

Efficient gene identification: combining novel sequencing technologies with established resource collections

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April 25, 2012, 15:30-16:30
AIT Tulln, Seminar Room – Ground Floor
Konrad-Lorenz-Straße 34, 3430 Tulln

Abstract

Plant genomes are complexes regarding many aspects, their large size that often reach gigabases, their polyploidy due to their multiple hybrid origins and the high percentage of repetitive elements that may represent the majority of the genome size. Next-generation DNA sequencing (NGS) technologies have revolutionized the genomic research in several domains, as it offers the capacity to obtain large amount of sequences in a short time. However, this approach is not sufficient to decipher the high complexity of plant genomes because of their size, their level of polyploidy and their high percentage in transposable elements. Bacterial Artificial Chromosome (BAC) libraries are still invaluable tools for plant genome analysis. They allow physical mapping, map-based cloning and sequencing projects. They facilitate gene cloning and contribute to rapidly identify homologous genes in polyploid species. During the last decade, BAC libraries from many plant species have been constructed worldwide. Therefore, in plant genomic context, BAC libraries are the unique tool to answer to various scientific questions. Screening BAC libraries gives the opportunity to isolate gene from large insert clones, to characterize disease locus, to make positional cloning, to study polymorphism, genome evolution and genetic variability or to explore the biodiversity.

The French Plant Genomic Resource Centre (CNRGV) is a national platform unique in France. Dedicated to plant genomics, the CNRGV is in charge of more than 9 millions unique samples among more than 100 plant genomic libraries of model and crop plant (<http://cnrgv.toulouse.inra.fr/en/Library>). The objectives of the CNRGV are to provide high throughput molecular tools to the scientific community.

However, the construction and organization of BAC libraries can be laborious and costly especially for large and complex genomes. These consuming steps are preventing widespread application of this

technology in the research community. In order to focus directly on a genomic region of interest in specific genotypes and rapidly isolate BAC clones spanning a genomic region, the CNRGV has developed a non gridded BAC library approach. The aim of this approach is to save time and reduce costs associated with the re-arranging, screening and storage of many BAC clones and to access more efficiently the sequence diversity of plant cultivars in specific regions.

This strategy of using non gridded library approach combined with NGS technology (using 454 technology), has proven to be an efficient way to directly target genomic region of interest and explore the variability among specific genotypes. An update on projects aiming at the characterization of loci in Bread Wheat lines involved in durable resistance to wheat pathogen will be presented.

Biosketch

Dr. H el ene Berg es is a natural born biologist. Her fascination with life is no doubt what helped her through eight long years of advanced studies in biology. "I've always wanted to understand what makes living organisms work since I was a child. Biology is not an easy subject, but my passion for it has got me through the years of study."

In 1996, she received her PhD in Molecular Biology and Genetics from University of Paul Sabatier, Toulouse in 1996 – Title: "Role of chaperons protein in the production of recombinants proteins in *Escherichia coli*". From 1997 to 2003 she did two post-doctoral trainings in the laboratory of interaction between plant and microorganisms at INRA-CNRS – France. First on « Regulation of *Sinorhizobium meliloti* genes involved in symbiotic nitrogen fixation » and second on: « *Sinorhizobium meliloti* whole genome expression analysis for nitrogen metabolism characterization ». Since 2003 she is Managing Director of the French Plant Genomic Resource Centre (CNRGV) at INRA, Toulouse. The Centre's target objectives are the collection, quality maintenance and distribution of biological material. H el ene Berg es is also member of the International Wheat Genome Sequencing Consortium and the Sugarcane Genome Sequencing Initiative.

<http://cnrgv.toulouse.inra.fr/en>

http://www.international.inra.fr/join_us/working_for_inra/portraits/helene_berges