustainability, or sustainability may be used to legitimize plant genomics. Understanding the relationships between legitimization, sustainability and plant genomics merits more analyses. From the perspective of sustainability, the approaches and assumptions of genomics can be seen as undesired and irreconcilable with its aims and approaches. This can be translated in the different perspective of holism versus reductionism. Whereas sustainability is seen as a holistic approach, plant genomics would be seen as the culmination of reductionism. More analysis is required to decide whether ecological agriculture and plant genomics are representatives of two essentially incompatible approaches, or can be combined. Can plant genomics fit in the approaches of ecological agriculture and if so, how? Vice versa, can any sustainable agricultural production scheme afford to deny the potential benefits of plant genomics? This creates a potential dilemma of sustainability that will be very interesting to analyze in a case-by-case approach. For the future of genomics, its applications and their relationship with sustainability should become better defined and clearer in society. Further analysis of the societal link between ecological agriculture and plant genomics may result in predictive capacities for the way plant genomics will be approached by society, or will have to be presented to society.

Plant genomics could be perceived as either a new way to change agriculture into a more natural, eco-friendly, low-tech production system or a next step in the further industrialization,

economization and mechanization of agricultural production, and may change the agro-food industry into a high-tech/high-value business. Which of these two options is a desire from and in the interest of society requires research attention, as does the question how the two options relate to sustainability. Research into the mechanisms of agenda setting in plant genomics research, the extent of corporate control and the diversity of society's evaluation of such issues is worth attention.

5. Implementation in the production chain

The advances in knowledge on genome organization, gene sequences, gene functions and gene expression are applied in marker-assisted breeding, transgenic crops and expression profiling. The bulk of the ongoing efforts are taking place in universities and research institutes, mainly funded by governments, i.e. public money. Because of the high costs of molecular genetic research, applications implemented by commercial companies can be found primarily in larger breeding companies involved in producing varieties in crops with a high economic impact. Application of marker-assisted breeding is most advanced in arable crops, such as maize and rice (large cultivation areas) and in vegetables such as tomato (high seed prices).

Transgenic crops cultivated globally encompass 8 varieties in 6 species, i.e. cotton, maize, canola, soybean, papaya and squash melon. Especially, the first four species represent bulk crops with a high economic value because of their large cultivation areas. In addition to development costs, costs for approving and adopting GM crops for market introduction and consumer acceptance are high and hamper large scale implementation in 'smaller' crops by smaller companies.

Expression profiling is based on linking specific quality traits to expression of specific genes, either during cultivation (monitoring crop health, disease infection status) or after harvesting (in storage, transport or at the retailers). The arrays used for this allow diagnostic sampling and monitoring of crop quality through the entire production chain. This facilitates crop cultivation management systems aimed at durable growth reducing the usage of agrochemicals and it enables producers, retailers and consumers to critically monitor product quality at all respective stages. Several specialized biotechnology companies are presently developing such expression arrays.

6. Potential Areas for concrete Points of Action

Regarding the state-of-the-art in technology, bioinformatics and societal aspects involved in genomics research as presented in the previous chapter several main points of action can be identified that will contribute to the desired transition into a sustainable agriculture in The Netherlands. These main points are resistance to pathogens, drought or salt tolerance, bio-based economy, consumer demands and chain management. Moreover, a clear and transparent, two-way communication about the issues involved and how to tackle them is a prerequisite. The establishment of a Technological Top Institute (TTI) on 'Green Genetics' in The Netherlands will stimulate and facilitate initiatives embedded within the BSIK program and co-ordinated by TransForum. Together with projects funded by IOP-Genomics and by other programs of the Dutch Ministries of Economic Affairs and of Agriculture, Nature and Food Quality the efforts on extending and exploiting plant genomics in The Netherlands can be significant and have a recognizable impact.

6.1 Resistance to pathogens.

In the year 2000 (most recent data available, CBS Voorburg/Heerlen) a total of 5.346.278 kg of chemical crop protectants (6.6 kg/ha) was used in the Netherlands. In 2001 in a joint initiative, representatives of the government and producers (farmers/growers) agreed to work towards a reduction in the use of chemicals in agriculture and horticulture. The formulated goal is to have a reduction in 2010 with 95% compared to the level of 1998. The obvious benefits of such a reduction would be on health and economic aspects for the growers themselves and for consumers (less exposure, less residues, less production costs, lower prizes), and on environmental aspects (less exposure of non-target organisms, less water contamination by spilling or washing out). The majority of the chemicals is used in the production of potatoes, bulbs and fruit. In these particular crops it proved to be extremely difficult if not impossible to achieve to goals set because of the open cultivation systems and the long or difficult conventional breeding processes. Sources of resistance are usually scarce and can be broken by the pathogens with relative ease. Stacking of multiple resistance genes or using non-host systems can contribute enormously to the durability of the trait and are explicit features that can be achieved using the full potential of plant genomics, either by molecular marker assisted breeding or by genetic modification. Integrated resistance management in cultivation or agro-systems can be greatly facilitated by the use of several types of diagnostics. For instance, using sampling and monitoring systems based on the known DNA sequences of important pathogens it can be easily established in cultivation at what point in time which pathogen is entering the field. Expression arrays can be used to monitor the onset of expression of genes involved in the plant's defense against patho-

gens, hence of infestation, prior to the moment at which infection becomes visible. This will make it possible to reduce the amount of chemicals necessary for control, enhancing durability in the primary production. Preventive spraying will not be required anymore. The main (not the only!) parties within the Dutch production chain with an interest in this trait are primary producers and specific consumer groups.

6.2 Drought or salt tolerance.

Although coping with adverse environmental conditions such as drought or salt stress is primarily a global problem at the moment, there are at least three arguments for tackling this problem also in The Netherlands. Changing climate conditions, such as the global warming up, could have consequences for The Netherlands in increasing the periods of time in which insufficient rainfall will take place or in increasing the surface of particular soil types, i.e. sandy soils, that are troubled by insufficient rainfall or by the reduced possibilities for artificial raining by pumping up and spraying surface water because of water shortages for this purpose. Another effect could be the rise of the sea level that could result in deeper penetration of salty ground water in coastal areas and thus creating more salt growth conditions for crops in those areas. Breeding companies based in The Netherlands are nowadays part of international conglomerates. This means that their skills and efforts should also be focused on global themes and problems. When they are to keep their leading position in plant breeding they should also work on developing crops tolerant to environmental stress conditions. For developing countries with large marginal areas, arid and salt, this is of great importance. The main parties within the Dutch production chain with an interest in this trait are breeding companies.

6.3 Biobased Economy.

A group of renowned experts and personalities prepared a vision document and presented it to the European Commission. It is called 'Plants for the Future – a European vision for plant genomics and biotechnology'. A few quotes from this vision to start this chapter: "investing more in researching plant genomics will pay potentially huge dividends", "there are enormous opportunities to use plants much more effectively to meet the challenges and demands facing European society in an environmentally friendly and sustainable way", "the future competitiveness of Europe's agricultural and food processing industries will depend on plant genomics, biotechnology and their smart application". Some of the approaches to the goals in exploiting as full as possible the potential of plant genomics that are suggested are compliant with the goals of TransForum, e.g. improve the genetic diversity of crop plants, develop renewable materials and develop more efficient biofuels.

The crucial starting point in the developing perception on the importance of a biobased economy is that today's society based on mineral oil and its derivatives can not last for ever. The

stocks of mineral oil are limited and will be exhausted in the near future. With the expanding economies of countries such as China and India and the need for their share of the oil stocks for maintenance and growth of their welfare and prosperity, in addition to the needs of the Western nations and other emerging economies, it is clear that we need to look for alternatives. Plants as efficient converters of solar energy into biological material can provide raw materials, specialty compounds and energy through biofuels. The main party within the Dutch production chain with an interest in this trait is the processing industry.

6.4 Plant Metabolites for human health

It has long been known that the metabolites in our food have a profound influence on our health in both positive and negative terms. One can immediately think here, e.g. of plant-based vitamins and micronutrients that are essential, or non-nutritional components in our daily diet that are required for maintenance of a healthy physiology. On the negative side, plants are also major sources of health-threatening metabolites such as toxins and poisons which, at very low ingestion levels can even prove fatal. Such metabolites have, contrastingly, frequently proven ideal lead compounds for the development of new drugs and pharmaceutical products with application in e.g. the treatment of cardiovascular disease (digoxin) and cancer (taxol, vincristin). As such, knowledge of the occurrence and biosynthesis of plant metabolites is important both to our understanding of the fundamental biochemical nature of our food as well as to the future analysis of the hugely under-exploited natural chemical biodiversity which is available within the plant kingdom. Currently, new tools are being developed for the rapid and broad analysis of the biochemical composition of plant extracts. Metabolomics has been reported to represent a major advance in our capacity to define biochemically biological materials which generates unique information with a broad application in the fields of e.g. food science, nutrition, plant breeding, processing technology etc.

6.5 Data integration for plant comparative genomics

In the wake of the whole genome sequencing projects, monolithic databases have been developed to accommodate data for a number of model organisms, the so-called Model Organism Databases (MODs). For plants, the first and most comprehensive one has been the Arabidopsis Information Resource (TAIR). With the accumulation of ever more complete genome sequences and associated datasets of ESTs, gene expression, and metabolites, a trend has set in to integrate these resources at higher taxonomical levels. The data warehouse solution EnsMart of the Ensembl MODs on vertebrate species is a prime example of this trend. Similar developments are underway for crops, e.g. the SOL Genomics Network website for Solanaceae. The power and successes of comparative genomic approaches underlie these developments: more can be learned about, e.g. Brassica through its comparison with Arabidopsis than by studying Brassica

alone. The taxonomic integration, however, still is much confined to genome sequence data, partly due to the unavailability of other datasets and partly because most computational tools for comparisons have historically been developed for DNA and protein analysis. An important direction for taxonomic data integration and software development will therefore be aimed at tools for cross-species comparative analysis of e.g. gene and metabolite expression datasets.

6.6 Implementation of the 'Omics' technologies in the production chain

Within the chain of agro-food production, physiological processes affect the quality of the produce. Factors that influence potential shifts in quality are manifold, including crop variety, developmental and physiological state of the product at the time of harvest, and post harvest and processing procedures and conditions. The development of dedicated arrays and diagnostic biosensors based on studying the genome (genomics), gene expression (transcriptome), gene protein products (proteomics), and the resulting chemical composition (metabolomics) will enable high-throughput monitoring and prediction of different aspects of plant or plant product quality at all stages of the production chain, information that is valuable for decision support in chain management. Genomics provides a diverse and powerful toolbox for the development of bio-marker based diagnostics, including e.g. microarray chips for monitoring shifts in gene expression, and metabolomics to discover key metabolites associated with physiological changes. The same genomics technologies are also instrumental to uncover the underlying metabolic and genetic basis of these processes, which in turn will deliver leads for breeding for product chain quality traits.

It will allow tracing and tracking of components (e.g. health-promoting substances), general product quality (off-flavors, decay), stress, senescence etc. as the result of storage or logistics or shelf-life. Based on these instruments all parties within the chain can decide whether or not to buy or sell the product.

6.7 Consumer demands

In the past, consumers have not always been the main determining factor in the development of new varieties. As a result of the discussions on GM crops and more generally as a result of more available time, financial means and opportunity through the internet for this, consumers have become more conscious, aware and interested in aspects of the production of food, feed and flowers. More and more they claim transparency and a role in determining traits that they would like to see in new crops or varieties. Traits such as increased shelf-life, good taste and healthiness are considered important. Also, the retailers support the consumers in formulating their desires or suggesting their needs. Although not always possible in all aspects of a crop, producers should communicate more frequently and more in depth with retailers and consumers in a two-way fashion on the aspects that determine a modern variety. Instruments for this type of communication need to be developed, if not available yet. The main parties within the Dutch production chain with an interest in this aspect are retailers and consumers.

6.8 Chain management

As stated in the previous paragraph it is important to involve all parties from the entire production chain, including end-users, in communicating and in determining the characteristics of new crops and varieties. Directing this process, making sure that all partners contribute and are taken seriously, that all partners comply with the goals that have been set jointly and take the necessary measurements for this, requires an appointed central coordinator, managing the entire chain. The tasks and responsibilities of such a chain manager need to be defined and accepted by all parties. The chain manager should increase the efficacy of implementing through the entire chain the results of the genomics research. All parties are stakeholders in this aspect.

7. Research Agenda and Societal Opportunities

TransForum brings together private companies, governmental bodies and knowledge institutes in projects aimed at the transition of agriculture into a sustainable enterprise. Scientific knowledge should be combined with applied knowledge and societal innovations. To this end, TransForum has two instruments, Innovative Practice Projects (IPs) and Scientific Projects (WPs). In the IPs the emphasis is on true integration of both scientific and applied knowledge present and available with all participants, who actively contribute to reach the project goals. Scientific methodologies, transition management and strategies for increased durability are aimed at testing in practice the strategies for innovation. In WPs some particular questions arising from the IPs can be addressed in more detail and in depth.

Resistance to pathogens has been the main target in several research initiatives, e.g. in Rosaceae such as rose, strawberry and apple, but also in Solanaceae such as potato and tomato (CBSP). The Innovative Practice Project, VC-010, Healthy pip fruit chain, is an example of a project, using genomics, aimed at making disease resistant fruit varieties, preparing a communication plan to inform the public and determining and monitoring decisive factors in formation and changing of public opinions. Implementation is guaranteed because of involvement of the appropriate representatives of fruit growers.

Industrial crops have been a subject for research for quite some time, firstly in identifying potentially interesting species and looking at problems or potentials in breeding such crops. Calendula and Crambe were taken further as crops with interesting seed-oil composition; hemp as a fibre crop and Miscanthus as an energy crop. Crambe is explored as an ice-breaker crop for GM applications in preparing a non-food, waxy esters (lubrication) producing crucifer in a collaborative efforts with scientists in Sweden. For Calendula, an international production chain has been formed in an IP, IN-008, Innovative Practice project Calendula, in which several aspects of using calendula oil as solvent in paints are tested in several facets of the chain.

