



A corrigendum to the phylogeny of the family Gammaridae (Crustacea: Amphipoda)

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Summary. We stated an error in our previous DNA analysis of Gammaridae. The right position of *Zenkevitchia* in the phylogenetic tree is close to marine and American *Gammarus* spp., far from the Dinaric troglolobitic *Typhlogammarus* group of genera. The morphologically diverse *Zenkevitchia* group supports the necessity of some parphyly in systematics.

After collecting samples of gammarids from the entire family area and necessary data of relevant marine relatives, we succeeded to establish the phylogenetic position of the important family Gammaridae and to construct a new, the first molecularly based phylogenetic tree of it (Hou & Sket 2016). We had to include some genera which had been supposed to represent independent families (mainly Bajkalian, e.g. Tahteev 2000). And, first of all, we dissolved the long lasting problem of genera with shortened uropod III endopodites (mainly '*Echinogammarus*' spp.). With a later work (Sket & Hou 2018) we also dissolved the position of some biogeographically strange taxa (e.g. the 'European *Eulimnogammarus*' of Stock, West-Mediterranean *Parhomoeogammarus* of Schellenberg (Sket & Hou 2018).

On the other hand the unusual position of the Caucasian troglolobitic (stygobiotic) *Zenkevitchia* which, according to our analyses appeared to be a close relative of the West-Balkan troglolobitic *Typhlogammarus* group of genera (with *Typhlogammarus*, *Metohia*, *Accubogammarus*) remained questionable. The question became more crying since Sidorov *et al.* (2018) sequenced a series of other Caucasian species and decided to erect for them an independent taxon, family Zenkevitchiidae. This resulted in a disjunct distribution of the new family between the Dinaric karst and Caucasian karst.

The disturbing position of our '*Z. admirabilis*', supposedly the type species of its genus, and genetic distribution of morphologically close *Zenkevitchia* spp. in two different clusters, forced us to check our previous tree construction. It happened that we had evidently done an error and we can now correct the position of *Z. admirabilis* Birštejn to a right position into the cluster of other *Zenkevitchia* spp. A new analysis of our sample put it into a logical position between its Caucasian congeners.

So, Dinaric and Caucasian karsts are inhabited by two not closely related, highly troglomorph monophyletic groups of species or genera (Fig. 1). The Dinaric *Typhlogammarus* group of genera is sister to the west-European *Echinogammarus* s. str. The Caucasian *Zenkevitchia* group is closely related to a couple of eastern North American *Gammarus* species, of which at least one (*G. minus* Say) is an eu-troglophile, which means a principally epigeal species including troglolobitic populations (Culver *et al.* 2013).

The status and composition of the morphologically diverse Caucasian genera *Zenkevitchia* Birštejn, *Anopogammarus* Birštejn, *Adaugammarus* Sidorov, Gontcharov & Sharina, probably *Kruberia* Sidorov and Samokhin (not yet molecularly studied) have still to be discussed (Fig. 2). Anyway, they have been shown to be clades within the *Gammarus* phylogenetic tree (Sidorov *et al.* 2018; this study). Among other problems, there is a lack of toptype samples of the members. Unfortunately, we do even not possess a toptype sample of the type species *Z. admirabilis* which would allow us to reliably fix the type taxon. The type locality was indicated (Birstein 1940) as the *peščera* (cave) *bliz Andreevki* or *Peščera andreevska*, nowadays the cave at Apra near Suhumi, Abhazija, Georgia (D. Sidorov *in litt.*).

