

Functional genomics of starch and grain quality

Prof. Alan H. Schulman is a leader of a Nordic multidisciplinary research program with aim to identify the key determinants of starch and grain quality in barley and, by extension, in the related crops wheat, rye, and oat. In the following he tells about his project and importance of Nordic co-operation for his research:

Starch is important

The cereal grain is our largest single primary food source, and thus among the most economically important structures in biology. The main nutritional components of the grain are starch, which is stored in the endosperm tissues that comprise the bulk of the grain, storage protein, also in the endosperm, phosphate, which is present in the outer aluerrone tissue, and soluble fiber (beta-glucan), present throughout. The relative quantities and specific structure of each of these components directly affect the suitability of the grain for various feed, food-, and non-food uses. In the Nordic region, because barley is the major crop, the properties of the barley grain are critical to agricultural success.

Goals of the project

The key properties of the starch, protein, and fibre of barley grains which determine their functionality in food and non-food uses are under genetic control. However, the number of genes is large and their interactions are not known. Furthermore, the development of the grain and its properties rest on a network of interactions extending from the gene level to that of the enzymes and proteins specified by the genes and onward to the storage compounds and grain physical structure.

The goal of the project has been to identify the key determinants of starch and grain quality in barley and, by extension, in the related crops wheat, rye, and oat, by the application of high-throughput analytical tools on each level of biological organisation. In order to do this, we have chosen a set of barley mutants affecting starch or soluble fibre content or structure, and studied them at multiple biological levels in order to identify the key parameters that vary. This has involved both the new tools of "genomics" including use of the microarrays which enable us to study the function of more than 20 000 genes simultaneously for in-depth analyses, and high-throughput chemometric methods for rapid screening of barley lines.

Rolfi



An example of staged materials for microarray analyses

Nordic production conditions demand matched plant material

Nordic consumers, and those abroad who buy exported Nordic food and beverage products, expect wholesome and nutritious ingredients with desirable sensory properties. The chain of consumer and market preferences (from “fork to farm”) must be matched by plant varieties suited to Nordic production conditions, environmental concerns, and climate that can deliver a harvest tailored to each stage of the production chain (from “farm to fork”). For cereals and potato tubers, which together represent more than half of the total land in the Nordic region in cultivation, it is the properties of the storage proteins and the carbohydrates, particularly starch, that are critical both to the final product and to the processing industry.

Our project focuses on barley, because barley is the most cultivated crop in Sweden, Norway, Denmark and Finland. It is also the fifth most important crop worldwide. The results will be, however, applicable also to rye, wheat, and oat, so both the Nordic and the worldwide impact is thereby considerable. Our approach to determine the genes and proteins controlling barley grain quality and starch properties in particular will provide the basis for breeding of barley with tailored qualities for industrial applications and added value varieties for the farmer. The ultimate goal is to provide the available tools for the plant breeder in a timely manner to meet the rapidly increasing consumer demands for high quality cereal products with specific functionalities. Whereas in North America very large breeding companies undertake the sort of work described here single-handedly for their target crops (maize, soybean), on the Nordic scale a collaborative approach to our niche crops is the most practical approach.

Nordic partners compliment each other

The approach we have taken to the scientific problem is both multidisciplinary yet unified. Each of the Nordic partners has specialised yet complementary skills which has given a good synergy to the project. If the Nordic region were one country of about 24 million, we could cooperate only internally, but until the return of the Kalmar union, we will need to collaborate on a regional scale. The EU Framework Programmes, furthermore, tend to focus on crops of greatest interest in warmer parts of Europe. Wheat, not a

major Nordic crop, gets the emphasis. For this reason, the Nordic context remains important.

Project highlights

We have analysed the gene expression pattern for 22 500 genes of a set of key mutants, Risø 16, Risø 17, Risø 29, amo-1; Carlsberg II; *shx*, as well as well-established the cultivars Bomi, Midas, and Saana. While the analyses are not yet complete, we have found differentially expressed genes in each case between the mutant and its normal parent. For example, between *shx* and Bomi to which it is a near isogenic line, there were 51 differences during endosperm development. This is enabling us to produce a set of candidate genes for the phenotypic change we see, and to correlate these to the differences on the protein, starch and beta glucan levels.

A way forward

The current project has studied a small set of barley mutants affecting beta-glucan and starch content in depth at the transcriptional, protein, and metabolite levels, as well as investigated verification of gene function using transformation approaches). These candidate genes identified in the project need now to be functionally tested. In addition, there are several sets of mutagenized barley populations produced for the TILLING method of reverse genetics for high throughput screening, in which genes responsible for the mutant phenotype can be quickly identified. The populations represent a valuable resource for identifying barley lines with novel and useful functionalities, and then determining the underlying basis for the change. We have submitted a new proposal to do this.

Likewise, an application is pending on the European level to produce a single nucleotide polymorphism –based haplotype map of key European barley varieties and then to carry out association genetics on key phenotypes including starch and beta glucan. The partnership is different and only involves the Finnish partner but, it will produce data that confers added value to the NKJ project data rather than merely extending it.

Project partners:

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