Crambe, being a crucifer just like the fully sequenced model crop *Arabidopsis thaliana*, can be used in exploring the potential of comparative genomics alongside parallel initiatives in Brassica, another cruciferous crop. An IOP-Genomics project proposal on Brassica Vegetable Nutrigenomics has recently been granted funding. Here, information available from *Arabidopsis* will be extrapolated directly to Brassica rapa. The first target compounds are glucosinolates, that are also a defined research target in Crambe. Through plant metabolites we are at the crossroads between bio-based economy items and health components defined by consumer demands. This is an example of divergent targets but convergence in approaches. The information generated in one project can clearly help progress in another project.

With the topics mentioned in chapter 2 and the examples and crop families as focal points mentioned here, the stage is set for the formulation of new IPs and WPs.

Utilising intrinsic robustness in agricultural production systems

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Abstract: This paper explores the potential of utilising robust crops and livestock for improving sustainability of agriculture. Two approaches for dealing with unwanted fluctuations that may influence agricultural production, such as diseases and pests, are discussed. The prevailing approach, which we call the 'Control Model', is to protect crops and livestock from disturbances as much as possible, to regain balance with monitoring and intervention and to look for add-on solutions only. There are a number of problems associated with the Control Model, including reduced animal welfare, environmental pollution and low public support. An alternative approach, which we call the 'Adaptation Model', is based on reducing the consequences of disturbances rather than taking disturbances out. Robust Design may be a promising methodology to utilise robust components and design the production process for minimal variation. For crops and livestock this means utilising and supporting their intrinsic ability to deal with disturbances by adaptation. Four main areas of research required for adopting the Adaptation Model were identified. Firstly, it is necessary to raise the awareness of the two approaches with all parties involved to stimulate innovation. Secondly, the methodology for robust design within and across animal and crop production systems needs further development. Thirdly, there are still many unanswered questions regarding optimal utilisation of biological robustness mechanisms, which requires technical research. Fourthly, as diversity of production systems increases, dissemination of knowledge will have to change from dissemination of solutions to dissemination of methods to identify the best solution for a specific context.

*"We cannot solve the problems we have created with the same thinking that created them!"
[Albert Einstein]*

Introduction

Following the Food and Mouth Disease outbreak in 2001, a group chaired by Dr Wijffels was invited by the Minister of Agriculture to advise on the perspectives for sustainable animal production in the Netherlands. Their report (Ministry of Agriculture and Food Safety, 2001a) and the 4th National Environmental Policy Plan (Ministry of Housing, Spatial Planning and the Environment, 2001) were the start of a change in governmental policy in favour of a transition to a sustainable agriculture (Ministry of Agriculture and Food Safety, 2001b, 2002). This transition requires a different kind of knowledge and expertise, and new ways of collaboration between commercial and research organisations. Supporting this process is the aim of TransForum. For this purpose, they invited scientists to explore existing expertise and expertise to be developed for key focus areas. The assignment for this paper was to explore the potential contribution of intrinsic robustness mechanisms for achieving a more sustainable crop and livestock production.

TransForum define a sustainable agricultural sector as follows when compared with the current situation³:

- It is economically sound;
- It provides high-value products and services;
- It is considerably less demanding and less detrimental to the environment;
- The minimum level of animal health and welfare is higher;
- It results in an attractive countryside;
- It is supported by the general public and well integrated within society.

We tend to evaluate the functioning of agricultural production systems as the average performance on the above-mentioned criteria under conditions that are considered to be "normal". However, as conditions vary and disturbances take place from time to time, stability of the production system is also an essential feature of its performance. Sensitive systems may on average meet the sustainability criteria, but may show strong deviations in case of unfavourable conditions. A sensitive farm may be profitable on average, but go out of business due to liquidity problems when prices are low.

There are two approaches to keep a system in balance and these are not mutually exclusive. The one approach is keeping away disturbances and the other approach is minimizing the impact of disturbances.

³ http://www.transforum.nl/transitie_duurzame_landbouw.htm#innovatie

The two approaches can be visualised by keeping a ball in position. On a flat surface, the ball only remains in position if it is protected from disturbances as draught. If the protection is unsuccessful, the ball has to be pushed back in position. In the second approach, the energy is spent on the design of the surface. If the ball is moved because of a disturbance, it rolls back in position afterwards (see Fig. 1). In both cases, the ball is in balance in ideal conditions, but the balance is more stable in the latter case.

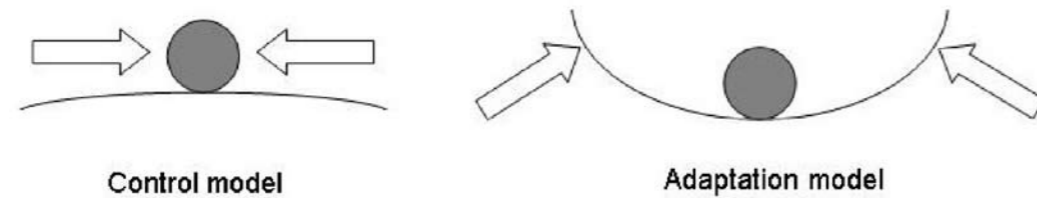


Figure 1. Under the Control Model, keeping the ball in position is by design dependent on protection and interventions, but under the Adaptation Model, returning to the original position after a disturbance is part of the design.

In this paper we contemplate approaches to achieving stability in agriculture. We argue that the current approach is mainly based on keeping away sources of variation and highly dependent on continuous monitoring and intervening. We call this approach the Control Model. We also set out the contours of an alternative model based on allowing and supporting systems to cope with disturbances through adaptation. In this case, maintaining stability in the face of foreseen and unforeseen problems is an integral part of the design process. We call this the Adaptation Model. It must be stressed that the Adaptation Model is not synonymous with organic farming, although many aspects of the Adaptation Model are implemented in organic farming. For example, the use of artificial fertilizer or genetically modified organisms is prohibited in organic agriculture, whilst under the Adaptation Model, there is no a priori restriction of methods.

It is evident that the Adaptation Model is closely linked with concepts as robustness (in the narrow sense: ability to switch between underlying processes to maintain the balance), resilience (ability to regain the balance after a disturbance) and resistance (insensitivity to disturbance)⁴. Yet none of the three concepts describes the Adaptation Model fully on its own. In the remainder of the paper we will use 'robust' and 'robustness' in the broad sense, which is minimal variation in a target feature following a disturbance, regardless of whether it is due to switching between underlying processes, insensitivity or quickly regaining the balance.

The objective of this paper is to discuss the potential for utilising intrinsic robustness mechanisms for achieving an inherently stable and sustainable agriculture.

⁴ For a system-theoretical discussion of robustness and related terms, see <http://discuss.santafe.edu/robustness> or Jen (2005).

The Control Model

Prior to World War II, agriculture in the Netherlands was characterized by small-scale production with substantial variation in production systems within and between regions. Plant and animal breeding was mostly local or regional and many local varieties existed for the various species. The post-war Dutch and European agricultural policy, aiming at securing a minimum level of food production, stimulated large-scale farming at the expense of small farms. In 1958, this common practice became official policy. In the process, agriculture became technology-driven with a single objective: maximum production at minimum cost.

These changes translated to designs for maximum productivity per unit, high labour efficiency and low production cost. Production was stabilised at the maximum level by keeping any disturbances away from animals and crops as much as possible, for example through killing bacteria with antibiotics and heavy pesticide use. Scale-enlargement caused the shielding from threats to shift from individuals to ever-increasing groups and acreages. This has led to beef, veal, pig and poultry production systems with high concentrations of animals per farm, low labour requirements, a high level of automation and protective environments. Crop production systems were characterized by the large-scale cultivation of monocrops with high fertilizer and pesticide input.

These systems show many features of the Control Model. The paradigm underlying the Control Model is that crops and livestock can be completely controlled and manipulated to attain maximum production and eradicate threats and disturbances. This protection involves frequent and intensive human interventions and neglected inherent robustness of the production system.

Although this approach was very successful in improving productivity, a number of problems became apparent. These problems concern the efficacy and the negative side-effects of the Control Model. Firstly, imperfect implementation of the intended design as well as freak incidents may have dramatic consequences, especially when the number and the concentration of animals or plants are high. This includes outbreaks of infectious diseases and in animal production, overburdening or a chronic stress response, if animals fruitlessly try to adapt to the adverse conditions. Secondly, the protection may only be effective temporarily, because of pests and pathogens developing resistance. Thirdly, negative side-effects include inadvertent environmental pollution, loss of biodiversity, loss of diversity of production systems and lack of public support.

The key features of the Control Model at the levels of individual animal or plant, crop, herd and production chain are:

1. Protection from exposure to disturbances as much as possible;
2. Maintaining the balance is by design dependent on monitoring and intervention. Interventions to regain the balance at one level are often applied at a higher level;
3. It is implicitly assumed that new problems or demands can be solved with add-on technology

Animal production

Infectious animal diseases

Infectious diseases on the list of “Diseases Notifiable to the OIE (World Organization for Animal Health)”⁵ are not considered in this paper, because dealing with these diseases is governed by international agreements.

Endemic infectious diseases are a serious problem for current animal production systems. Infectious diseases rarely fade away in these systems, because of the high concentration of animals and the constant influx of unchallenged animals. An outbreak of an infectious disease therefore often has long-term consequences for the profitability, because of higher mortality, higher veterinary costs and lower productivity. Avoiding outbreaks of disease has become a very critical issue in animal farming. Given their existing production system, there is little farmers can do but to increase biosecurity, and veterinarians advise accordingly. It is now common in animal production to restrict the number of visitors to the farm to the minimum, to have shower facilities or provide visitors with boots and over-alls, to restrict intake of animals and clean and disinfect pens regularly. This increases the cost of production substantially, but within the given system it is cost-effective.

For an animal, an infectious disease may pose a threat to its life and welfare. Developing the immune system and mounting an immune response therefore get priority over production traits. For this reason, farmers and veterinarians tend to combat the pathogen rather than utilise the animal’s immune response. Apart from vaccinations and stimulating colostrum intake, there is hardly any structured approach to training the innate and adaptive immune system. This has led to scientists extrapolating the hygiene hypothesis from humans to farm animals (Van der Weijden and Schrijver, 2004; Van Eden, 2005). They hypothesize that the immune system of farm animals is insufficiently challenged because of hygienic conditions, which would leave the animals vulnerable to otherwise harmless micro-organisms. In other words, the reliance on human interventions leaves inherent mechanisms to deal with pathogens unused and underdeveloped. This view, however, is highly controversial among veterinary scientists.

More recently, pressure from the production chain has pushed farmers even more in the direction of freedom from certain micro-organisms. Farmers have the obligation to prove that their stock is free of certain micro-organisms, for example *Salmonella* spp. in the case of broiler producers. If they fail to do so, they risk a penalty or may even lose their contract.

Overburdening of animals

The experience of the last four or five decades has provided a wealth of information regarding maximisation of production from farm animals through breeding, feeding, housing and management. The average milk production per cow has increased from just over 4,000 kg to

⁵ http://www.oie.int/eng/maladies/en_classification.htm

nearly 9,000 kg per 305 days lactation. Pigs reaching 100 kg of body weight in 130-140 days are no longer exceptions. Broilers weigh more at 40 days of age than many mature laying hens of 20 weeks and older.

Animals with high levels of production often struggle in suboptimal conditions. Suboptimal conditions under the Control Model imply that interventions at herd level to regain the balance at animal level, as envisaged in the design, don’t take place or are ineffective. Dairy cows at the peak of lactation often stop the oestrous cycle temporarily when they are in a negative energy or protein balance. In this way the body protects the cow against complete depletion of body reserves. In other cases, the body is not able to cope with the high level of production in suboptimal conditions. Beef cattle, slaughter pigs, broilers and turkeys often accumulate body weight so rapidly, that slippery floors, overstocking and poor housing facilities cause damage to feet, bones and joints. It can equally well be argued that it is the genetic potential, the actual high level of production or the suboptimal environment, which is responsible for the overburdening. Breeders have the responsibility to genetically select for the full range of existing production systems and farmers should aim for a level of production that animals can sustain given the conditions on the farm, or otherwise improve the conditions.

Chronic stress in animals

A chronic stress response is the result of structurally not fulfilling certain needs. Imperfect implementation of the Control Model at the level of the production system will invoke an adaptive response of the animal, but since the design of the production system relies on interventions for maintaining the balance, expression of the adaptive response is not supported or even counteracted. Frustration because of fruitless attempts to adapt will in many cases lead to a chronic stress response. For example, an animal that is cold and wants to go to a more comfortable spot but has nowhere to go in a pen with just one climate, will become restless and frustrated. In many of the current production systems for pigs, poultry, beef and veal, animals show symptoms of a chronic stress response, such as stereotypic behaviour, damaging behaviour directed to pen mates, elevated cortisol levels and depression. A chronic stress response may also suppress the immune function, leaving animals more exposed to opportunistic pathogens. Another cause of chronic stress is inhibiting species-specific behaviour, such as rooting or dust-bathing on a concrete floor.

At herd level

Disturbances at herd level that cause variation in the level of sustainability include variation in feed quality (storage, variation in raw material), wear and tear of equipment, corrosion, accumulation of dust and obnoxious gases in the air, pests (such as insects or rodents), a transport ban, a power cut, changing legislation, but also variation in individual requirements of animals managed as groups. Many of these challenges are dealt with according to the ‘protect or intervene’ approach although in some cases this is the only option.

Arable production

Soil degradation

High inputs of artificial fertilizers made crop production systems less dependent on the quality of the soil and the soil was therefore mainly seen as a substrate. The use of solely artificial fertilizer may lead to a reduced soil organic matter content, which plays a critical role in the maintenance of soil structure and water holding capacity. Intensive soil cultivation may aggravate the soil degradation process.

