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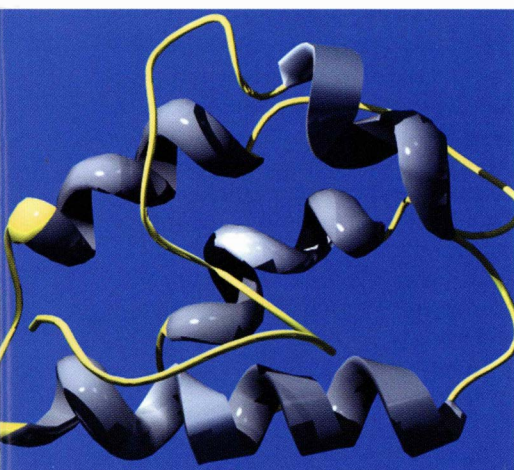
Wheat genes, proteins and quality

Research on durum wheat and bread wheat is intended to improve the quality of cereal-based products (pasta, bread, biscuits...) and to develop new tools for breeding, such as molecular markers. Proteins involved in a given characteristic are identified and characterized biochemically, thus yielding data for the isolation of the relevant genes. These genes are then investigated (regulation, structure), mapped and/or used as markers in breeding.

In the national Génoplante programme, a genomic approach is currently being developed: 100,000 ESTs (Expressed Sequence

Tags) will be produced from different libraries of cDNA (complementary) from mRNAs (messenger) extracted from ripening seeds. The goal is to identify all the seed proteins that play a part in the wheat quality and also to use these ESTs for genetic mapping in order to define Quantitative Trait Loci (QTL) usable in selection.

Frédéric de Lamotte, © UBBMC-INRA



Studying proteins involved in wheat quality to develop new breeding tools

Syntenic and parallel chromosome walking in the Poaceae

The grass family (*Poaceae*) is remarkable for the conservation of the basic structure of their genome: conservation of synteny (distribution of genes between chromosomes) and of colinearity between homologous chromosomes. This conservation is seen despite great genome diversity stemming from the frequency of anonymous repeated sequences (of undetermined function) and the ploidy level (number of copies of the basic chromosomes in the cells). This parallelism allows interspecific transposition of information and creation of common analytical and biological resources. The model species is rice, which among the *Poaceae* has the simplest genome, which is now being sequenced. Libraries of large fragments of DNA, constituted in Bacterial Artificial Chromosomes (BACs), have

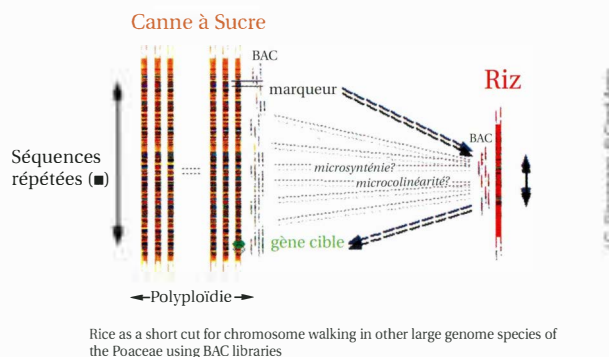
Studies are under way to investigate proteins of importance in the value of wheats, notably the thioredoxin system.

The thioredoxin system is used to improve the breadmaking quality of wheat varieties deemed unsuitable for breadmaking

The proteins in flour are responsible for the viscoelastic properties of dough. The reserve proteins (gliadins and glutenins) are the major constituents of the gluten obtained after kneading dough under a fine stream of water. Depending on the rheological properties of gluten, the bread will be more or less developed after fermentation. Although numerous chemical bonds are involved, disulphide bonds are believed to play an important part in the elasticity of the dough. The NADP-dependent thioredoxin system (an enzymatic system) is able to reduce the disulphide bridges of the reserve proteins but also of other small proteins especially rich in disulphide bridges. This generates free -SH groups which can then be reoxidized by creating inter-protein bonds, thus facilitating the network development and contributing to dough elasticity. The controlled addition of the different components of this thioredoxin system therefore allows to improve the breadmaking quality of varieties deemed to be unsuitable for breadmaking.

Biochemical and molecular studies of the thioredoxin system have yielded several isoforms and their relevant cDNAs. The proteins encoded by these cDNAs are produced in heterologous hosts so as to study their structures and functions.

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been constructed for the main species such as rice, sorghum, sugar cane or wheat. The next step is genomic analysis of characteristics such as resistance to diseases, grain quality, plant architecture and drought tolerance.

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