

SPECIAL ISSUE: *CANTHARELLUS*

EDITORIAL

Towards completing the world inventory for *Cantharellus*

This special issue on *Cantharellus* presents several papers that focus on tropical African or American chanterelles using a combined morphological-molecular approach. This important update on the taxonomy and biodiversity of *Cantharellus* in the world presents a total of 11 new species, five from tropical Africa and six from North America; it also introduces one new endemic section for Africa and it confirms the isolated position of the South American *C. guyanensis*, as already suggested by Shao *et al.* (2014), as sister to the Afro-Asian *C.* subg. *Afrocantharellus* thereby making it a good candidate for the recognition of an additional subgenus in *Cantharellus*.

This special issue also illustrates the importance of obtaining sequence data from available type material and of the process of epitypification in the stabilization of species concepts in the genus. Indeed, *Cantharellus* more and more reveals itself as an assemblage of species that have extremely flexible and variable phenotypes. As the microscopical diversity among the various species in the genus is rather limited, general field characteristics such as overall color, size and shape have always taken a very important place in the delimitation and identification of species. As a consequence, the use of molecular data to delimit species in *Cantharellus* may result in a reduction rather than a multiplication of accepted species, contrary to what can be observed in other genera of the cantharelloid clade, such as *Hydnum* (Feng *et al.* 2016). This is here particularly well illustrated by the extreme example of the newly described *C. velutinus* (Buyck *et al.* 2016e), the variability of which has met with much disbelief among colleagues. It is therefore not surprising that recent revisions of European chanterelles (Olariaga *et al.* 2015, 2016) resulted in a rather impressive reduction of the currently accepted European *Cantharellus* from 24 (Eyssartier & Buyck 2000) to merely eight species, each of these being highly variable in overall color, as well as in size and general habit. This special issue also presents first sequence data for the holotypes of two of the earlier described North American chanterelles (Buyck *et al.* 2016c), both of which apparently have been ignored due to the preponderance of particular macroscopic features in defining their morphological species concept. When available type specimens are resistant to sequencing, neotypification or epitypification with newly sequenced collections that fit the original description, are the only means of stabilizing the earlier introduced names and corresponding species concepts. Such an issue no longer concerns North American *Cantharellus* (Buyck *et al.* 2016c) and has equally been dealt with for the European species (Olariaga *et al.* 2016) but it remains a major issue for most of the African and even Asian chanterelles. In this special issue, five mainland African (Buyck *et al.* 2016a,b; De Kesel *et al.* 2016) and one Malagasy *Cantharellus* (Buyck *et al.* 2016g) are epitypified but there is still a long way to go before the taxonomy of African chanterelles will be entirely based on phylogenetic species concepts.

In contrast with the above-mentioned highly variable phenotypes within a single species, several sometimes unrelated species may present near-identical field habits, such as the African *C. miomboensis* and *C. pseudomiomboensis* (De Kesel

et al. 2016) or the various American species of subg. *Cinnabarinus* (Buyck *et al.* 2016d), thereby making identification impossible without sequence data or without at least carefully checking the microscopic features. With respect to the latter, it is now clear that the diagnostic value of spore measurements can only be appreciated when presenting mean values for length, width and length/width ratio. Such simple statistical values are nevertheless not always provided, not even in several recent descriptions of new chanterelles. Also hyphal extremities of the pileus surface can orient one toward specific species or species complexes, as again illustrated here for several species complexes among North American chanterelles (Buyck *et al.* 2016e,f)

In view of the huge, observed differences when comparing known biodiversity of *Cantharellus* among individual continents (Fig. 1), what can we anticipate for the inventory of *Cantharellus* for the next few years? With respect to its long-standing tradition of intense mycological exploration, the situation is not likely to change very much in Europe where glaciation periods very likely wiped out most of the earlier biodiversity. In North America, however, the description of new species has exploded over the past five years and this is likely to continue for some time, especially since the mycological community can now benefit from a nearly complete coverage of the presently 29 described species by representative sequence data (Buyck *et al.* 2016c). Over the next years, we have also high expectations from massive sequencing of *Cantharellus* collections in the USA, not only with respect to the discovery of new species, but particularly with respect to species distribution patterns. These appear to be much wider than previously assumed for some species, but presently available data also clearly indicate that more restrictive distribution patterns may exist (Buyck *et al.* 2016f). In the past, the variable ITS region of *Cantharellus* species has also been responsible for the systematic exclusion of the genus from results based on DNA analyses of soil samples (Buyck *et al.* 2014). Several field observations indicate for example the existence of more

