famine approach' to plant nutrition has many disadvantages, especially by contributing harmful effects to the environment and will continue to show the inequalities in achieving yield potential of crops. There is a need to scientifically evaluate the soil fertilizer-management practices under the 'life-cycle assessment (LCA) approach'[3].

The systems approach which has components such as inventory analysis, impact analysis and improvement analysis, will help evaluate the environmental consequences of fertilizer application from 'cradle to grave'. The ultimate goals of the LCA approach include comparison of environmental performance of agricultural practices or products, and to make eco-efficient improvements in the system. The LCA requires a great deal of data[4] and is a decision-support tool. Sustainable development in agriculture requires this approach to use natural resources efficiently and to minimize the waste. Or else, the current 'feast and famine approach' to plant nutrition can only remind us about the action of that unknown butcher, who feeds his goat with water to its full stomach, so that he benefits from the increased weight. Global concerns on the environment strongly necessitate that agricultural management at the farm level is on the basic tenet of the LCA approach, in order to utilize the natural resources efficiently and to prevent environmental degradation.

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NEWS

MEETING REPORT

Pre-harvest sprouting in cereals: A global scenario*

In order to assess the progress in research towards understanding the physiology, genetics and molecular biology of pre-harvest sprouting in cereals, an international symposium is being organized every four years. Starting in 1975, ten such symposia have been already organized[1]. In this sequence, the 11th International Symposium on Pre-harvest Sprouting in Cereals was held recently in Argentina. About 54 delegates representing 12 countries attended the symposium.

Pre-harvest sprouting (PHS), i.e. precocious germination of grains in the ear following physiological maturity, leads to a reduction in grain functionality, grain yield and viability of seed, resulting into significant economic losses. The sporadic occurrence and complex biology of PHS is a major challenge faced by crop geneticists. The aim of the symposium was to discuss different aspects of the PHS phenomenon and the possibility of minimizing the incidence of its adversity. The key aspects that were discussed in the meeting included the following:

(i) Physiological, genetic–molecular and environmental control of dormancy in cereals. (ii) Physiology and molecular biology of the cereal grain post-germination growth. (iii) Physiology of deterioration in the sprouted grain.

Daryl Mares chaired the opening session and highlighted the importance of agronomic management for PHS/dormancy. Daniel J. Miralles (Argentina) underlined the problem of PHS in wheat and barley, particularly in the context of expansion of agriculture to the marginal areas of Argentina favouring sprouting. He also discussed empirical models available for some barley cultivars for predicting PHS risk. Hickey *et al.* (Australia) presented their findings on rapid screening for PHS-resistant grains.

The significant role of genotype and environment in determining the expression of seed dormancy and PHS was reiterated by Nyachiro (Canada) and Gualano and Benech-Arnold (Argentina). For instance, in malting barley grains, under high temperature conditions, air temperature is the key determinant of the dormancy release pattern during the final stage of grain-filling. Further, Gualano and Benech-Arnold reported a linear relationship between temperature in the 'sensitive window' and germination index after physiological maturity.

Chandler[2] (Australia) presented experimental results on the involvement of gibberellic acid (GA) and abscisic acid (ABA) in dormancy[2]. Using GA mutants of barley, they demonstrated that GA response is not required for germination, if dormancy has been lost but ABA is important in maintaining dormancy of barley grains. In sorghum, RT–PCR analysis showed that dormancy blocks the rise in GA levels, which may be partly due to strong ABA signalling in dormant grains. In barley, caryopsis protein ABAP1 regulates genes involved in germination (Rodriguez *et al.*).

Rathjen (Australia) presented results of the study on the movement of water in seeds using magnetic resonance microimaging and reported that neither the rate of increase in water content nor the distribution within dormant and non-dormant grains differed significantly. They em-

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phasized that the inhibitor present in the seed coat is transferred to the embryo during imbibitions and causes dormancy.

Adkins (Australia) reported that dormancy is localized in different parts of the seed like seed hull, seed coat and seed embryo. For instance, in *Themeda triandra*, the hull modifies the water distribution patterns within the endosperm and is also responsible for lower uptake of oxygen and hence seed dormancy.

