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A plea for a concerted nomenclature for arbuscular mycorrhizal fungal genes

During the last 5 years, more and more genes from arbuscular mycorrhizal (AM) fungi have been identified, and gene fragments have been cloned and sequenced. It therefore seems to be opportune and necessary that researchers agree on a nomenclature for AM fungal genes. Following a discussion started within the framework of the EU project GENOMYCA (QLRT-2000–01319), a number of conclusions were reached which we would like to put forward to the international community in order to achieve this aim:

1. Names for genes are written in italics with the exception of the numbering of loci and alleles. Lower-case and capital letters can be used. Names for proteins are exclusively in non-italic capitals.
2. The first four letters indicate the species starting with one capital followed by three lower-case letters, for example: *Glomus intraradices*, *Gint*; *Gigaspora rosea*, *Gros*; *Scutellospora castanea*, *Scas*.
3. The next letters indicate the function of the deduced protein. The number of letters is up to the author, but should not be more than necessary, for example: phosphate transporter, PT; chitin synthase, CHS; metallothionein, MT.
4. These letters should be followed by a number for the locus and a letter for the allele. This seems to be very important, because one can expect to have gene families for certain functions and different alleles among the nuclei of one isolate. The first allele of the first β-tubulin gene isolated from *Glomus mosseae* is therefore named *GmosBtub*1a, and the corresponding protein GMOSBTUB1A.
5. Many sequences are derived from non-targeted approaches, like sequencing of cDNA libraries or differential display analyses. However, subsequent data base searches often do not lead to any similarities to known genes. In these cases, the source of biological material of such an expressed sequence tag (EST) can be indicated. In order to distinguish it from an abbreviation for a function, it should be given in parentheses, for example for ESTs: from germinating spores of *Glomus mosseae*, *Gmos*(*Gsp*)1; from extraradical hyphae of *Gigaspora margarita*, *Gmar*(*Exhy*)1; from mycorrhiza of *Glomus intraradices*, *Gint*(*Myc*)1.

It is obvious that this nomenclature excludes certain information, like the AM fungal isolate or the plant species which has been used, or if the biological material was isolated from pots or from in vitro cultures. It also does not say if sequences were derived from genomic or cDNA clones and if it is only a fragment or the full size open reading frame. However, one has to find a compromise, because names for genes should not be too long. The participants of GENOMYCA (http://www.dijon.inra.fr/bbceipm/Genomyca/) would like to open a discussion with these proposals and receive comments or suggestions from other scientists inside or outside this field of research.

On behalf of the GENOMYCA Consortium

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