



Plant structure ontology: How should we label plant structures with doubtful or mixed identities? *

BRUCE K. KIRCHOFF¹, EVELIN PFEIFER² & ROLF RUTISHAUSER²

¹Department of Biology, University of North Carolina at Greensboro, Greensboro, USA. E-mail: kirchoff@uncg.edu

²Institute of Systematic Botany, University of Zurich, Switzerland. E-mail: rutishau@systbot.uzh.ch

* In: Minelli, A., Bonato, L. & Fusco, G. (eds) *Updating the Linnaean Heritage: Names as Tools for Thinking about Animals and Plants*. Zootaxa, 1950, 1–163.

Table of contents

Abstract	103
Introduction	104
Morphological nomenclature: The Plant Structure Ontology	104
Case studies	105
“Leaves”	105
“Roots”	108
“Flowers”	110
Morphological nomenclature: five complementary approaches	112
Approach 1 = Standardized vocabularies	112
Approach 2 = Developmental genetics	112
Approach 3 = Continuum Model and Fuzzy Morphology	113
Approach 4 = Process morphology, i.e. dynamic morphology	114
Approach 5 = Character cladograms	117
Conclusions and outlook	119
Acknowledgments	120
References	120

Abstract

This paper discusses problems with labelling plant structures in the context of attempts to create a unified Plant Structure Ontology. Special attention is given to structures with mixed, or doubtful identities that are difficult or even impossible to label with a single term. In various vascular plants (and some groups of animals) the structural categories for the description of forms are less distinct than is often supposed. Thus, there are morphological misfits that do not fit exactly into one or the other category and to which it is difficult, or even impossible, to apply a categorical name. After presenting three case studies of intermediate organs and organs whose identity is in doubt, we review five approaches to categorizing plant organs, and evaluate the potential of each to serve as a general reference system for gene annotations. The five approaches are (1) standardized vocabularies, (2) labels based on developmental genetics, (3) continuum morphology, (4) process morphology, (5) character cladograms. While all of these approaches have important domains of applicability, we conclude that process morphology is the one most suited to gene annotation.

Key words: Character cladogram, Continuum, Evo-devo, Flower, Flowering plants, Gene ontology, Intermediate organs, Leaf, Morphological nomenclature, Organ identity, Plant ontology, Plant structure ontology, Root