Emerging pest, weed and disease problems

The large-scale cultivation of monocrops may initiate pest and disease problems as insect pests can effectively track and colonise crops and diseases can spread fast in monocrops by plant to plant infection. The heavy use of fertilizers may make crops vulnerable for attack by insect herbivores and pathogens (Matson et al. 1997). Many agricultural pests, such as aphids, leafhoppers and planthoppers, have shown strong population increases in response to nitrogen fertilization. The use of broad-spectrum pesticides disrupts pest regulation by natural enemies and the development of resistance against chemical pesticides in insect herbivores, weeds and pathogens has become a serious problem (Clarke et al. 1997). For instance, insects and weeds often evolve resistance within one and two decades, respectively. Similarly, crop resistance to pathogens generally lasts only a couple of years.

The interrelation between arable and animal production

The paradigm underlying the Control Model also caused animal and arable production to become detached from each other. With the introduction of chemical fertilizers and the globalisation of the market for feedstuff, different agricultural sectors had the opportunity to maximize production independently. One of the effects of the disengagement of the arable and the animal sectors was that poultry and pig production could grow enormously without an associated arable sector for producing the feedstuff. This resulted in a huge surplus of manure. Meanwhile, the arable sector had grown accustomed to the use of chemical fertiliser, which at the time was considered to be much easier for precisely meeting the plant requirements at the right time. Manure was therefore only used for the limited amount of land that the poultry and pig farmers did possess, thus creating an environmental problem. Another problem introduced by the detachment of animal and arable production is quality and risk management of globally traded ingredients of animal feed.

Negative side-effects of the Control Model in animal and arable production

Toxic residues

Pesticides applied to arable fields may result in significant doses of pesticides reaching adjacent ecosystems via leaching or aerial drift, where it can have a strong impact on non-target organisms. Also abundant use of veterinary medication may lead to metabolic residues accumulating in the environment.

Loss of biodiversity

Scaling-up of field sizes, removal of non-crop habitats and large-scale monocropping have led to simplified agro-ecosystems with only few and fragmented non-crop habitats left. Together with the frequent and intensive disturbances in crops, these developments have contributed to a rapid decline of biodiversity in rural landscapes (Benton et al. 2003). At the present time, most biodiversity in intensively used areas is concentrated in field edges and non-crop habitats. In animal production, the number of lines and breeds has decreased significantly after the process of intensification and scale-enlargement commenced. This is a direct consequence of the removal of local sources of variation, which made locally adapted populations redundant.

Loss of cultural diversity

With the introduction of production systems that were independent of the local context, local variation in customs, practices and production systems gradually disappeared. This has led to an increasingly monotonous countryside, aggravated by the scale-enlargement. Pig and poultry production units generally make a dull and closed impression to the general public.

Lack of public support

With increasing biosecurity, animal production systems have become inaccessible for the general public. This makes people wonder what is going on. Many are also concerned about the above-mentioned problems and it is easy to blame the farming community.

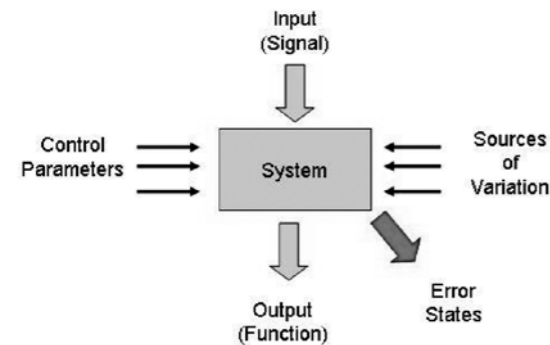
Adaptation model

The key element to the Adaptation Model is that systems at all levels are designed to reduce the consequences of sources of variation, rather than taking out the sources of variation. It is a matter of managing sources of variation where possible, and removing them where easy or necessary. In this way, robust cropping and animal production systems contribute to a stable and sustainable agricultural sector on the basis that a complete prevention of threats is not feasible.

Under the Adaptation Model, the design of production systems and processes is optimised for stable performance in the normal bandwidth of sources of variation. This means that financial income no longer is the optimisation criterion, but a stable and reasonable income is used as a precondition in the design process. In fact, some productivity is traded for stability.

For the design of a robust production system (Fig. 2) it is necessary to have a measure of the ideal function of the production system. Disturbances that one cannot or decide not to remove will result in a functioning that deviates from the ideal function. In addition, there are control parameters, of which some will have an impact on the level of functioning and others on the variation of functioning in the presence of disturbances. The concept of robust design is to use robust components and set control parameters in such a way that deviations from the ideal function caused by the present disturbances are minimal. This concept has been implemented for quality control in engineering cars and microchips ("Robust Engineering Design", "Robust Design", "Taguchi Methods", see Phadke, 1989; Dehnad, 1988; Taguchi, 2004).

Figure 2. Schematic representation of a production system



As an example, the system could be a production system with pigs. The input is feed. Sources of variation are seasonal changes in climate, presence of pathogenic micro-organisms, pres-

ence of an aggressive pen mate, etc. Control parameters (in the design process!) are stocking density, pen size and layout, building layout and distance between buildings, but also management procedures for weaning and moving pigs and changing feed. The deviation from the ideal function (the output) could be the total loss to anyone (pig, farmer, buyer, society) of a pig produced or it could be the loss of welfare to the pig.

Using robust components implies utilising intrinsic robustness mechanisms. For a discussion of biological robustness, see Kitano (2004). In animal production, these mechanisms include behavioural, physiological and immune responses at the animal level and a stable micro-flora at the herd level. Relying on these mechanisms does require confidence in the natural ability of animals to cope. Sometimes it is argued that our domestic animals are too far removed from their wild ancestors to be able to cope with natural stressors. However, several studies showed that pigs (Jensen, 1988; Stolba and Wood-Gush, 1989) and poultry (McBride et al., 1969; Wood-Gush et al., 1978) are very well able to live a natural life after being released into the wild or in a semi-natural enclosure.

For cropping systems, intrinsic robustness mechanisms exist at the level of the plant and the field or farm. Diversification at all levels is regarded as a promising strategy to safeguard food production with only limited dependence on agrochemicals. Diversified cropping systems may be less sensitive to invading weeds, pests and diseases for a number of reasons: a more efficient use of resources, a higher occupancy of niches, a more abundant and diversified community of natural enemies, less effective transmission of pathogens and more favourable structural and micro-climatic conditions, which together may reduce the impact of yield-reducing agents.

It must be stressed that stability of sustainability cannot be achieved by just using robust crops and animals. It will require a re-design of systems at many levels, from animal or crop, herd, production chain and sector to national and international arrangements in order to utilise robustness.

The key features of the Adaptation Model at the levels of individual animal or plant, crop, herd and production chain are:

1. Allow to cope where possible, but protect where necessary
2. Utilise intrinsic adaptation mechanisms, allow them to learn-by-doing and support them
3. Consider the possibility that fundamental re-design may be necessary

Animal production

Infectious diseases

There are two main ways to avoid clinical disease symptoms (hence not including sub-clinical disease). Firstly, to avoid exposure of the animal to the pathogen and secondly, to avoid that infection results in clinical symptoms. The third way, which is to avoid that exposure results in

infection (e.g. genetic resistance to F18 E. coli in pigs), is too rare to be used as a general strategy. Under the Adaptation Model, it is a conscious decision whether one of the two or both are employed to minimise clinical disease. For some pathogens, there is no alternative option to avoiding exposure, as animals will be dead before they have mounted an immune response (e.g. highly virulent Asian Influenza strains) or because of international agreements (Diseases Notifiable to the OIE)³. In practice, it is probably best to start up with the highest health status that can be maintained for a considerable period of time.

As yet, there are no systems that are consciously optimised for avoiding that infection results in clinical disease. It requires that animals are prepared for exposure, in case it happens, and that the production system hamper pathogens spreading and replicating rapidly. The latter has consequences for density of animals, contact structure between animals, age structure of the population and management of microflora in the environment, among other things.

The ability of an animal to deal with infection depends on its genetic potential, its experience and, at the time of exposure, its physiological state and the support it gets for adaptation. Concerning general resistance to clinical disease, we should not expect large gains from breeding and selection. A good overview of what is possible and what not in poultry breeding is given in Muir and Aggrey (2003). Although there are examples that unbalanced genetic selection caused increased sensitivity to a specific pathogen and examples that selection against a specific pathogen was successful, there is no evidence that the genetic potential for immune-competence has deteriorated or is insufficient.

Building up experience may occur through low-level exposure under some form of protection, through which the immune system learns to mount an appropriate response. It has been suggested for this purpose to use vaccinations, keep animals in more natural social groups (weaning them at a later age), bring animals into well-controlled contact with non-pathogenic micro-organisms early in life, and manage the intestinal microflora by enriching diets with roughage and pre- and probiotics, in order to prepare animals for exposure (Van der Weijden and Schrijver, 2004). For some of these suggestions, however, there is only circumstantial evidence. A concerted approach is required to determine the best over-all strategy.

An appropriate response at the time of exposure also requires that the immune system is not suppressed through a chronic stress response, that the animal has sufficient metabolic resources available and that the environment supports an appropriate response, for example by providing a micro-climate with a higher temperature.

Non-infectious sources of variation

Situations of chronic stress should be avoided, not only to avoid immune-suppression, but also because they generally arise from a breach of welfare. This means that animals should be kept in an environment in which they can behave and adapt as they require, including species-specific behaviour. The ability to adapt successfully again requires sufficient genetic potential, building up experience and getting the opportunity and resources to adapt. Optimising pro-

duction systems and processes for building up experience and supporting adaptation is a new perspective and many questions are still unanswered. What is the best way to prepare animals for a dynamic environment? What role do social skills play and how can they be developed? What support is needed for successful adaptation?

Dealing with disturbances at herd level for minimal deviation from the target output (however defined) through the design will be a challenge. It requires that production systems are already in the design phase exposed to these disturbances. It also needs to be assessed what kind of disturbances in terms of incidence and seriousness should be included in a Robust Design approach.

Arable production

Soil health

Improving soil quality with an approach that focuses on a sustainable soil management is a major key for the Adaptation Model. Improving soil quality means improving physical, chemical and biological conditions of a soil for a stable crop growth. Sustainable soil management might be achieved through a site-specific approach, a sound crop rotation, good-management practices and fertilization including organic soil amendments. The use of animal and green manure, cover crops and reduced tilling may raise the organic matter content of soils and enhance the diversity of soil organisms. These features are associated with enhanced disease suppression, nitrogen-mineralization and a favourable soil structure. A healthy soil is therefore the basis for robust crop growth.

Plant/Field level

Yield stability can be obtained by the use of varieties that have specific traits that makes the crop less vulnerable to unfavourable conditions and yield reducing agents. For instance, varieties with a deeper rooting system are more tolerant to drought, a dense crop canopy improves the competitive potential of the crop and hairy leaves make the crop less attractive for aphids (Lammerts van Bueren et al. 2002). Diversification at the plant level may entail the breeding or genetic engineering of crops that are resistant to pathogens (e.g. Phytophthora infestans) or pests (e.g. crops that produce Bacillus thuringiensis toxin). The world-wide reduction in pesticide use by the use of Bt-corn and cotton are tremendous. However, if their deployment is to be sustainable, resistant crops must be used in conjunction with methods that promote natural occurring antagonists. Otherwise their effectiveness is prone to neutralization by resistance in the same manner as with pesticides. To date, there is considerable resistance towards the use of genetically modified organisms among the general public in the Netherlands. The use of genetically engineered crops with subtle changes, for instance crops containing resistance genes originating from related plant species, are likely to be less controversial. Diversification at the within-field level may involve agroforestry, multicrops, cover crops, variety mixtures, or beetle

banks that act as sources of predators that may control pest populations. Good results have been obtained by the use of variety mixtures, resulting in a substantial reduction of pesticide use (e.g. Zhu et al. 2000). Although multicropping is common in the tropics, it is hardly used in the temperate zone because it requires careful selection of plant species, intensive and careful management and there is a lack of machinery tailored to harvest multiple crops grown at the same time in the same field. Precision agriculture may be used for local interventions with pesticides when yield reducing agents seem to go out of control. Diversification at the field level may involve the establishment of field margins, inclusion of fallow periods and crop rotation. Field margins may reduce drift of pesticides and may act as sources for natural enemies that may control pest densities in crops. However, in particular cases field margins have also been shown to support for pests. Careful selection of plant species is therefore essential to enhance the diversity of field margins, but without the stimulation of pests, weeds and diseases.

Farm/landscape level

Diversification at the farm or landscape level may involve the establishment of hedgerows and other semi-natural habitats and the re-introduction of arable-livestock systems. Arable-livestock systems allow favourable nutrient management (e.g. potential to close nutrient cycles at the farm level). Diversified landscapes composed of arable fields intermingled with natural habitats have in general a more abundant and diverse natural enemy community and often lower pest densities in crops (Thies and Tschardt 1999). Many processes in pest and disease development act at spatial scales exceeding the farm scale. Farmers should therefore join forces for effective pest and disease management. An example of a project aiming at the diversification at higher spatial scales is the Functional Agro-biodiversity Project (2005) which aims to enhance biodiversity and suppress insect pests by the large-scale establishment of field margins in de Hoeksche Waard.

The interrelation between arable and animal production

In natural ecosystems synergistic interactions among plants and animals are common. Such interactions between plant and animal production may help both types of production to become more stable. Animal production may help to stabilise crop production through widening of crop rotation or grazing under-crops, such as grass-clover or lucerne. This may support soil health and weed suppression. Plant production may stabilise animal production through removing excess minerals and reducing disease burden in pig or poultry outdoor yards or by growing crops for animal feed at minimal cost. Plant and animal production could also mutually benefit from cooperation by optimally utilising the excess of manure from animal production systems. Another example is keeping poultry and sheep in orchards, where the trees provide shade, the poultry reduce the burden of harmful insects and the sheep reduce the development of fungi by eating weeds, grass and old leaves (Bloksma et al., 2002).