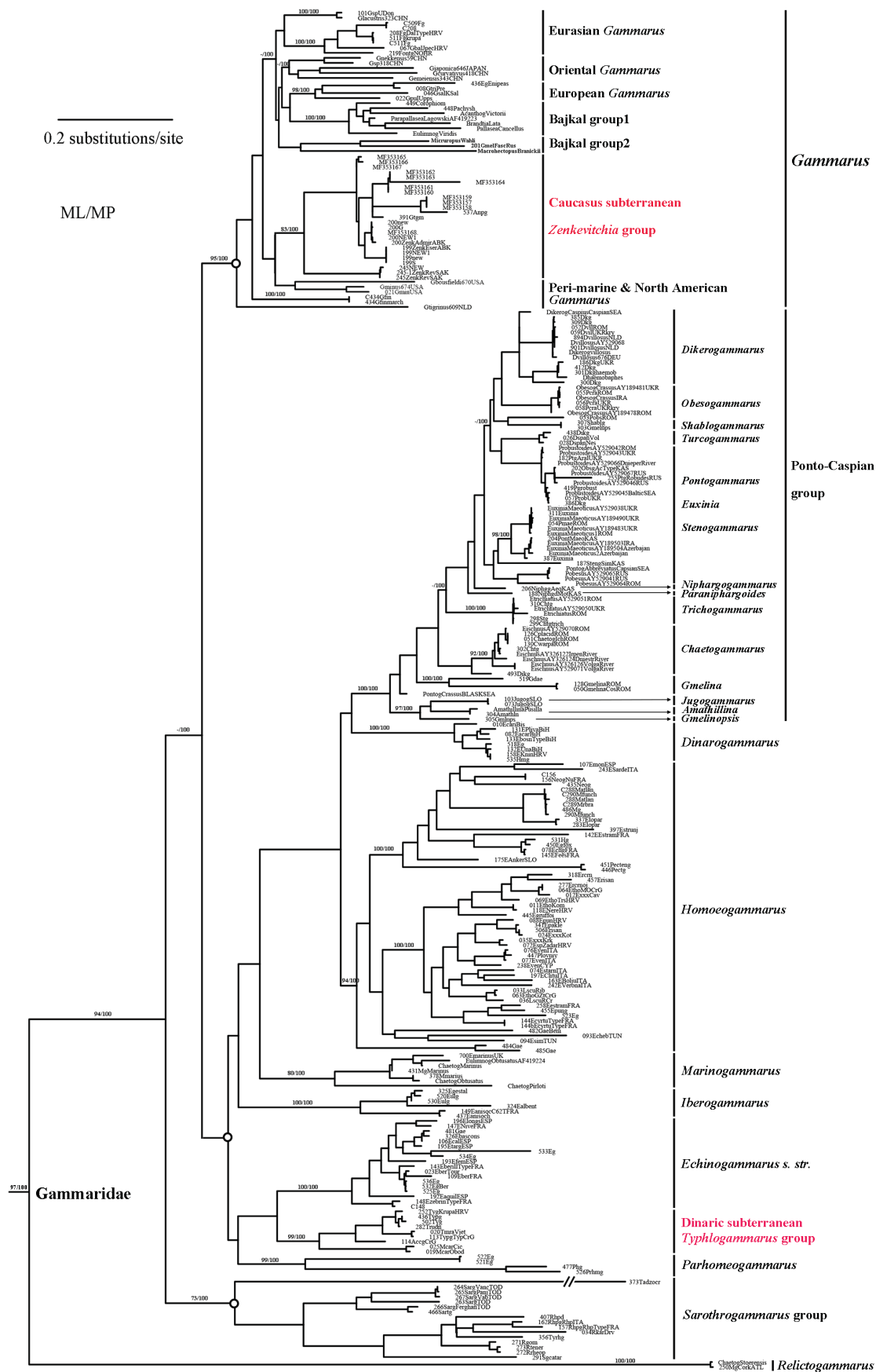


FIGURE 1. Maximum likelihood phylogenetic tree of Gammaridae based on the combined analysis of mitochondrial (COI) and nuclear (28S, 18S and EF-1a) markers. Numbers represent statistical bootstrap supports of nodes in order for maximum likelihood (ML) and maximum parsimony (MP).

Although we can not totally avoid paraphyly in the systematics, we would like to avoid it whenever possible (Nordal & Stedje 2005; Farris 1974). Therefore, we are not enthusiastic with separation of the Caucasian group as a separate family. Its status is similar to Bajkalian genera, which are strikingly diverse and often regarded as several separate families, although they are phylogenetically members of the genus *Gammarus* Fabricius (Hou & Sket 2016). Remarkable is also the morphological diversity of the *Zenkevitchia* group, although it is molecularly compact (Table 1). The mean genetic distance of the 28S rRNA gene between the species of the *Zenkevitchia* group is 0.028 (the exclusion of *Z. revazi* Birštejn & Levuškin leaves the rest even at 0.02), while the pairwise uncorrected p-distance for 28S rRNA gene between European freshwater *Gammarus* spp., which are morphologically less diverse, is 0.053.

