The aleurone layer is part of the endosperm and consists in a
organ derived from the maternal tissues (more information at

The maize kernel is classified botanically as a caryopsis. In
organ whose major function is to accumulate nutrient reserves,
earten, the embryo occupies most of the seed and is
basically a storage organ that accumulates starch and proteins.
The aleurone layer is part of the endosperm and consists in a
continuous layer of large cubical cells, which accumulate protein
and lipid granules and surrounds most of the endosperm. In
the area of the pedicle, which connects the seed to the mother plant,
the cells adopt a special morphology, typical of transfer cells
and form the basal transfer cell layer. The embryo consists of an
embryonic axis and a single cotyledon, which is called the
scutellum. The embryo axis is formed by the plume, covered
by the coleptile and the radicle, covered by coleohizia. All these
organs are almost completely surrounded by the scutellum, an
organ whose major function is to accumulate nutrient reserves,
mainly lipids and proteins. A single layer of cells directly in contact
with the endosperm, which is called the scutellar epithelium, is
important in the digestion and transport of the nutrients from the
endosperm to the embryo axis during germination. Both
endosperm and embryo derive from the fusion of gametes, but
while the embryo is derived from the fertilized egg, triploid
endosperm is derived from fertilized polar nuclei. Surrounding
the endosperm and embryo lays the pericarp, a protective
organ derived from the maternal tissues (more information at

Full genome sequencing allows the identification of the complete
catalog of genes in a species. However, the roles of a high
proportion of these genes remain unknown. The description of
temporal and spatial gene expression patterns is a first step in the
determination of the functional roles of the genes. Microarrays are
a useful tool to study gene expression in a tissue but, because
it integrates data from all cell types used for RNA extraction,
most spatial information is lost. On the other hand, it requires
the existence of a microarray chip containing all, or at least most
of the genes in the genome, which is not yet available for many
plant species. Laser microdissection allows obtaining RNA samples
from more homogeneous cell types and has been successfully used,
for example, in the study of the maize shoot apical meristem or
pericycle cell transcriptomes (Brooks et al., 2009; Dembinsky et al.,
2007). The combination of laser microdissection with microarray
hybridization is a very promising technique that has been allowed
to produce, for example, a cell type transcriptome atlas in rice (Jiao
et al., 2009). A complementary strategy is to define the specific
cellular expression patterns by in situ hybridization (ISH). ISH is a
high-resolution technique for the analysis of gene expression
that allows determining the steady state concentration of a specific
mRNA at the cellular level. ISH has been successfully applied in
maize (Fontanet and Vicient, 2008). Large-scale surveys of gene
expression patterns based on ISH analyses have been performed
for animals as, for example, Drosophila melanogaster (Zhao et al.,
2010), mouse (Richardson et al., 2010) and other mammals (Olsen
et al., 2004). In plants, it has only been performed for wheat (Drea
et al., 2005).

MASISH (Maize Seed In Situ Hybridization; http://masish.uab
.cat/) consists of a database of patterns of gene expression in maize
seeds based on ISH and a web-based interface that enables users to
search and display images and related gene annotations (Fig. 1).
The database contains two types of entries. Approximately half
of the entries arise from the systematic search of PubMed (http://
www.ncbi.nlm.nih.gov/pubmed/) for publications on maize seed
ISH. ISH images of the other genes were generated by the authors
themselves as previously described (Fontanet and Vicient, 2008)
without relying on labeled RNA probes and paraffin-embedded
samples (and labeled as “unpublished”). Some minor differences
were introduced in the protocol in order to facilitate the systematic
analyses. For example, hybridizations with two different probes
were performed in a single slide using silicone insulators (Grace
Bio-Labs JTR20-1.0). The probes used were obtained from clones of
cDNAs derived from scutellum dissected 30 days after
pollination (Genebank entries AM937797 to AM938286). Control
images (hybridization with sense probe) were performed for some
of the genes, showing no hybridization. These control images are also available in the report of the corresponding genes, while genes still lacking controls are clearly labeled as ‘unverified’. The database includes information concerning the possible functions of genes, GenBank entries and related publications. This database is expandable, so that the final aim is to obtain spatial information of the expression of all those genes that are transcribed in the maize seed at any point of development.

MASISH database is a relational MySQL database installed in a Linux Ubuntu Server. The searching interface is written in PHP and is wrapped in a Joomla web site that further includes information on the project and tools for the authors to easily maintain and update the database. MASISH database interfaces with GenBank database (http://www.ncbi.nlm.nih.gov/) and the AMIGO Gene Ontology web site (http://amigo.geneontology.org/cgi-bin/amigo/go.cgi) to retrieve information from these databases and link out gene reports. Information is accessed through browsing the MASISH database by gene name, expression pattern, reference or Gene Ontology ID and through text-based queries by gene symbol/name/synonym, PubMed ID, authors or GenBank accession, either including or excluding unpublished and/or unverified genes. Images for each gene are displayed initially as a set of thumbnails. Each thumbnail image is linked to the original full-sized image that can be downloaded.

Great efforts are being made in the recent times in the identification of all genes and their roles in maize. A second draft of the maize genome has been recently released, which contains most of the maize B73 genome sequence (http://www.maizesequence.org/; B73 RefGen_v2). Bioinformatics tools have been recently developed in order to identify and annotate the maize genome (Andorf et al., 2010; Montalent and Joets, 2010). High-throughput pyrosequencing of Expressed Sequence Tags (ESTs) has been applied in order to determine a maize transcriptome atlas at the organ level (Vega-Arreguín et al., 2009) and will also be of great help in the maize gene annotation. In this context, the establishment of an expandable expression pattern database such as MASISH provides a body of knowledge to suggest hypotheses that can facilitate the identification of the functions of genes that encode proteins of currently unknown function. In addition, it may also be helpful for comparing gene expression patterns of homologous genes in different species.

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