Impact on aspects of sustainability

It is evident that much more work is required before the impact of adopting the Adaptation Model on sustainability can be assessed accurately. Nevertheless, there is great potential when considering the definition by TransForum (see Introduction). With regard to profitability for an agricultural producer, productivity of the herd will reduce and the price per unit of product will reduce as well, unless the product fits a niche market. This means that the cost of production has to be reduced considerably, especially the fixed cost. However, there are already some promising examples (Heineken, 2004). With regard to product quality, there is a potential for product differentiation for niche markets (e.g. agricultural production methods that embrace local customs or heritage may be sold as regional products), but there is also a potential for producing uniform products for bulk markets with diverse production systems when farmers get used to optimising for minimum variation. The environmental burden may be lessened if the use of medication and chemical crop protection is reduced (e.g. reduced toxic residues in the environment) and the emission of nitrogen and phosphate is minimised. Concerning animal health & welfare, a well-prepared immune system in combination with a stable micro flora and an appropriate biosecurity may improve animal welfare through a reduction of clinical diseases symptoms. Allowing animals to adapt may reduce the undesirable side-effects of chronic stress. Allowing biodiversity of wildlife to increase will improve the attractiveness of the countryside (e.g. flowering plants in field margins are often appreciated by the general public). We anticipate that the above will have a positive impact on public support, especially when the positive contribution is also intuitively clear.

Towards sustainability even in adverse conditions

Our vision for agriculture in the future is one of an agriculture that is sustainable not just in ideal conditions, but in the entire bandwidth of normally occurring disturbances. This requires a shift in paradigm from the Control Model to the Adaptation Model.

Current situation

In the Netherlands, a move towards more sustainable animal production has already started. Support from the general public, impact on the environment and animal health and welfare are increasingly taken into account. Yet there is still a long way to go.

The primary strategy to improving sustainability, however, is largely based on the Control Model: solutions aim at protecting against sources of variation and require technical or human intervention. Examples from animal production are biosecurity as the single means of improving animal health and filters in the air outlet of pig and poultry sheds to reduce environmental pollution. The solutions need to be almost perfect as failure has potentially far-reaching consequences.

In animal production, the interest in aspects of the Adaptation Model is restricted to a number of non-veterinary scientists and a small number of predominantly organic farmers. Utilising inherent robustness of animals is therefore controversial. Many veterinarians and farmers consider inherent robustness to be irrelevant for existing production systems or lack the confidence to rely on it. The perception of the general public is that animals have lost inherent robustness because of continued genetic selection for production traits. Our view, however, is that existing production systems ignore inherent robustness and counteract any attempts of animals to deal with threats.

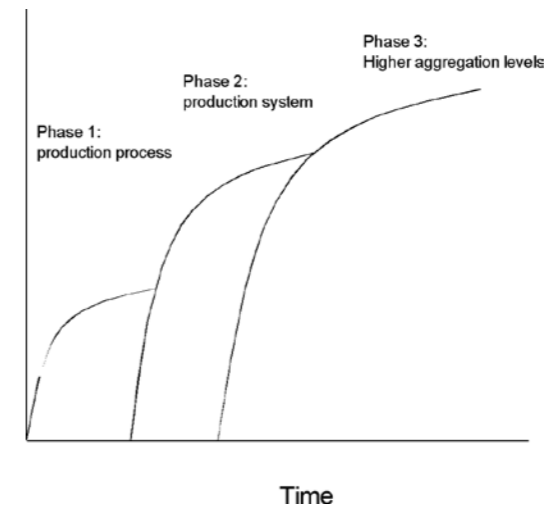
In crop production a gradual shift towards more sustainable production systems is also evident. Even though nearly all crop varieties used are developed for maximum yield under optimal conditions and some farmers still adopt practices associated with the control model (e.g. calendar sprays), there is an increasing interest in agricultural production systems that utilise internal self-regulation processes and are therefore less dependent on human intervention. For instance, integrated pest management (IPM) strategies are now widely used and farmers become more and more interested to use functional biodiversity to enhance the resilience and buffering capacity of the agro-ecosystem. In addition, organic farmers form a small group of front runners that develop cropping systems that are robust without dependency on agrochemicals.

Achieving the vision

A transition towards a more sustainable agriculture consists of many, largely autonomous processes. Small technological innovations may gather momentum if sufficient people take up the idea and develop it further, and if the conditions are right. If such innovations lead to changes at a higher aggregation level and to changes in perception, attitude and behaviour in society, then it has evolved into a system innovation.

The shift from the Control Model towards the Adaptive Model can be considered as a development process that involves three phases (Sterrenberg and Brandt 1996). The first phase involves changes in the production process. Amendment of the production process can be realised within the current production system and may entail a reduction of stocking densities or the shift from calendar sprays to spraying according to damage thresholds. Although such an altered production process can be implemented relatively quickly, the expected benefit resulting from these changes may be modest (Figure 3).

Figure 3. Improvements in sustainability per phase over time (Sterrenberg and Brandt 1996)



The second phase entails the transition of production systems. These changes often involve considerable investments, such as replacement of cage-housing of laying hens by an outdoor free-range housing system or the shift from conventional to organic farming systems, and can only be implemented in the longer term. The expected benefit, however, is likely to outweigh that of amendments in the production process.

The third phase contains changes at higher aggregation levels (e.g. regional level or production chain). Tuning production systems at larger spatial may result in the closure of nutrient cycles or the suppression of pests and diseases by habitat management and crop rotation. The implementation of these changes that exceed the system level require effective communication between farmers but hold promise of substantial benefits (Fig. 3).

Stumbling blocks

Legislation and regulations can easily stand in the way of the transition process. Pioneering farmers who want to implement new ideas, not seldom find themselves confronted with restrictions because of legislation and regulations. For example, if legislation about mineral losses in animal husbandry is implemented strictly, it is not possible to test and develop various alternative housing systems because the ammonia emission may be too high. Of course, a too high ammonia emission is not acceptable for systems in practice, but legislation should not be restrictive to innovation in a promising direction.

Legislation that allows for making an exception for promising initiatives may be instrumental in stimulating the innovative potential of farmers. This requires effective communication

between policymakers of different disciplines and the agricultural sector. Also, a different approach in legislation and regulations may be helpful. Many regulations, such as the Dutch quality assurance for pig production (IKB), are at the level of the means, rather than the objectives. Instead of exactly prescribing how a farmer should do something, the regulations could provide a framework of only a few important preconditions within which a farmer has to achieve certain goals, for example a mortality below a certain maximum. In this way, general goals can still be achieved and farmers have more freedom for developing innovative solutions. Another stumbling block is the organisational structure of many of the agricultural production chains. Firstly, there is a lack of trust between primary production and other links. Secondly, there is a concentration of power in links other than primary production, such as retailers, leaving primary production fragmented with virtually no power. The lack of trust is also an issue between primary production and the various governments.

Research agenda

1. Raising awareness

Technological innovations based on the Adaptation Model will not be successful unless an increasing number of people adopt the Adaptation Model as a conceptual framework. The Adaptation Model must have sufficient critical mass in order to progress. It means that research should raise the awareness among farmers, specialists, scientists, the supplying and processing industry and the general public of the differences between the two paradigms.

Projects in this area could demonstrate the process of interactively designing for a normal bandwidth in a given context. This could be done at three levels: designing new production processes within existing systems, designing new production systems and processes, and designing new economic structures, production systems and production processes. It requires an interdisciplinary and interactive design approach to develop stimulating and thought-provoking prototypes. The objective of such demonstration projects is not to develop ready-made solutions, but to change the perspective for innovations.

A second issue in this area is perception and management of risk. Especially the notion of a zero-risk is a potential time bomb for the farmers' profitability and the consumers' confidence. The change in risk perception is necessary to build the trust of the general public, and to make the various parties involved prepared to make an effort.

Related to this is also the problem of allocation of costs of calamities, especially when the consequences increase with a reducing risk. Under the Control Model, the society always paid for the costs of for example environmental pollution (clean water management) through taxes and not via more expensive products. In this way, the true costs of the current production system are not visible (Kalverkamp and Van Hoytema, 1989).

2. Designing for robustness

The methodology required for developing inherent robust agricultural production processes and systems is not available. The theory, however, exists and has been developed for industrial production processes (Robust Design). This largely statistical theory needs to be changed and adapted for agricultural production systems and tested for suitability. Following the adaptation of the general methodology for agriculture, it would be helpful to have a simple protocol or tool that a farmer can use to evaluate alternative practices for impact on variability. This needs to be developed and disseminated in practice.

Additional work is also needed to further develop system approaches to achieve more inherently robust production systems of agricultural products. Kitano (2004) argued that robustness is a fundamental feature of evolvable complex systems. Special emphasis is therefore required for self-learning systems at all levels, that evolve through learning-by-doing.

For new systems to contribute to a more sustainable agriculture, it is necessary that there is a continuous reflection on presuppositions and possible negative side-effects and partitioning issues that come with it (Beck, 1992). This requires a much stronger interaction between social and technical sciences and a substantial involvement of society in the design process, for example through citizen groups.

3. Technical research

The change from the Control Model to the Adaptation Model also raises many technical questions. For example in animal production, there are still many unanswered questions regarding optimum utilisation of the animal's ability to adapt through genetic selection, training and support. The answers may also vary for the various classes of non-zoonotic and zoonotic pathogens and non-infectious environmental stressors. Another issue is the avoiding of chronic stress. Is it possible to apply the current knowledge to existing production systems in the short term and design improved systems in the longer term? A third issue is avoiding of damaging behaviour to pen mates, in case a chronic stress response inadvertently occurs. Managing the micro-flora to control pathogenic micro-organisms and keeping it stable may be another promising area.

In crop production, robust crop varieties are currently not available. Breeding programs may select varieties that attain good yields under a wide range of conditions. Further, multi-cropping systems may solve much of current problems concerning yield reducing agents, but are not used in practice. The identification of well-balanced crop combinations and development of machinery to harvest multiple crops in the same field may make mixed cropping systems feasible for practice. Finally, there is little knowledge of how the diversity of soil biota, extra-field vegetation and natural habitats may enhance crop production. In particular, effects of incentives at larger scales (e.g. cooperation between farmers) have received little attention.

With regard to integrated cropping and livestock production systems, there is a need for developing and testing one or two appealing concepts for fully utilising the synergy for achieving a sustainable agriculture. The objective would be to stimulate the development of novel ideas in practice.

4. Development and dissemination of knowledge

Under the Adaptation Model, local sources of variation are taken into account in the design. This means that the result is a more diverse and context-based type of agriculture. It also means that the concept of centrally developing innovations and disseminating them into the commercial practice has become void. A different concept for knowledge development and dissemination is required. The project 'Netwerken in de Veehouderij'⁶ in 2004/2005 provided a lot of valuable experience for an alternative concept, which would be quite appropriate for

⁶ <http://www.verantwoordeveehouderij.nl/index.asp>

working with the Adaptation Model.

Critical in a more context-based agriculture is the ability of a farmer to develop the best production system for the specific context of the farm. Farmers learn by observing, sharing experience and combining forces to get answers to shared problems. Input from scientists is needed for a broader development of concepts, for other contexts and in-depth knowledge of underlying processes. Hence, projects should aim at teaching farmers to observe and researchers to listen.

As a consequence, dissemination of knowledge shifts to a large extent from dissemination of solutions to dissemination of ways to solve context-specific issues. This requires a different way of technical support. In the new situation, solutions are owned by innovative farmers, who may not be interested in providing their solutions to the others, except if they get something in return, for example in a farmers' study group.

The Adaptation Model does not stop at the farm gate, but affects the entire production chain. More study is needed to obtain an organisational structure that builds mutual trust and creates an environment in which innovations arise and prosper.

Conclusions

Many of the current problems in agriculture related to sustainability, seem to be associated with the way how agriculture attempts to achieve stability. Developing and utilising intrinsic robustness of animals and cropping systems, instead of solely relying on protection and intervention, seems to be a major step in the direction of an agriculture that is sustainable in the entire bandwidth of normal conditions. This requires a raising of awareness among all parties involved, development of methodology, fundamental and applied technical research and a change in the way that knowledge is developed and disseminated.

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IT Innovatie en Nieuwe Organisatiestructuren in de Nederlandse Bloemensector

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Abstract

This position paper summarizes the main characteristics of the flower industry in the Netherlands and proposes a research agenda to investigate further development of the sector up until 2015, by analyzing the impact of IT applications, IT infrastructure, supply chain integration, new organizational forms and coordination mechanisms.

In the 20th century, the flower industry in the Netherlands has developed into a very successful internationally operating sector, with a total turnover value of flowers and flower bulbs of 4,000 million euro in 2005. In 2004, 90% of the total flower volume in the Netherlands was produced by about 15,000 small or medium sized enterprises, the Dutch flower growers, but total imports for specific flower types are growing rapidly. Eighty percent of the total flower volume in the Netherlands is exported on a worldwide scale. A key role in the sector is played by a small number of auction organizations (such as FloraHolland and Aalsmeer), which are cooperatives owned by many small growers. Another key role is for the large wholesale organizations and combinations (such as VBG and HBAG).

The sector is now at a turning point in its development. Threats and opportunities emerge due to internationalization of markets, supply chain integration, and innovations in IT, chain logistics, and new cooperative forms, also known as IT-enabled network organizations.

We propose a research agenda in order to develop practical knowledge on the impact of IT applications and IT infrastructure development on the formation of successful network organizations and supply chain integration in the flower industry in the Netherlands.

1. Inleiding

De Nederlandse bloemensector heeft zich de afgelopen decennia ontwikkeld tot een economisch krachtige sector. Er is echter, na een periode van sterke groei in de tweede helft van de 20e eeuw, sprake van een fase waarin een aantal hardnekkige problemen aan de orde zijn. De sector loopt op tegen ecologische en maatschappelijke grenzen. Daarnaast wordt de schaarse ruimte in toenemende mate geclaimd voor wonen, recreatie, natuurontwikkeling en waterbeheer. Ook de vraag naar bloemen is onderhevig aan verandering. Steeds vaker koopt de consument via alternatieve kanalen zoals supermarkten of benzinestations. De concurrentiekracht neemt af en de technologisch gerichte, aanbodgedreven agro-kennisinfrastructuur wordt steeds vaker als een zwakte ervaren (www.transforum.nl)

Een transitie van de bloemensector lijkt dan ook noodzakelijk, wil deze op de langere termijn toekomst hebben. De transitie zal een forse verandering moeten inhouden in de richting van een ecologisch, economisch en sociaal meer duurzame ontwikkeling: een transitie naar een duurzame agrosector en een mooi en leefbaar platteland (www.transforum.nl).