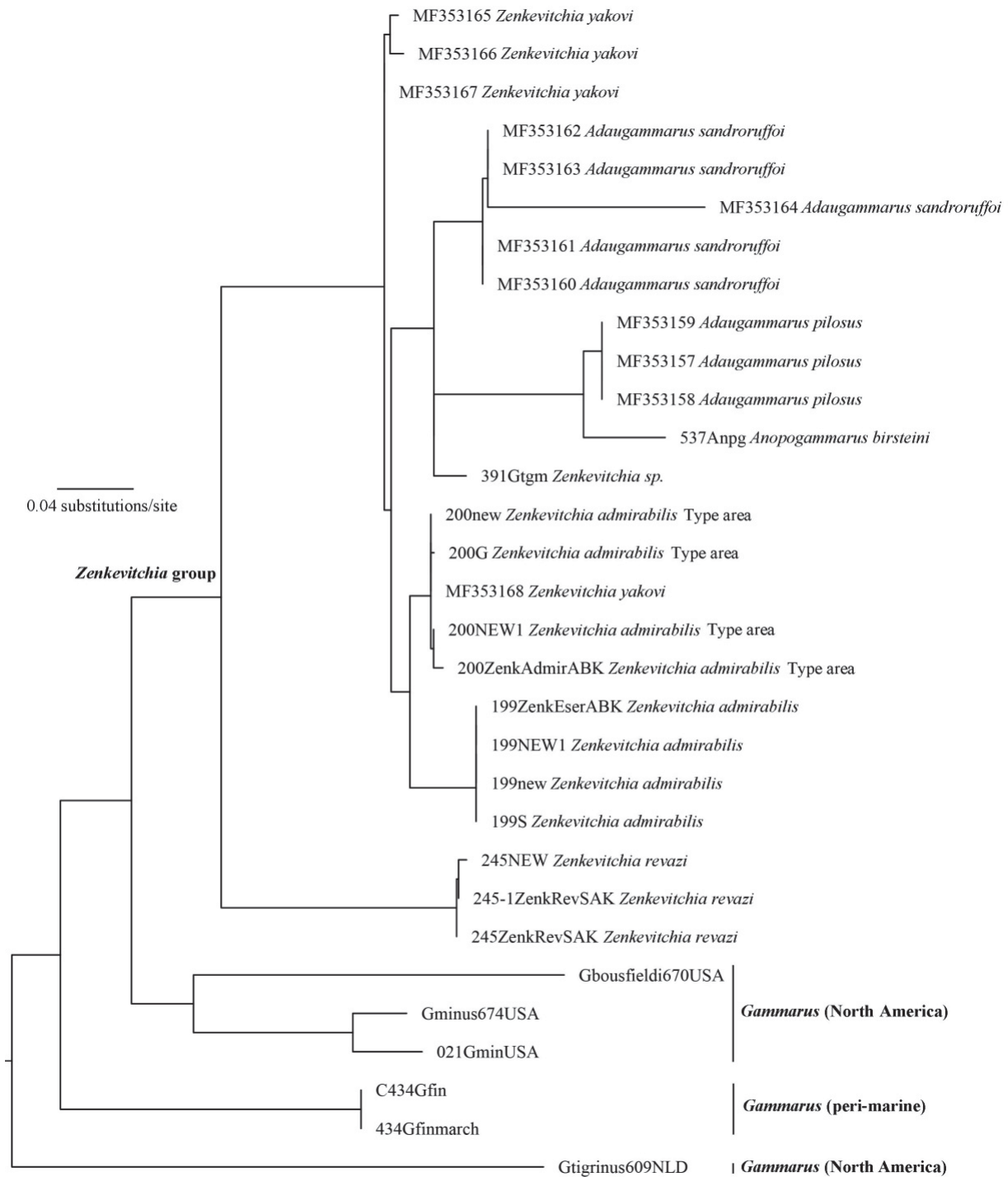


FIGURE 2. Enlarged the relevant part of the tree from Fig. 1, including the *Zenkevitchia* group of species and its relatives. Taxonomic identification after Sidorov *et al.* 2015.

TABLE 1. 28S rRNA gene distances among zenkevitchiid species

28S Pairwise distance	245 ZenkRevSAK <i>Zenkevitchia revazi</i>	537	199	200
537Anpg <i>Anopogammarus birsteini</i>	0.0633			
199new <i>Zenkevitchia admirabilis</i>	0.0858	0.0174		
200new <i>Zenkevitchia admirabilis</i>	0.0608	0.0101	0.0014	
MF353157 <i>Adaugammarus pilosus</i>	0.0752	0.0078	0.0187	0.0098
MF353160 <i>Adaugam. sandroruffoi</i>	0.0688	0.0125	0.0133	0.0067
MF353165 <i>Zenkevitchia yakovi</i>	0.0636	0.0118	0.0075	0.0032
391Gtgm <i>Zenkevitchia sp</i>	0.0625	0.0124	0.0014	0.0023

TABLE 1. (Continued)

28S Pairwise distance	MF353159	MF353160	MF353165
537Anpg <i>Anopogammarus birsteini</i>			
199new <i>Zenkevitchia admirabilis</i>			
200new <i>Zenkevitchia admirabilis</i>			
MF353157 <i>Adaugammarus pilosus</i>			
MF353160 <i>Adaugam. sandroruffoi</i>	0.0131		
MF353165 <i>Zenkevitchia yakovi</i>	0.0126	0.0092	
391Gtgm <i>Zenkevitchia sp</i>	0.0117	0.0092	0.0055

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