Environmental Genomics

Symposium: Environmental Genomics — November 2, 2001

The first theme of our seminar series on Current Themes in Ecology dealt with the timely subject of Environmental (or Ecological) Genomics. The technological developments in the area of genomics have alighted the interest of many ecologists. Environmental genomics is all about applying genomics to natural systems in their natural environment. By using genomics we can get insight in species' adaptations to variable circumstances. In addition we aim to use genomics to progress evolutionary and ecological theory and enhance our understanding of ecosystem functioning and biodiversity.

The speakers presented not only their own work from the molecular biology point of view but place it in a wider context and to think about ecological and evolutionary issues such as: interaction of the genome with the environment, the functioning of organisms in a variable environment, the possibilities/pitfalls of extrapolating/changing from model species to ecologically more interesting species, how to use sequence data to solve complex evolutionary and ecological problems.

The symposium started with a contribution by one of our present day most famous Dutch scientists: Ronald Plasterk, who needs little introduction in the world of molecular biology. Two other speakers (Rens Voesenek, an ecophysiologist and Kate Lessells, a behavioural ecologist) presented their view on the value of genomics for ecology and they are challenged to bridge the (decreasing) gap between molecular biology and ecology.

Organisation

Organisation:
Prof. Hans de Kroon, Department of Experimental Plant Ecology, University of Nijmegen, Nijmegen.

Logistics: Marieke Bootsma, Netherlands Institute of Ecology.

Advice and overview: Hans de Kroon

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Environmental Genomics,

2 November 2001, Wageningen

Programme

09.30 – 10.00	Welcome and coffee
10.00 – 10.40	**Dr. Stephen Wicks and Prof. Dr. Ronald Plasterk** (Netherlands Institute for Developmental Biology, The Hubrecht Laboratory, Utrecht, The Netherlands) SNPs in C. elegans: mapping the eddies of evolution?
10.40 – 11.20	**Dr. Marta L. Wayne**, (Assistant Professor, Department of Zoology, University of Florida, Gainesville, USA) Discovering Candidate Genes De Novo: Integration of Microarray and Quantitative Genetics
11.20 – 12.00	**Prof. Dr. David Baulcombe,** (Senior Scientist and Head of Laboratory, Sainsbury Laboratory, John Innes Centre, Norwich, Great Britain) Fast forward genomics using gene silencing technology in plants
12.00 – 13.00	Lunch
13.00 – 13.40	**Dr Philippe Reymond and Prof Dr. Edward E. Farmer,** (Gene Expression Laboratory, Institute of Ecology, University of Lausanne, Switzerland) Expression profiling in plant defence
13.40 – 14.20	**Prof. Dr. Rens Voesenek,** (Plant Ecophysiology, Utrecht University, The Netherlands) The mechanism of flooding-induced shoot elongation: an eco-molecular approach
14.20 – 14.50	**Dr. George A. Kowalchuk,** (Netherlands Institute of Ecology, Centre of Terrestiral Ecology, Heteren, The Netherlands) Genomics and Microbial Ecology: Potential and Possibilities
14.40 – 15.20	Tea
15.20 – 15.50	**Prof. Dr. Willem M. de Vos** (Laboratory of Microbiology and Wageningen Center for Food Sciences, Wageningen, The Netherlands) Functional and Comparative Genomics of Low GC Gram Positive Bacteria: From Environment to Application
15.50 – 16.20	**Dr. Kate Lessells**, (Senior Scientist, Department of Animal Population Biology, Netherlands Institute of Ecology, Centre of Terrestrial Ecology, Heteren, The Netherlands) Letting the genomics-genie out of the bottle: can genomics replace ecology?
16.20	Discussion

SNPs in C. elegans: mapping the eddies of evolution?

Dr. Stephen Wicks,

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Caenorhabditis elegans (isolate N2 from Bristol, UK) is the first animal of which the complete genome sequence was available. We sampled genomic DNA of natural isolates of C. elegans from four different locations (Australia, Germany, California, and Wisconsin) and found single nucleotide polymorphisms (SNPs) by comparing with the Bristol strain.

SNPs are under-represented in coding regions, and many were found to be third base silent codon mutations. We tested 19 additional natural isolates for the presence and distribution of SNPs originally found in one of the four strains. Most SNPs are present in isolates from around the globe and thus are older than the latest contact between these strains. An exception is formed by an isolate from an island (Hawaii) that contains many unique SNPs, absent in the tested isolates from the rest of the world. It has been noticed previously that conserved genes (as defined by homology to genes in Saccharomyces cerevisiae) cluster in the chromosome centers. We found that the SNP frequency outside these regions is 4.5 times higher, supporting the notion of a higher rate of evolution of genes on the chromosome arms. We have re-sequenced a significant fraction of the C. elegans genome in the Hawaiin strain and characterised a dense set of SNPs.
Reproductive isolation of a sub-population such as this Hawaiin isolate is characterized by significant phenotypic divergence. SNPs represent a powerful set of markers for mapping the loci which are responsible for the phenotypic variation within sub-populations of a species that occurs en route to speciation.