It was reiterated that grain colour and dormancy/PHS are correlated, a feature on which research[3,4] can be traced back to as early as 1900. In order to study the role of seed-coat pigment and dormancy in barley, NILs of Nishinohoshi for 12 proanthocyanidin-free genes (involved in the flavonoid synthesis pathway in seed coat pigment) were analysed for seed dormancy. These genes had a negative effect on seed dormancy (Tanooka, Japan). In weedy rice, Foley and coworkers[5] cloned and characterized *qSD7-1*, a QTL associated with red pericarp/testa colour and reported that it has pleiotropic effects on seed dormancy, red pericarp colour and grain weight. Hence, they concluded that this dormancy gene could not be used to improve resistance to PHS in white pericarp colour varieties.

DePauw (Canada) emphasized the importance of the genotype RL4137 in wheat breeding. RL4137 has two mechanisms for PHS resistance: one associated with kernel colour and the other not associated with it. RL4137 is important in breeding white-seeded wheat and has been reported to contribute PHS resistance in a number of wheat varieties like HY361, AC Vista, Snowbird, Kanata and Snowstar.

PHS dormancy is a complex trait and is controlled by many genes showing significant interaction with the environment. Hence, developing molecular markers linked to this trait will be useful not only in selecting resistant genotypes, but also in breeding resistant varieties in cereals. Six papers dealing with QTL mapping added information to a growing body of data on the location of QTL for resistance to PHS. Two new QTLs for seed dormancy on chromosome 2H and 3H using a population derived from a cross between Samson barley (dormant) and TR118 in barley were reported by Nyachiro. Mohan (India) presented experimental findings on a single locus and two-locus QTL analysis and reported[6] two major QTLs for PHS tolerance on chromosomes 2A and 3A. Hamphreys (Canada) reported co-location of QTLs on chromosome 4B in wheat for three PHS traits, i.e. falling number, germination and sprouting index. This information will be useful in pyramiding useful alleles to develop future PHS-resistant wheat cultivars. Mares (Australia) discussed the mechanism and genetic control of dormancy in red and white-grained wheat[7]. He reported a new QTL, close to *R-Bla*, on chromosome 3B and suggested that this QTL appears to be linked to increased expression of genes controlling key enzymes in the flavonoid pathway. Ullrich (USA) reported in barley that although most PHS and dormancy (DOR) QTLs coincide, some unique QTLs for these traits were also present[8]. They further reported that PHS susceptibility and DOR are not always represented by opposite alleles at a locus.

Taking into account the new trends in comparative biology, Holdsworth (UK) outlined the importance of comparative biology, development and implementation of bioinformatics tools based on knowledge in model species like *Arabidopsis* and rice[9]. Using bioinformatics tools, he reported new candidate loci in barley. Using a comparative approach, Gerjets and co-workers (UK) have studied the gene expression between wheat and *Arabidopsis*, and examined whether germination-associated genome expression is conserved/consistent between these species.

Another issue addressed at the symposium was the importance of late maturity α-amylase (LMA), also termed prematurity α-amylase (PMA), which refers to the presence of LMA activity in mature wheat grains in the absence of sprouting. LMA is a genetic defect present in some wheat genotypes and has been inadvertently disseminated to wheat breeding programmes around the world. Excessive LMA activity in flour lowers both the bread-making quality and Hagberg falling number (HFN). Farrell *et al.* (UK) reported that not only genotype but also environmental factors, particularly the temperature during grain-filling, play an important role in producing high LMA in grains. Mrva (Australia) presented her research findings on the effect of semi-dwarf (*Rht1*) phenotype on LMA expression and concluded that *Rht1* and *Rht2* reduce expression of LMA and require a cool temperature shock as trigger for LMA synthesis[10]. Taking into account the importance of both PHS and PMA in wheat, a large UK-based LINK project that aims to bring a multidisciplinary approach to both PHS and PMA is currently underway. As part of this link project, Phillips (UK) presented findings on biochemical and molecular mechanisms involved in PMA induction.

The symposium covered different aspects of the problems related to PHS and there was unanimity in the view that active research effort are needed to understand the genetic mechanism underlying this complex trait in cereals. In the concluding session, the need for breeding new high-yielding varieties in cereals that are resistant to PHS was recognized. A major effort is also needed to incorporate PHS tolerance in the Indian cereal-breeding programme, as the major wheat growing region, i.e. the Indo-Gangetic Plain, receives heavy rain during harvest and causes loss in yield and quality.

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