Om deze resultaten te bereiken, zal de huidige technologie- en aanbodgedreven agro-kennisinfrastructuur moeten veranderen in een vraaggedreven, interactieve en transdisciplinair werkende kennisinfrastructuur. De nieuwe organisatie TransForum heeft als doelstelling het bevorderen van die transformatie (www.transforum.nl).

Dit position paper is geschreven in opdracht van TransForum. Het beschrijft de huidige situatie in de Nederlandse bloemensector met de nadruk op het gebruik van IT, de effecten van IT op de prestaties van organisaties in de sector en de ontwikkeling van ketens en netwerken. De drie uitgangspunten voor dit paper zijn:

1. inventarisatie van wetenschappelijke inzichten rond netwerkorganisaties en supply chains die van toepassing zijn in de landbouwsector, meer in het bijzonder de bloemensector.
2. de identificatie van concrete aangrijpingspunten die bijdragen tot de transitie naar duurzame landbouw in Nederland. In het bijzonder wordt er gekeken naar potentiële ontwikkelingen op het vlak van supply chain en netwerking die de werking van de bloemensector kunnen stimuleren.
3. het opstellen van een research agenda om de kansen voor de bloemensector in de komende 10 jaar te identificeren.

Het paper is gebaseerd op kennis binnen de discipline Informatiemanagement van de economische faculteit van de Universiteit van Tilburg, aangevuld met een literatuurstudie en gesprekken met experts uit de sector (een workshop in januari 2005 en individuele reacties uit onder andere de Bloemenveiling Aalsmeer) en contacten met de initiatiefnemers van het florilog project (www.transforum.nl).

Het paper is bedoeld als uitgangspunt voor verder onderzoek.

In hoofdstuk 2 wordt de bloemensector geanalyseerd vanuit een supply chain standpunt. De verschillende partijen worden beschreven alsook de manier waarop ze zich ten opzichte van elkaar verhouden. Hoofdstuk 3 geeft een eerste analyse van de bloemensector, gericht op inzicht in het functioneren van de markt, de verwachtingen voor de volgende jaren en de rol die IT hierin kan spelen. In hoofdstuk 4 wordt een voorstel gedaan voor verder onderzoek.

2. De bloemensector in Nederland

2.1 Facts & Figures

Nederland is van oudsher een bloemenland. Het beschikt over een gunstig klimaat en heeft zeer hechte en innovatieve sierteeltclusters (productie, toelevering, handel & logistiek) (Zimmermann 2003). Het is zeer gunstig gelegen ten opzichte van het afzetgebied Europa en loopt voorop op het vlak van productontwikkeling en teelttechnieken.

De sector is gekenmerkt door een groot aantal kwekerijen (6.500 onder glas, 8.200 volle grond) en vertegenwoordigt een tewerkstelling van 57.000 FTE's (Bloemen-bureau Holland, 2005). De sector realiseert een productie van 4.090 miljoen Euro (bloemkwekerij & bollen) waarvan het grootste deel bestemd is voor export (zie tabel 1). Sommige partijen verwachten een sterke omzet groei van 45% in de sector in de periode 2006-2012 (Hogervorst, 2005).

Productie (bloemen & bollen)	4090 miljoen euro
Import (bloemen)	481 miljoen euro
Export (bloemen & bollen)	3667 miljoen euro
Percentage geëxporteerd	80,2 %

Tabel 1: Bloemensector in cijfers (gebaseerd op Bloemenbureau 2005)

De voornaamste afnemers zijn Duitsland, UK, Frankrijk en Italië. De VS heeft aan belang ingeboet door de lage wisselkoers van de dollar. In tegenstelling tot de gangbare opvatting zijn niet de tulpen het belangrijkste product, maar rozen en chrysanten. Tulpen nemen de derde plaats in.

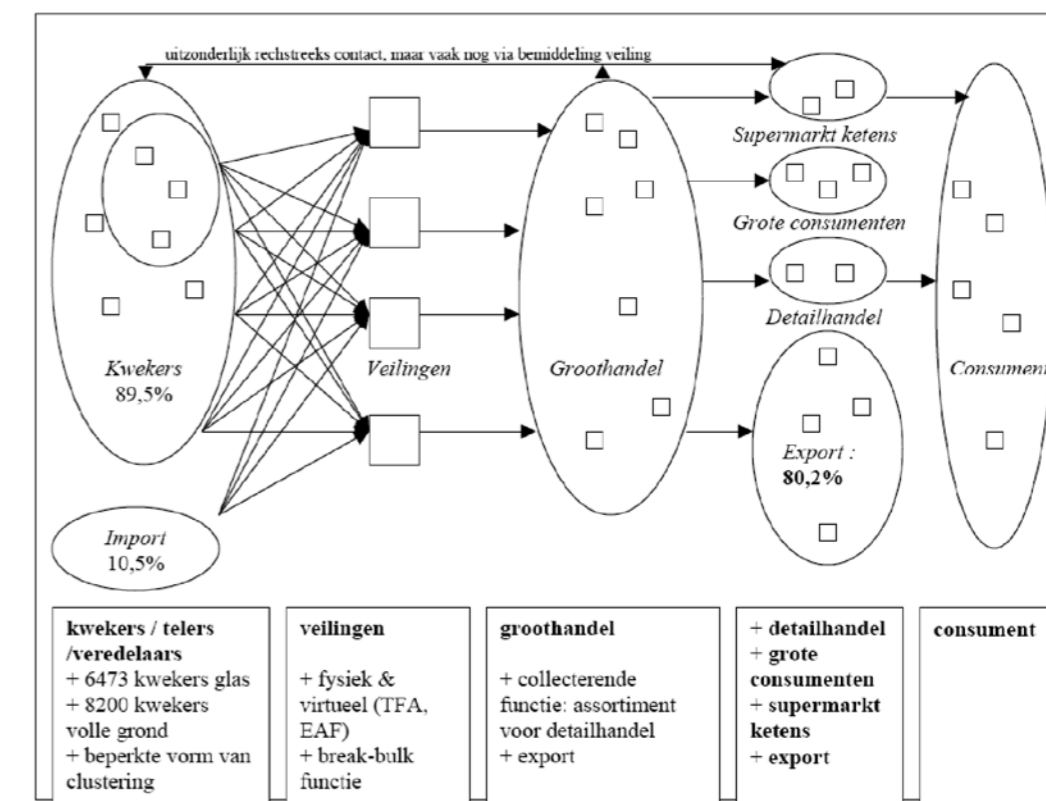
Nederland is niet alleen koploper wat de productie van bloemen en bollen betreft, het bekleedt eveneens een dominante positie in het verhandelen ervan. Niet minder dan 66% van de Europese import verloopt via Nederland. Meer dan een vijfde komt van buiten de EU, veelal van Nederlandse kwekers. De veilingen nemen een centrale rol in bij het verhandelen van bloemen.

2.2 De waardeketen in de bloemensector

Een typische waardeketen binnen de Nederlandse bloemensector bestaat uit 5 schakels: de kweker, de veiling, groothandel, detailhandel en consument (Den Hertog 2001). In onderstaande figuur wordt deze keten grafisch weergegeven. Vervolgens worden de verschillende schakels uit de keten onderzocht.

2.2.1 Kwekers, telers en veredelaars

Traditioneel wordt de bloemenproductie in Nederland gekenmerkt door een lage concentratiegraad. Er zijn zeer veel relatief kleine bedrijven die niettemin innovatief zijn en voorlopen op productontwikkeling en teelttechnieken. (Zimmerman 2003, thesis). Nederlandse kwekers bewerken ook gemiddeld een kleinere oppervlakte dan buitenlandse kwekers. Een voorbeeld: in Kenia (de belangrijke importeur) beschikt een kweker over 5 tot 15 maal meer landbouwareaal (Wynands 2003). Al dient opgemerkt dat in Nederland vaak meer intensieve landbouwtechnieken worden gebruikt zodat de productiviteit per oppervlakte vaak veel hoger ligt in vergelijking met buitenlandse kwekerijen. Het aantal ha gebruikt voor het kweken van siergewassen daalt licht in de afgelopen jaren van 46.520 ha in 2002 naar 45.904 ha in 2004 (Bloemenbureau 2005).



Er is bij de Nederlandse kwekers een trend ingezet naar toenemende schaalvergroting en concentratie (Doorduyn, 2004). Dit wordt geïllustreerd door de cijfers uit tabel 2. Er vindt een sterke evolutie plaats naar schaalvergroting en clustering aan kwekerszijde (o.m. via telersverenigingen).

Traditioneel zijn de Nederlandse telers lid van een (coöperatieve) veiling. Dit betekent dat ze onderworpen zijn aan een afrekenplicht (soms ook veilingplicht genoemd). De financiële afrekening van de gerealiseerde afzet wordt via de veiling geregeld, ongeacht of deze gerealiseerd werd via de klok (zie infra) of via rechtstreekse verkoop aan klanten.

Kwekers kunnen ook opteren voor een aanvoercontract. In dat geval zijn ze geen lid van een veiling, maar kunnen ze hun afzet toch realiseren via de klok, zij het tegen hogere kosten.

De veiling is voor de telers niet alleen een afzetmechanisme maar fungeert ook als afscherming van de Nederlandse telers (zie verder). Wanneer men dit koppelt aan de waarneming van Blok (2003) dat in de sector sociale aspecten een belangrijke rol spelen (iedereen kent iedereen), dan kan men stellen dat de Nederlandse bloemenmarkt moeilijk toegankelijk is voor buitenstaanders. Binnen de groep Nederlandse telers speelt de concurrentie wel volop en kan men spreken van een open markt.

	2002	2004
aantal telers glas	7516	6473
aantal telers volle grond	9800	8200
ha siergewassen onder glas	6214	6107
ha siergewassen in volle grond	40306	39797
ha siergewassen onder glas / aantal telers glas	0,827	0,943
ha siergewassen in volle grond / aantal telers volle grond	4,112	4,853

Tabel 2: Schaalvergroting en concentratie in de Nederlandse sierteelt

2.2.2 Veilingen

Er zijn twee types veilingen actief. Enerzijds de traditionele veilingen die onder de vlag van het VBN fungeren (bv: Aalsmeer, FloraHolland, Oost-Nederland en Vleuten). Deze veilingen zijn vaak coöperatieven waarvan de telers deel uitmaken. De bloemen worden er per klok geveild. Daarnaast is er een opkomst van een alternatieve veilingvorm: de elektronische veiling Tele Flower Auction (TFA), die een relatief klein maar constant volume verhandelt. Ze richt zich tot kwekers die maximaal rechtstreeks willen afzetten.

In een markt met vele vragers en aanbieders waarbij het product een zekere mate van homogeniteit bezit (zoals dit het geval is met de bloemenmarkt) wordt een veilingssysteem als een goed en kostenefficiënt mechanisme gepercipieerd voor de allocatie van producten (Van Den Berg, 2001).

De bloemenveilingen zijn typisch aanbod gestuurd. Telers bieden hun producten in bulk aan waarna de veiling zijn rol als break-bulk vervult. Een probleem daarbij is dat de bloemeteelt deels afhankelijk is van externe factoren zoals weer en ziektes. Hierdoor fluctueert het aanbod en de kwaliteit van de bloemen en is het niet mogelijk om lang op voorhand het aanbod te voorspellen. Dit wordt in de hand gewerkt door de beperkte houdbaarheid van bloemen waardoor het aanleggen van voorraden met de huidige stand van technologie⁽¹⁾ slechts een marginale oplossing kan bieden.

De traditionele veilingen werken met een veilingplicht voor hun leden (zie boven). Dit betekent dat de aangesloten kweker er zich toe verbindt zijn afzet te realiseren via de veiling. Dit betekent niet dat de gehele afzet via de klok wordt verkocht. Directe verkoop aan klanten is mogelijk, maar dan zal de financiële afhandeling typisch via de veiling gebeuren. Afzet via externe organisaties, buiten de veiling om, is uitgesloten.

De veilingen organiseren naast de veiling per klok ook andere types afzetondersteuning zoals bemiddeling tussen kwekers en grote klanten. Ondanks het stijgende aantal transactie dat niet via de klok wordt afgehandeld is de handel via deze alternatieve mechanismen voorsnog beperkt. De stijgende verkoop via de grootwarenhuizen kan deze evolutie naar nieuwe afzetondersteuning evenwel versnellen.

Daarnaast moet opgemerkt worden dat buitenlandse kwekers geen toegang hebben tot de coöperatieven.

2.2.3 De groothandel

De groothandel heeft een collecterende functie. Zij tracht het aanbod van verschillende aanbieders op het juiste tijdstip bij elkaar te voegen om een compleet assortiment aan te kunnen bieden aan de detaillisten.

Zoals bij de kwekers is ook bij de afnemers een schaalvergroting en concentratie beweging ingezet. Dit is vooral op twee vlakken merkbaar:

1. Inkoopbeslissingen worden genomen door een kleinere groep professionele inkopers. Dit zijn goed geïnformeerde onderhandelingspartners die relatief grote hoeveelheden verhandelen. Hierdoor ontstaat een relatief kleine prijselasticiteit.
2. De fusies en acquisities hebben geleid tot het ontstaan van enkele grote holdings van exporteurs. Zij omzeilen steeds vaker de veiling door directe afspraken te maken met kwekers.

¹ In Wageningen bestudeert men in 2005 nieuwe koeltechnieken die lange transporten over zee mogelijk maken met beperkt of geen kwaliteitsverlies. Dit type technologieën kan een doorbraak betekenen in de bewaring van bloemen.