Discovering Candidate Genes De Novo: Integration of Microarray and Quantitative Genetics

Marta L. Wayne

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Despite much recent interest, a direct link between genotypes and phenotypes remains elusive. QTL mapping is necessary for determining physical locations of genes causing variation in the trait of interest. However, many genes map to a given QTL which do not contribute to such variation. In contrast, microarray technology generates a list of genes whose expression differs among genotypes; but the association between phenotype and expression is not evaluated. We combined these approaches to identify genes responsible for phenotypic differences of interest. A set of recombinant inbred lines were assayed for ovariole number in *Drosophila melanogaster* and QTL for this trait identified. Forty deficiencies spanning the QTL were employed to further refine the map position of genes contributing to variation in this trait between parental lines, with six deficiencies showing significant effects. Next, parental lines were assayed for expression differences using Affymetrix microarray technology. Candidate genes for ovariole number were identified which map to regions identified by QTL and deletion mapping, and whose expression varied significantly between parental lines.

Fast forward genomics using gene-silencing technology in plants

Prof. dr. David Baulcombe

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I will describe the mechanisms of gene silencing and the development of gene-silencing technology for identification of gene function in plants. I will also describe applications of this technology for the identification of genes required for various types of disease resistance in plants. The success of this approach indicates the potential of gene silencing technology for analysis of plant responses to a range of biotic and abiotic stimuli.

Expression profiling in plant defence

Dr Philippe Reymond and Professor Dr. Edward E. Farmer

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Recent progress in understanding plant defence has highlighted a complex, interacting network of signaling pathways leading to the induction of numerous genes. The advent of new technologies for the global analysis of gene expression is fundamentally affecting research in biology, and studies on plant defence benefit from these new approaches. We use DNA microarrays containing thousands of genes from the model plant *Arabidopsis thaliana* with the goal to understand the role of defence-related genes during mechanical wounding and plant-insect interactions. The association of a particular signaling pathway with a defence response are tested with microarrays and defined Arabidopsis mutants. Comparison of transcript profiles after biotic and abiotic stresses reveals overlapping activation of defence-related genes and defines new concepts on how plants may cope with multiple aggressions. Furthermore, the combination of expression data with metabolite measurements yields new and complementary information.

The mechanism of flooding-induced shoot elongation: an eco-molecular approach

Prof. Dr. Rens Voesenek,

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The amphibious plant *Rumex palustris* has the capacity to respond to complete submergence with stimulated elongation of petioles. This adaptive reaction allows the survival of this plant in habitats with sustained high water levels by re-establishing contact with the aerial environment. Ethylene plays a key role in stimulated shoot elongation in *R. palustris*; however, other plant hormones and gases also effect this submergence response. Upon submergence ethylene accumulates in submerged tissues due to the extreme slow diffusion rate of gases in water compared to air. The interaction between ethylene and its receptor protein appears to operate as a sensing device for the under-water environment. A cDNA, homologous to the ethylene receptor from *Arabidopsis thaliana*, was isolated from a *R. palustris* cDNA library. Further downstream in the transduction pathway a fast and substantial decrease of the endogenous ABA concentration and a certain threshold level of endogenous GA are required to maximize petiole elongation. Cross-talk of ethylene, ABA and GA results in a significant increase of the *in vitro* cell wall extensibility in submerged petioles. Furthermore, the pattern of transcript accumulation of a *R. palustris* Expansin gene correlated with the pattern of petiole elongation upon submergence.

Genomics and Microbial Ecology: Potential and Possibilities

Dr. George A. Kowalchuk

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Microbes represent the world's greatest source of genetic and functional diversity. The relatively small size of microbial genomes and their potential for rapid response to external stimuli, make these organisms particularly accessible via genomics approaches. I will present four general genomics study areas that show the greatest potential to further our understanding and application of microorganisms: (1) Complete genome sequencing and functional genomics, (2) Use of bacterial artificial chromosomes (BACs) to uncover metabolic potential, (3) Use of microarrays for phylogenetic and metabolic assessments of the microbial metagenome (4) Microbial Bioinformatics. Progress to date and current research directions will be used to exemplify these key microbial genomics strategies.

Comparative and Functional Genomics of Low GC Gram-Positive Bacteria: From Environment to Application

Prof. Dr. Willem M. de Vos

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Low GC Gram-positive bacteria (LGB) constitute a prominent group of abundant microorganisms all surrounded by a single membrane that are evolutionary related and involved in a wide range of environmental, medical or food applications. The genomes of several representatives have been determined and range in size between 2 and 5 Mb but a great variety of LGB have not been analyzed at the genome level and show considerable diversity as shown by their 16S rRNA sequences. This includes LGB from environmental samples such as soil, GI tract or foods that are active but not yet cultured or have recently been isolated and show unique physiological properties. To advance the understanding of the diversity, activity and interactions of these LGB, we have applied a series of comparative and functional genomics approaches, including specific PCR amplification of 16S rDNA and relevant genes, microarray analysis, and differential hybridization and display technologies. An overview of these combined approaches will be presented to illustrate their potential and limitations.

Letting the genomics-genie out of the bottle: can genomics replace ecology?

Dr. Kate Lessells

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The rapidly expanding application of genomics in ecology has allowed ecologists to address an impressive array of previously unanswerable questions: what organisms are there? what are they doing? how do they do it? what evolutionary trajectories are open to them? These questions seem to span the gamut of ecological enquiry and to threaten to leave traditional ecology as an obsolete dinosaur of the pre-genomics era. However, while genomics has undoubtedly broken the log-jam in our understanding of the detailed mechanisms underlying ecological processes, broad ecological theory is still needed to understand how those mechanisms contribute to the functioning of larger ecological entities such as individuals, populations and communitities. Rather than replacing ecology, genomics will complement the study of broad ecological processes in our endeavours to understand how organisms interact with each other and their environment.