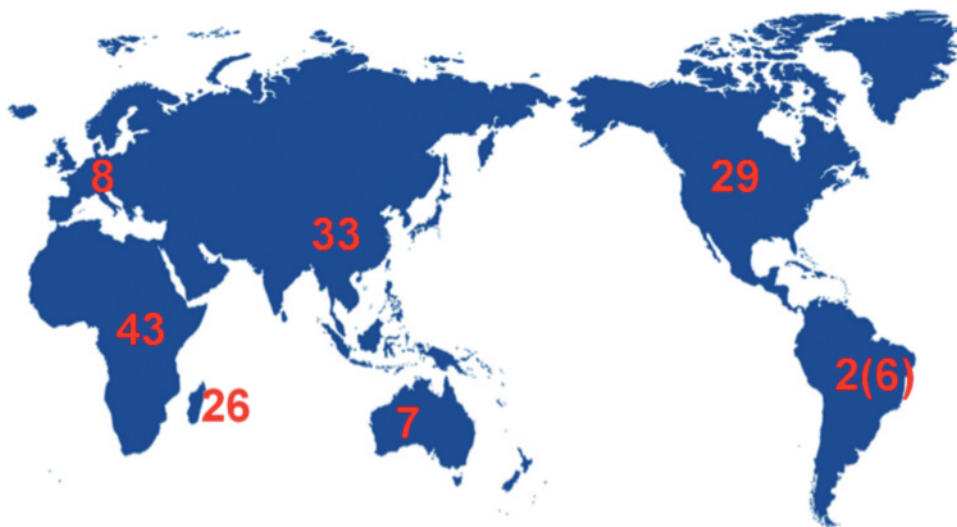


Fig. 1. Estimations of known species richness for *Cantharellus* on individual continents and Madagascar based on published accounts.

or less specific associations with certain hosts or habitats such as for the European *C. roseofagetorum* (Olariaga *et al.* 2016) or the here newly described American *C. velutinus* (Buyck *et al.* 2016e) which has a pink form restricted to the Appalachian Mountains, while it seems mutually exclusive with *C. lateritius* in Texas where it seems to prefer habitats in which American beech is an obvious component. The example of the here equally newly described *C. coccolobae* is to our knowledge one of the rare examples of a highly specific host association among American *Cantharellus*.

Mainland Africa, which already surpasses by far all other continents with its 43 presently described endemic *Cantharellus* species (De Kesel *et al.* 2016), is certainly going to comfort its leading position as evidenced by the many, many new species that continue to be uncovered through the increasingly frequent fungal inventories in both the rain forest area and the surrounding woodlands (De Kesel *et al.* 2016; Buyck, unpubl.). We estimate that, at this moment, more than 20 undescribed taxa have already been identified and many more are likely to follow. Yet, a major priority, to which several papers in this special issue have contributed, remains the urgent epitypification and molecular characterization of the many African chanterelles described by Heinemann (1958, 1966).

A considerable contribution to the world inventory of *Cantharellus* can also be expected to come from Asia as already suggested by the few past publications on this genus (Corner 1966, Eyssartier *et al.* 2009; Shao *et al.* 2014), as well as by unpublished results from preliminary inventories in China (Shao 2011) and Taiwan (V. Antonin, pers. com.).

At the opposite, and in strong contrast with the high *Cantharellus* biodiversity on the abovementioned continents (with the exception of Europe), Australia and South America do not seem to harbor that many *Cantharellus* species and this notwithstanding many decennia of mycological inventories. South America revealed a rich mycota for other genera in Cantharellales, such as *Clavulina* (Henkel *et al.* 2011) and *Craterellus* (Henkel *et al.* 2014), but even preliminary molecular data (Buyck unpubl.) seem to indicate the presence of only very few, distinct species in *Cantharellus*.

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