Volgens Deneux & Luten (2001) is dit vooral het geval met buitenlandse kwekers die hiertoe meer mogelijkheden hebben dan Nederlandse bedrijven (door o.m. veilingplicht).

Let wel, de geraadpleegde experts stellen dat het beschikken van een alternatief afzetkanaal (veiling) kan uitgespeeld worden bij directe onderhandelingen tussen kweker en afnemer. Zij stellen dat dit de onderhandelingspositie van de kweker kan versterken.

Daarnaast is er een evolutie merkbaar waarbij groothandelaars (of geaffilieerde bedrijven) hun dienstenpakken uitbereiden. Er worden diensten aangeboden zoals verpakking en labeling van de bloemen, expeditie, cash & carry.

2.2.4 Detailhandel, grote consumenten, supermarkten. export

Het leeuwendeel van de Nederlandse productie (ongeveer viervijfde) is bestemd voor export. De export van snijbloemen vertegenwoordigt een omzetcijfer van maar liefst 3.052 miljoen euro (ter vergelijking: de totale productie van snijbloemen bedraagt 4.090 miljoen euro). Daarmee neemt Nederland een dominante positie in op wereldvlak. Daarnaast fungeert Nederland als transitland (zie boven).

Momenteel ontwikkelen er zich elders in de wereld enkele distributiecentra die op termijn afbreuk kunnen doen op de dominante positie van Nederland in de distributie van bloemen. Ook de sterke positie van de euro t.o.v. de dollar speelt in het nadeel van Nederland.

De verkoop van bloemen aan de Nederlandse consumenten gebeurt voornamelijk via kleinhandel. Detaillisten kopen half afgewerkte producten bij de groothandel en verwerken die tot hoogwaardige afgewerkte boeketten. Zij profileren zich als speciaalzaken die een gevarieerd en hoogwaardig assortiment willen aanbieden en die maximaal kunnen inspelen op de individuele wensen van hun klanten.

Naast de detailhandel ontstaan in snel tempo andere distributiekanaalen. Bloemen worden verkocht in benzinestations, supermarkten, enz. Dit is een trend die vooral in Engelstalige landen al ver is doorgezet. Merk echter op dat de relatie tussen de groothandelaars en de nieuwe distributievormen sterk verschillen met de relatie groothandel – detaillist. Een supermarkt keten is niet op zoek naar half afgewerkte producten, maar wenst kant en klare boeketten aan te kopen. Ze streven naar een beperkt gestandaardiseerd assortiment en verlangen uniformiteit, leverzekerheid en traceerbaarheid.

Uiteraard is dit laatste moeilijk realiseerbaar via de veiling. Men gaat op zoek naar alternatieve aankoopmogelijkheden zoals bemiddeling en lange termijn contracten met telers. Veilingen spelen hierop in door de diensten die ze op dit vlak reeds aanboden (zie boven) verder uit te werken en aan te bieden naast de traditionele klok (bemiddeling, tracking & tracing,...).

2.2.5 De consument

Het consumptiepatroon kan sterk verschillen van cultuur tot cultuur. Dit komt tot uiting wanneer de consumptie van snijbloemen in de verschillende landen onder de loep wordt genomen. Vooreerst is er een groot verschil in het budget dat per capita aan bloemen wordt gespendeerd (tabel 1).

Land	Consumptiegebruik per capita in euro
Nederland	53,1
België	42,7
UK	41,1
Denemarken	40,6
Duitsland	36,4
Zwitserland	83,8

Tabel 3: Consumptie per capita (gebaseerd op Bloemenbureau 2005)

Er zijn landen waar consumenten eerder opteren voor een boeket met traditionele bloemensoorten en kleuren (bijvoorbeeld UK, Spanje) terwijl andere consumenten graag experimenteren en voorstanders zijn van nieuwe soorten en kleuren (bijvoorbeeld Nederland en België). Daarnaast is er ook een wezenlijk verschil vast te stellen in de redenen die consumenten opgeven om over te gaan tot een aankoop. In Nederland bijvoorbeeld is de aankoop van een boeket in 46% van de gevallen gerelateerd aan speciale gelegenheden (feestjes etc). In het Verenigd Koninkrijk daarentegen is consumptie voor speciale aangelegenheden veel beperkter (bloemen als cadeau bij een feestje wordt als te intiem ervaren en is "not done"). De piekdagen in de Engelse verkoop zijn dan ook donderdag en vrijdag: tijdens de wekelijkse inkopen wordt een boeketje gekocht om het huis op te fleuren. Met andere woorden, in het Verenigd Koninkrijk worden bloemen voornamelijk gekocht voor eigen consumptie terwijl in Nederland bloemen vaak gelieerd zijn aan speciale gelegenheden. (Jennissen). Dit verschil in het consumptiepatroon biedt een mogelijke verklaring voor het succes van de distributie van bloemen via supermarktketens in het Verenigd Koninkrijk.

2.3 Veranderingen in de keten

In de afgelopen decennia is er veel veranderd in de internationale sierteeltsector, waarvan de bloemensector en de potplantensector deel uitmaken. Door Bloemenvveiling Aalsmeer worden de volgende trends onderscheiden die belangrijk zijn voor de ontwikkelingen tot 2015 (Hogervorst, 2005):

1. toenemende internationalisatie van zowel productie als verkoop;
2. ketenverkorting en ketenomkering (naast verkoop via de veiling ook rechtstreekse verkoop tussen producent en met name het supermarktkanaal)
3. toenemende complexiteit van de fysieke distributie (vgl. Flor-i-log project): klanten willen vers kopen en op maat; reduceren voorraadrisico's; kleinere transacties met hogere frequenties; rolverschuivingen van transporteurs naar dienstverleners);
4. splitsing van distributiekanaalen van traditionele bloemenwinkels naar supermarkten;
5. toename van schaalgrootte en kostprijsreductie: afname van het aantal spelers; toename bedrijfsomvang; toename van procesefficiëntie;
6. verdere professionalisering: hoger opleidingsniveau, toename transparantie in de ketens, toenemende samenwerking en netwerkvorming;
7. vraag naar risicobeheersing neemt toe: garanties en certificering van product, proces en arbeid.

3. Netwerkorganisaties in de bloemensector

In hoofdstuk 2 blijkt dat in de bloemensector sprake is van verticale en horizontale integratie en van intensivering van de samenwerking tussen organisaties in ketens en netwerken. Ook is er sprake van toenemend gebruik van IT (met name in de handel).

In dit hoofdstuk worden enkele soorten netwerken (waardeketsen) in de bloemensector onderscheiden op basis van enkele beschikbare theoretische modellen. Het doel is om de werking van de sector in meer detail te onderzoeken en op basis daarvan enkele voorspellingen te doen voor de nabije toekomst. Hierbij wordt aandacht besteed aan de mogelijkheden en beperkingen die IT in deze context oplegt alsook de interactie tussen IT en de organisatie van de waardeketen.

3.1 Het ontstaan van netwerkorganisaties

Traditioneel wordt ervan uitgegaan dat slechts twee fundamenteel verschillende processen bestaan waardoor goederen bewegen door een waardeketen (Williamson, 1993, Malone et al 1987):

1. Markten: Goederen worden doorgegeven van de ene schakel (organisatie) in de keten naar de andere schakel via handel of markt. Deze markt wordt beheerst door prijsmechanismen: kopers en verkopers vinden elkaar bij een bepaald prijsniveau.
2. Hiërarchieën: Ketens worden geïnternaliseerd in hiërarchieën: een bedrijf verzorgt intern verschillende stappen in de waardeketen. De stappen worden beheerst door interne besturingsmechanismen.

Waardeketens van het eerste type zijn gekenmerkt door de aanwezigheid van veel (kleine) bedrijven die flexibele relaties onderhouden met leveranciers en afnemers, gebruik makend van open markten. Waardeketens van het tweede type bestaan uit slechts enkele (grote) organisaties die minder gebruik maken van markten en dus meer activiteiten intern uitvoeren. Verondersteld wordt dat in een waardeketen een structuur ontstaat van markten en hiërarchieën, zodanig dat de totale marktkosten en organisatiekosten zijn geoptimaliseerd.

Sinds 1990 wordt een derde vorm onderscheiden: handel via 'hybrid governance' of ook wel netwerkorganisaties. Dit zijn nieuwe organisatiestructuren waarin zelfstandige bedrijven in nauw contact staan met elkaar en er naar streven om de marktkosten te drukken door wederzijds vertrouwen. Zij werken samen in clusters van individuele bedrijven (Adler 2002). Hoewel de bedrijven van de cluster in staat zijn om op individuele basis meerwaarde te creëren wordt er vooral gestreefd naar meerwaarden en mogelijkheden die voortvloeien uit hun nauwe relaties (Johnston & Lawrence 1988). In dit type waardeketens verandert de focus van competitie op bedrijfsniveau naar competitie tussen netwerken van bedrijven (Holland 1995).

De Nederlandse bloemensector is in essentie een waardeketen van het eerste type. Individuele bedrijven bieden hun producten aan via markten. De veilingen vervullen in dit type waardeketen een intermediaire rol. Veilingen zijn een tool om de overgang van producten tussen de producenten en de groothandel op een optimale en kostenvriendelijke manier te laten gebeuren.

IT ondersteuning is in deze context vooral gericht op het zo kostenefficiënt en snel mogelijk afhandelen van transacties.

Niettemin kan men een geleidelijke verschuiving verwachten naar waardeketens van het derde type (netwerkorganisaties), onder meer onder druk van de nieuwe afzetkanalen (figuur 1). Supermarktketens en anderen streven naar een constant, gestandaardiseerd en voorspelbaar aanbod. Het veilen van bloemen is minder geschikt voor deze waardeketen, vanwege de onzekerheid in aanbod qua hoeveelheid en assortiment en de beperkte houdbaarheid. Men zal dan ook sneller terugrijpen naar (lange termijn) afspraken tussen de betrokken partijen die een stabiele samenwerking moeten stimuleren. De traditionele rol van de veilingen komt onder druk te staan. Dit wordt geïllustreerd door de vaststelling dat steeds meer handel buiten de traditionele klok om gebeurt (zie boven).

IT wordt gezien als een noodzakelijke voorwaarde om tot netwerkorganisaties te komen. Het bevordert de communicatie en ondersteunt diverse samenwerkingsvormen (collaborative software, tweede generatie Enterprise Resource Planning software, enz.). De IT infrastructuur richt zich niet meer uitsluitend naar het afhandelen van transacties, maar naar de ondersteuning van een netwerk. Het tot ontwikkeling komen van een netwerk van organisaties en de maturiteit van de IT binnen dit netwerk gaan hand in hand. Ontwikkeling op het ene vlak dient gevolgd door nieuwe ontwikkelingen op het andere vlak en vice versa.

3.2 De invloed van IT op netwerkorganisaties

Ook de bloemensector ontsnapt niet aan de verschillende informatiseringsgolven. De introductie en het gebruik van IT heeft fundamentele invloed op alle mogelijke aspecten van productie en handel. Het is ondoenlijk om een volledig overzicht te geven van alle mogelijke veranderingen die IT kan teweeg brengen in een sector. Niettemin worden hieronder enkele van de meest markante verwachtingen geschetst aan de hand van drie theorieën.

Het hoeft geen betoog dat het correct kunnen beoordelen van de impact van de steeds verder schrijdende informatisering en het correct kunnen inschatten van de gevolgen van nieuwe IT investeringen cruciale elementen zijn voor een geslaagd pro-actief en duurzaam beleid.

3.2.1 'Electronic markets' theorie

Deze theorie stelt in essentie dat de introductie van IT twee belangrijke effecten heeft op markten (Malone, 1987):

- In de eerste plaats zal de introductie van IT leiden tot een groei van de markt. Dit kan verklaard worden door het verbeteren van de markttoegang (bv. via elektronische computer-aansluiting hoeft men niet fysiek in de veiling aanwezig te zijn om te bieden) en door de meer open competitie die daaruit voortvloeit.
- In de tweede plaats voorspelt Malone een stijging van het aandeel van de elektronische markten ten koste van fysieke markten. Immers, het inzetten van IT kan de transactiekosten (de kosten om een geschikte koper te vinden en de transactie af te handelen) significant doen dalen (Wigand, 1997) even als de coördinatiekosten per eenheid.

Malone stelt verder dat de mate waarin deze trends zich voordoen afhankelijk zijn van de complexiteit van de productbeschrijving en de specifieke eigenschappen van het product dat in de keten wordt verhandeld. Dit laatste wordt aangeduid met de term 'asset specificity' en duidt op de mate waarin middelen die nodig zijn om goederen of diensten te leveren, specifiek zijn voor elke transactie (plaats, fysieke activa, kennis, tijdsperiode). Zowel de complexiteit van de productbeschrijving als de 'asset specificity' kunnen elektronische handel ernstig belemmeren.

Vertaald naar de bloemensector betekent dit dat de introductie van IT zal leiden tot meer elektronische handel (bijvoorbeeld Tele Flower Auction) omdat hierdoor de transactiekosten en de coördinatiekosten zullen dalen. Niettemin zal het succes van de elektronische handel sterk afhangen van het vermogen om de productbeschrijving van het op afstand verkochte product adequaat op te stellen en de mate waarin de specifieke eigenschappen van bloemen (asset specificity) de elektronische handel niet bemoeilijken.

Interessant in deze context is het Linnaeus project waarbij men sectorbreed tracht de omschrijving van producten op een hoger plan te tillen (www.vbn.nl) en de ontwikkeling naar het veilen op basis van informatie op de klok in plaats van de fysieke aanwezigheid van bloemen onder de klok (Hogervorst, 2005).

3.2.2 'Electronic hierarchy' theorie

De introductie van IT kan aanleiding geven tot clustervorming. Onder meer via bedrijfsoverschrijdende informatiesystemen (bijvoorbeeld logistieke applicaties en elektronische bestelsystemen) kan een geprivilegieerde toegang ontstaan tot data die de samenwerking van een beperkt aantal bedrijven in een sterke cluster (of hiërarchie) in de hand werkt (Johnston & Lawrence, 1988).

