(146-149) Four proposals to amend the Code to provide for naming genomically preserved plants

In order to accommodate the naming of genomically preserved plants and in the spirit of *Code* Preamble 4, which calls for providing for future nomenclature, four modifications of the *Code* are proposed. A detailed discussion of genomically preserved plants and their nomenclature is published separately in this issue (Werth & Lellinger, Taxon 41: 513-521. 1992).

(146) Reword the first sentence of Preamble 7 and amend footnote 2:

"*7.* The rules and recommendations apply to all organisms treated as plants (including fungi and blue-green algae but excluding other prokaryotic groups[1]), whether fossil, non-fossil, or genomically preserved[2]."

"[2] In this Code, the term "fossil" is applied to a taxon when its name is based on a fossil type, the term "non-fossil" is applied to a taxon when its name is based on a non-fossil type (see Art. 13.3), and the term "genomically preserved" is applied to a taxon when its name is based on features attributable solely to the presence and expression of its genome in a polyploid species of hybrid origin (see Art. 13.3)."

These rewordings recognize that genomically preserved plants represent a third category of plants that exist and may be named under the Code.

(147) Add a new paragraph to Art. 7:

"*7.18bis.* The holotype of a taxon of genomically preserved plants is an illustration of a set of its likely unique features that are present in and determined from its polyploid derivative (e.g., isozyme band patterns, restriction fragment band patterns, or DNA sequences). The illustration must be labelled or annotated if it is necessary to distinguish features of the genome of the genomically preserved plant from features of the genomes of other taxa. For the purposes of this provision, a list of DNA base pairs in sequence is considered to be an illustration."

This provision recognizes that, in the absence of a physical holotype, a set of unique data must be used to characterize the taxon and that these data can best be displayed as an illustration.

(148) Amend Rec. 32B.1 by adding a second sentence, so that it reads:

"*32B.1.* The description or diagnosis of any new taxon should mention the points in which the taxon differs from its allies. The description or diagnosis of a taxon of genomically preserved plants should emphasize characters that are most directly observable directly from its genome, such as allozyme or karyotype data or nucleotide sequences, and should include an explanation of the means by which the features were determined."

This amendment establishes the special kinds of data that descriptions and diagnoses of taxa of genomically preserved plants should include.

(149) Add a new Art. 39bis:

"*39bis.1.* In order to be validly published, a name of a new taxon of genomically preserved plants must be accompanied by the designation of the name of a single

polyploid species to which it is ancestral and in which its genomic material is carried and from which the holotype illustration is derived."

This Article will avert any confusion as to the identity of the taxon of genomically preserved plants in cases where the taxon may have contributed a genome to more than one hybrid species.

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(150-156) Seven proposals to amend Art. 7 of the Code

The *Code* does not explicitly indicate the elements that are to be regarded as the original material associated with a name. The footnote to Art. 7.4 of the Berlin *Code* (Greuter & al., 1988) implies that only specimens and illustrations examined by an author of a name prior to the publication of the name and associated by the author with the concept of the named taxon are original material. Below is a summary of the more important contradictions that exist between this concept of original material and other provisions of the *Code*.

Art. 7.16 states: "A name validly published by reference to a previously and effectively published description or diagnosis (Art. 32.3) is to be typified by an element selected from the context of the validating description or diagnosis, ...". This conflicts with the concept of original material above since the material may not have been seen by the author of the name. Nevertheless it is current practice to refer to such types as lectotypes and not as neotypes.

An author may also validate a name using a previously unpublished description written by another, or with a description based on a previously unpublished description provided by another, without having examined the material on which that description was based. Although the *Code* does not clearly indicate the basis for typification of such names, it is customary to typify them (e.g. *Poa cilianensis* Allioni; see Perry & McNeill, 1986) by an element on which the validating description was based.

The *Code* does not state that the holotype (Art. 7.3), or the isotype(s) (Art. 7.6), or the syntype(s) (Art. 7.7) must be elements seen by either the author of the name or the author of the validating description. Further, despite the fact that an isotype or a syntype need not be part of the original material and the unequivocal instruction in Art. 7.5 that a lectotype must be selected from the original material, Art. 7.4 states that "An isotype, if such exists, must be chosen as the lectotype. If no isotype exists, the lectotype must be chosen from among the syntypes, if such exist." This means that, under certain circumstances, the *Code* dictates that an element that is not part of the original material must be designated as the lectotype of the name.