In de bloemensector zou dit het geval kunnen zijn indien een grote afnemer (bijvoorbeeld een supermarktketen) via elektronische weg informatie uitwisselt met enkele bevoorrechte (buitenlandse) kwekers. Deze informatie zorgt voor een betere afstemming tussen productie en vraag waardoor een nauwere samenwerking ontstaat. Dit bemoeilijkt uiteraard de concurrentie door andere bedrijven.

Kortom, men kan stellen dat de introductie van IT volgens de electronic hierarchy theory de verschuiving van de waardeketen van type 1 naar type 3 versnelt (zie boven).

3.2.3 'Move to the middle' theorie

De introductie van IT vergemakkelijkt communicatie en de uitwisseling van data (zie boven). Maar daarnaast vergt de introductie van IT eveneens hoge investeringen (gunstig voor lange termijn relaties). De combinatie van beide resulteert volgens deze theorie in (Clemons, 1993):

1. meer outsourcing: het wordt makkelijker om een deel van de taken uit te besteden (bv. drukken van labels in China);
2. daling van het aantal partners in een supply chain, maar met hechtere en langduriger relaties.

Ook deze theorie geeft aan dat de introductie van IT het traditionele business model binnen de bloemensector onder druk zet. Er zal een verschuiving ontstaan naar netwerkorganisaties en er zullen meer gespecialiseerde bedrijven ontstaan die taken overnemen die kwekers of handelaren niet tot hun core business rekenen.

3.2.4 'Resource based view' theorie

De drie theoriën hierboven benadrukken sterk het kostenaspect van markten en hiërarchieën en verklaren daarmee het ontstaan van (nieuwe) organisatievormen in ketens. Een heel ander perspectief ontstaat vanuit de resource based view en de resource dependency theorie (Barringer & Harrison, 2000).

Deze theorie stelt dat het succes van een (netwerk-)organisatie wordt bepaald door de unieke combinaties van 'resources' die ze heeft verzameld uit de omgeving, inclusief de inter-organisatiele relaties. De unieke combinatie van resources maakt het mogelijk om waarde toe te voegen in een netwerkorganisatie.

Voor IT betekent dit onder andere dat onderscheid wordt gemaakt tussen IT applicaties (software toepassingen) in een organisatie, de applicaties tussen organisaties en de IT infrastructuur waarbinnen de applicaties kunnen functioneren. De IT infrastructuur is 'de set van gemeenschappelijk beschikbare voorzieningen (de resources) en kan bestaan uit hardware, software, communicatienetwerken, standaarden en IT-diensten (Weill et al, 2002). Let wel, wat als in-

frastructuur (cq resources) wordt beschouwd in een organisatie kan een applicatie zijn op het niveau van een netwerk.

Een voorbeeld van een belangrijke IT infrastructuur voor ketenintegratie is de 'business bus'. Dit is een IT-netwerk met gestandaardiseerde 'stopcontacten' waarmee organisaties met een 'stekkerverbinding' virtueel deel kunnen uitmaken van een netwerkorganisatie (Oesterle et al, 2000). Dit stelt hoge eisen aan de 'networkability' van organisaties en aan standaarden in ketens.

3.4 Machtsrelaties in netwerkorganisaties

Machtsverhoudingen hebben een belangrijke invloed op de ontwikkeling en de structuur van netwerkorganisaties. Om de impact van de verschillende spelers in een waardeketen te analyseren wordt wel gebruik gemaakt van 'machtsanalyse'. Met dit instrument worden de krachtsverhoudingen tussen leveranciers en klanten in kaart gebracht. De machtsituatie in een keten kent vier categorieën (Cox, 2001 a,b):

1. buyer dominance
2. inter-dependence
3. in-dependence
4. supplier dominance

'Buyer dominance' is een situatie waarbij de koper dominance (>) of inter-dependence (=) heeft over de leveranciers in alle schakels van de supply chain tot en met de leveranciers van grondstoffen. Een voorbeeld hiervan is geschetst in onderstaande figuur. Dit type machtsverhouding komt het vaakst voor in food retail, aerospace, automotive, IT hardware, process construction projects, chemical processing en contract manufacturing. Het omgekeerde, i.e. 'supplier dominance', vindt men vaak terug in sectoren zoals IT services, strategic consulting services, retail banking services en high volume food processing (bijvoorbeeld de suikerindustrie).

De bloemenindustrie wordt gekenmerkt door een hoog niveau van inter-dependency. Dit kan verklaard worden door een combinatie van een groot aantal spelers (zowel kwekers als groothandelaars) en de veilingplicht die ervoor zorgt dat kwekers en groothandelaars het leeuwendeel van hun transacties via de veiling laten verlopen. Ze zijn op elkaar aangewezen om hun activiteit te kunnen uitoefenen.

Zoals beschreven in deel 1 is er een concentratiebeweging gaande binnen de sector, zowel binnen de groep kwekers als de groep groothandelaars. Men kan verwachten dat hierdoor een machtsverschuiving zal plaats vinden ten voordele van de schakel met de hoogste concentratiegraad.

Ook voor de veiling is dit van belang omdat hun inkomsten rechtstreeks worden beïnvloed door de macht van de verschillende schakels in de keten. Immers, de (omkering van de) machts-

verhouding tussen kopers en verkopers heeft een rechtstreekse impact op de veilingprijzen. Daarnaast dient vermeld dat het voor kwekers minder gemakkelijk is om buiten de traditionele keten om handel te drijven (veilingplicht) terwijl dit voor groothandelaren minder een probleem is. Dit heeft uiteraard een gunstige invloed op de power van de groothandel.

Merk op dat de verdere inrichting van de supply chain en ontwikkeling van de IT infrastructuur voornamelijk gedomineerd wordt door de schakel met de grootste power. Met andere woorden: de huidige concentratie bewegingen in de bloemensector zullen bepalend zijn voor het power evenwicht en dus ook voor de richting waarin het ondersteunende IT platform zich zal ontwikkelen.

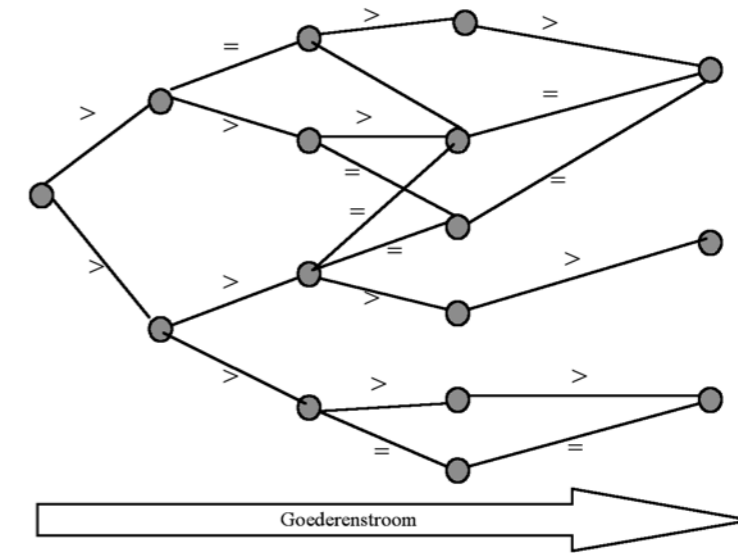
3.5 Afhankelijkheid en vertrouwen in netwerkorganisaties

In een waardeketen is niet alleen de macht van de ene schakel over de andere van belang. Diverse onderzoeken tonen aan dat ook elementen zoals onderlinge afhankelijkheid en vertrouwen belangrijk zijn (Sako, 1998; Teece et al, 2001, Ibrahim & Ribbers 2005).

De mate van onderlinge afhankelijkheid wordt gekenmerkt door de toegevoegde waarde door partners en de vervangbaarheid van partners in de keten. IT heeft vooral impact op dit laatste element. Enerzijds maakt informatisering een hoge mate van standaardisering mogelijk waardoor partners beter vervangbaar worden. Anderzijds kunnen hoge investeringskosten in IT de afhankelijkheid verder verhogen. De introductie van bedrijfsoverschrijdende ERP systemen is hier een voorbeeld van. Enerzijds verhoogt het de kwaliteit en flexibiliteit van communicatie en gegevensoverdracht maar tegelijk fixeert het de bestaande waardeketen. Immers, uitstappen is vaak een te dure optie. De bloemensector dient zich niet alleen de vraag te stellen hoe ze IT maximaal kan benutten. Ze moet zich tevens bewust zijn van het mogelijk institutionaliseren van afhankelijkheden via IT investeringen.

Mogelijk belangrijker dan macht en onderlinge afhankelijkheid is de mate van vertrouwen binnen een keten. Vertrouwen is het sleutelwoord bij de ontwikkeling en het succes van inter-organisatiele samenwerking en waardeketens. Het vereist nauwe samenwerking, een goede communicatie, degelijke informatie en kennis uitwisseling tussen partijen. Het wordt opgebouwd door accumulatie van goed afgehandelde transacties.

Een 'transparante keten' wordt wel gedefinieerd als 'een keten waarin de totale marge op het eindproduct of de dienst verdeeld wordt over de deelnemers naar rato van relatieve waarde-toevoeging' (Van Kooten, 2000). Dit benadrukt het belang van wederzijds vertrouwen tussen partijen in een ketenrelatie en verklaart (mede) waarom veel partijen in de bloemensector worstelen met transparantie (Hogervorst, 2005).



Figuur 2. Voorbeeld van machtsanalyse in een netwerkorganisatie bestaande uit 16 organisaties met 21 relaties. (de symbolen staan voor gelijke macht (=) of suprematie (< >)).

4. Voorstel voor verder onderzoek

In hoofdstuk 2 zijn diverse kenmerken en ontwikkelingen in de bloemensector beschreven, waarna in hoofdstuk 3 een eerste analyse is gemaakt van de structuur, het functioneren, de rol van machtverhoudingen en vertrouwen in de bloemensector.

De bloemensector in Nederland is volop in beweging: groeiende buitenlandse concurrentie (bijvoorbeeld Kenia), toenemende informatisering, toetreden van nieuwe spelers in de ketens (zoals supermarkten), groeiende concentratie bij zowel producenten als groothandel. We onderscheiden de volgende factoren:

- (i) de tendens tot schaalvergroting,
- (ii) internationalisering,
- (iii) verticale en horizontale integratie,
- (iv) ketentransparantie en ketenomkering en
- (v) (hoewel langzaam) de toenemende automatisering in de sector.

Centraal thema voor verder onderzoek in de bloemensector is het ontstaan van diverse vormen van samenwerking en netwerkorganisaties in de sector. Onderwerp voor verder onderzoek dient te zijn de verdere ontwikkeling van de sector tot 2015 en de invloed van IT applicaties en IT infrastructuur. De tijdshorizon van vijf tot tien jaar is gebruikelijk bij onderzoek naar de impact van IT op een sector (Van der Zee en Ribbers, 2000). We onderscheiden drie groepen onderzoeksvragen.

Specifieke vragen ten aanzien van de ontwikkeling van nieuwe organisatievormen, ketenintegratie en coordinatiemechanismen zijn:

1. Welke soorten netwerkorganisaties en samenwerkingsverbanden (verticaal, horizontaal) ontstaan er in de sector en hoe succesvol zijn die?
2. Welke partijen/organisaties zijn lid van welke netwerkorganisaties?
3. Hoe is de positie van midden- en kleinbedrijven in de netwerkorganisaties??
4. Wat is de rol van ketenregisseurs?

Specifieke vragen ten aanzien van de ontwikkeling van IT zijn:

5. Welke IT applicaties worden gebruikt door welke actoren in de sector?
6. Welke IT infrastructuur bestaat in de sector, in de netwerkorganisaties in de sector en in de afzonderlijke ondernemingen?
7. Door welke partijen (aanbieders, ketenregisseurs) worden de applicaties en infrastructuur aangeboden?

² zie bijvoorbeeld Smits et al (2006) voor een uitwerking van de bijzondere positie van het MKB in IT gebaseerde netwerkorganisaties.

Specifieke vragen ten aanzien van de interactie (alignment) tussen organisatieontwikkeling en IT-ontwikkeling zijn:

8. Welke veranderingen in de sector kunnen we verwachten ten gevolge van de inzet van IT.
9. Welke (nieuwe) IT applicaties en IT infrastructuur zijn nuttig voor de sector en haar participanten?

In dit hoofdstuk wordt verder aangegeven hoe dit onderzoeksvoorstel zich verhoudt tot Flor-i-Log (4.1), hoe de ontwikkeling van netwerkorganisaties (vragen 1-4) wordt onderzocht met de NEFETI methode (4.2) en hoe de ontwikkeling van IT applicaties, IT infrastructuur en ketens (vragen 5-8) wordt onderzocht met de TICS methode (4.3) en hoe IT-applicaties kunnen worden ontworpen (vraag 9) (4.4).

4.1 Gerelateerd TransForum onderzoek: Flor-i-log

Sinds 2005 bestaat het TransForum onderzoeksprogramma Flor-i-log. In Flor-i-log werken de bloemenveilingen (FloraHolland en Aalsmeer), sierteelthandel (VGB en HBAG) en de universiteiten van Rotterdam en Wageningen samen om de Nederlandse regiefunctie in de sierteelt te versterken. Centraal staat de Nederlandse potplantenindustrie die het uitstekend doet in Duitsland, Frankrijk en het Verenigd Koninkrijk. Ook handelsstromen uit Denemarken en Italië lopen steeds vaker via Nederland. De komende decennia zal de teelt van potplanten ook in andere Europese landen sterk groeien. Voor de sierteeltsector is het cruciaal dat Nederland de commerciële regie in handen houdt. Dit vraagt om grote veranderingen in de sierteeltsector. Op dit moment ligt het accent van de handel en export op sierteeltproducten die fysiek via Nederland naar de afnemers gaan.

De ambitie van Flor-i-log is om een internationaal netwerk op te zetten. Zo hoeven bijvoorbeeld potplanten die in Italië gekweekt zijn voor de markt in Zuid-Duitsland niet fysiek naar Nederland te komen. Wel kan vanuit Nederland de distributie worden gecoördineerd. Dit beperkt de transport- en logistieke kosten, terwijl de service voor afnemers verbetert. (www.transforum.nl)

Het spreekt voor zich dat het project Flor-i-Log voor de potplantensector diverse raakvlakken heeft met dit position paper voor de bloemensector. Voor beide projecten is van belang een analyse van de sectorstructuur, (inter-) nationale ketens en netwerken, ketenintegratie en ketenbesturing.

Verschillen tussen dit position paper en Flor-i-log zijn bijvoorbeeld:

1. het specifiek domein: de potplantensector verschilt substantieel van de bloemensector vanwege het verschil in asset-specificity (zie hoofdstuk 3),
2. de focus op IT applicaties en IT-infrastructuur in de bloemensector versus de focus op logistieke ketens in Flor-i-log,
3. de focus op dynamiek in netwerkvorming in de bloemensector versus de focus op reorganisatie van logistieke processen in Flor-i-log,
4. de effecten van IT op transacties in de ketens (veilen en alternatieve mechanismen) in de bloemensector en de inrichting van logistieke ketens in Flor-i-log.

Dimension	Description	Sample question
Strategic drivers and incentives	The objectives, motives, perceptions and expectations of organizations and stakeholders involved in a network	What are the business and IT drivers for networking and how are they perceived by the organizations in the network?
Enabling conditions	The conditions that enable or stimulate the emergence and formation of the network	What are the critical organizational and managerial conditions and capabilities for networking?
Design	The structuring of the network responsibilities, decision-making units, and coordination mechanisms	What organizations are involved in the network, what functions, tasks and responsibilities?
Functioning	The inter- and intra-organizational processes and (transactional or informational) activities	What are core processes in the network and what is the role of IT?
Infrastructure	The telematics infrastructure of the network	Which standards are used? What is the position of legacy systems? How is data quality assured?
Performance	Impacts and effects of the networks	When is the network (perceived) as successful, and how are the impacts shared across the network?

Tabel 4: Voorbeeldvragen uit de NEFETI methode

Het ligt voor de hand dat bij de opzet en uitvoering van verder onderzoek in het kader van TransForum afstemming dan wel samenwerking zal plaatsvinden tussen beide onderzoeksprogramma's. Dat zou bijvoorbeeld kunnen plaatsvinden in het kader van de onderzoeksonderwerpen genoemd in 4.2 – 4.4.

4.2 Ontwikkeling van netwerkorganisaties

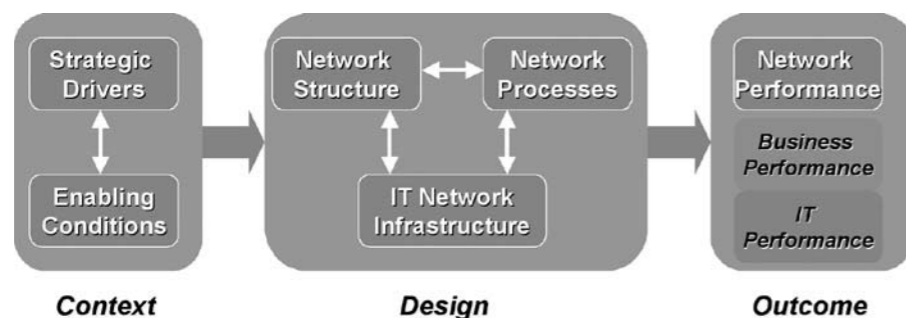
De ontwikkeling van netwerkorganisaties kan worden onderzocht met behulp van de NEFETI methode. NEFETI staat voor Network Enterprises of the Future Enabled by Telematics Infrastructure en is ontwikkeld door CRISM in een onderzoeksprogramma in samenwerking met het Telematica Institute in Enschede (www.telin.nl).

De NEFETI-methode identificeert toekomstige werkingsmodellen, economische structuren en de kritische succesfactoren van netwerkorganisaties. De methode ondersteunt de analyse van IT strategieën, IT architecturen en IT diensten, in relatie met organisatorische veranderingen in netwerken. De theoretische basis wordt gevormd door de theorieën genoemd in hoofdstuk 3.

De NEFETI methode is gebaseerd op een conceptueel model waarin zes elementen zijn samengebracht die nauw met elkaar zijn verweven (figuur 3). Het model bestaat uit de volgende zes componenten:

1. 'Strategic drivers': inventarisatie van de onderliggende motieven voor samenwerking en netwerkvorming van het management en de andere stakeholders. Voorbeelden zijn commerciële doelen, kwaliteitsverbetering, efficiëntie verbetering, enz.
2. 'Enabling conditions for networking': inventarisatie van de condities die samenwerking en netwerkvorming mogelijk maken en/of stimuleren (bijvoorbeeld: analyse van voorgaande ervaringen, de aanwezigheid van applicaties, infrastructuur, netwerkstandaarden, enz).
3. 'Network structure': vaststellen van de structuur van de netwerkorganisatie (inventarisatie van participanten, netwerkstructuur, machtsverhoudingen (zie boven), enz.).
4. 'Network processes': in kaart brengen van de wijze waarop de netwerkorganisatie functioneert, hoe de participanten samenwerken in inter- en intra-organisatie processen, hoe transacties verwerkt worden in het netwerk, hoe coordinatie plaatsvindt, enz.
5. 'IT network infrastructure': inventarisatie van de IT infrastructuur van de netwerkorganisatie en de afstemming tussen IT ontwikkeling en de bedrijfsdoelen in het netwerk.
6. 'Performance of the network organisation': meten en evalueren van de bedrijfs- en IT-prestaties van het netwerk.

Deze zes elementen zijn generiek, dat wil zeggen, kunnen worden beschreven voor netwerkorganisaties in alle bedrijfstakken (Smits, 2002). Door inventarisatie op verschillende tijdstippen kan de ontwikkeling van netwerkorganisaties, prestaties en IT worden gevolgd. De zes elementen worden in kaart gebracht op basis van interviews met stakeholders en –voor elke organisatie in de netwerkorganisatie- door het beantwoorden van een lijst van 30 vragen, ongeveer 5 vragen per component (zie tabel 4).



Figuur 3. NEFETI model voor de analyse van netwerkorganisaties (Smits, 2002)

4.2 Ontwikkeling van IT in netwerkorganisaties

De ontwikkeling van IT applicaties en de IT infrastructuur in een netwerkorganisatie kan worden onderzocht met behulp van de TICS methode. Deze methode is ontwikkeld om de dynamische afstemming ('alignment') te onderzoeken tussen enerzijds de bedrijfsprocessen en bedrijfsstrategie van organisaties in netwerken en anderzijds de IT applicaties en infrastructuur (Smits & Kuo, 2003).

De methode combineert modellen uit de operations research en information management (IM). Het operations research perspectief levert vooral inzichten in supply chain management en het meten van supply chain prestaties (zie o.m. Harrison & New, 2002; Grieger, 2003). Het IM perspectief focust op de groei en ontwikkeling van business netwerken en samenwerkingen tussen organisaties (IOS) en het belang van een infrastructuur van (gedeelde) resources in de keten (hoofdstuk 3; Bakos, 1998; Klein & Selz, 2000; Turban et al, 2000).

Figuur 4 toont het 'extended strategic alignment model' uit de TICS methode. Het bestaat uit twee verschillende analyse niveaus.

1. het intra-organisatie niveau: business strategie, IT, supply chain management en structuur, geanalyseerd vanuit het perspectief van een individueel bedrijf (lijnen 1 en 2).
2. het inter-organisatie supply chain niveau waar de verschillende organisaties die deel uitmaken van een netwerk beslissen over supply chain- en IT zaken (lijnen 3-6)

De TICS methode en het extended strategic alignment model zijn gebaseerd op de volgende vijf bouwstenen:

1. Business strategie en supply chain management. In dit onderdeel wordt vooral gefocust op de impact die de bedrijfsstrategie heeft op zowel de scope van de supply chain (met wie willen we samenwerken, in welke configuratie) als op het niveau van integratie in de keten.
2. Supply chain structuur. De structuur wordt beschreven op basis van de machtsanalyse van Cox (zie hoofdstuk 3) en het classificatiemodel van Sarkat et al (1998). Zij gebruiken vier parameters om de structuur van een netwerkorganisatie te beschrijven:
 - het aantal organisaties/ schakels tussen grondstof en afgewerkt product (channel length);
 - het totaal aantal organisaties dat betrokken is in de supply chain (inclusief intermediairen);
 - de mix tussen virtuele (informatie) kanalen en fysieke distributie-kanalen;
 - onderscheid tussen lineaire en parallelle sequentie van activiteiten.
3. IT en Inter-Organisational Systems. Een IOS kan variëren van een eenvoudig programma om transactiegegevens uit te wisselen tot zeer complexe systemen om bijvoorbeeld het cash management te beheren van een supply chain (Holland, 1995). De analyse van IT en IOS in een supply chain start met een relatief eenvoudige inventarie van IT applicaties, IOS en infrastructuur binnen de organisaties die deel uitmaken van de netwerkorganisatie. Verdere analyse behelst o.m. het documenteren van de bedrijfsprocessen, IT processen en informatiestromen binnen en tussen organisaties. Daarna wordt de impact van IT, IOS en infrastructuur op de prestaties van de netwerkorganisatie bepaald.
4. Business-IT alignment. Met de term alignment wordt de afstemming bedoeld tussen het business domein (bedrijfsstrategie en bedrijfsprocessen) en het IT domein (IT strategie en IT processen) in een organisatie. Alignment wordt nagestreefd op twee niveaus: enerzijds is er de afstemming tussen de strategieën en de interne infrastructuur en processen (strategic fit) en anderzijds is er de afstemming tussen de business en IT (functional integration). Slechte afstemming resulteert onvermijdelijk in sub-optimale prestaties, ondanks zware investeringen in IT. Luftman (1996) ontwikkelde op basis van empirische bevindingen een model dat tracht te beschrijven hoe het alignment proces kan plaatsvinden. Hij stelt dat alignment drie belangrijke componenten telt die een strategische veranderingen kunnen verklaren: driver, lever en impact. Hij ontwikkelt op basis van deze componenten twee perspectieven op alignment:
 - De bedrijfsstrategie is de "driver" voor de bedrijfsprocessen en/of IT strategie (levers), die uiteindelijk de IT processen beïnvloeden (impact).
 - De Informatie strategie is de driver voor IT processen en/of bedrijfsstrategie (levers), die uiteindelijk ook de bedrijfsprocessen beïnvloeden.
5. Prestaties van de supply chain. De prestaties van de supply chain kunnen op verschillende manieren gemeten en beoordeeld worden: bv. meer flexibiliteit, betere klantgerichtheid, customizatie, betere kostenefficiëntie (Kleijnen en Smits (2003); Gunasekaran et al (2004)

Het analyseren van de netwerkorganisatie volgens deze bouwstenen leidt tot dieper inzicht in de structuur en de werking van het netwerk. Het biedt ook de mogelijkheid tot simulatie waarbij bijvoorbeeld kan worden nagegaan wat de mogelijke gevolgen zijn van investeringen in elektronische communicatie-infrastructuur.

De TICS methode is generiek, dat wil zeggen dat de methode kan worden toegepast in de bloemensector om vast te stellen welke afstemming plaats vindt tussen bedrijfsprocessen van de verschillende partijen in de keten en op welke wijze IT applicaties en IT infrastructuur kan bijdragen aan goede prestaties.

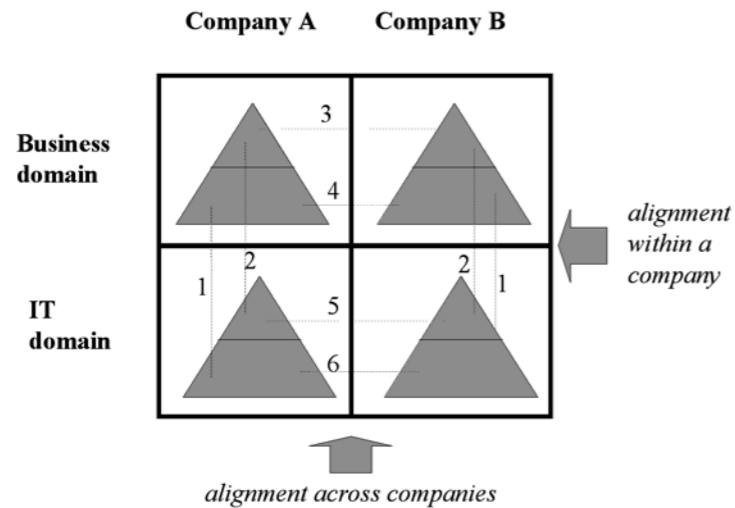


Figure 4. Het 'extended strategic alignment model' waarin wordt weergegeven de afstemming tussen bedrijfsdomein en IT domein binnen een organisatie (verticaal) en tussen organisaties in een netwerkorganisatie (horizontaal).

4.3 Ontwerp van IT applicaties voor netwerkorganisaties

Het onderzoek zoals genoemd in de voorgaande secties leidt tot inzichten in ketenlogistiek in de plantensector (door Flor-i-Log), netwerkontwikkeling in de bloemensector (met behulp van de NEFETI methode) en afstemming tussen IT en bedrijfsprocessen (met de TICS methode). Deze inzichten kunnen aanleiding zijn voor het ontwerpen van nieuwe of verbeterde IT oplossingen voor de bloemensector. Het verdient aanbeveling om enkele toepassingsgebieden te selecteren waarvoor applicaties dienen te worden ontworpen.

Beproefde methoden en technieken voor applicatieontwerp in ketens zijn beschikbaar (procesmodelleren, actormodelleren, interactiemodelleren, DEMO methode, enz). Met behulp van mockups en prototyping kan een ontwerp worden ontwikkeld dat geschikt is voor verdere commerciële ontwikkeling en implementatie, buiten het kader van dit onderzoek.

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