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Original Article

# New distributional records, taxonomy, morphology, and genetic variations of the endangered brackish-water species *Lamprothamnium succinctum* (Charales: Charophyceae) in Japan



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#### ABSTRACT

Members of the brackish-water species *Lamprothamnium succinctum* (Charales, Charophyceae) are widely distributed from tropical to temperate regions, including East Asia. In Japan, *L. succinctum* is listed as an endangered species and is protected by the government, because it was recorded only at two localities, Lake Hachiro-gata (Akita Prefecture) and Oo-ike pond (Deba-jima Island, Tokushima prefecture), and has become extinct in the former. In this study, we identified five new localities of this species in Japan. The morphological characteristics of their thalli agreed with those provided in the original description of this species, with distinctive reproductive characteristics. Moreover, the oospores of Japanese specimens of *L. succinctum* were examined for the first time using scanning electron microscopy. The oospores of Japanese specimens exhibited granulate fossa wall patterns, which were consistent with those described in previous studies. Our genetic analyses based on the DNA sequences of two chloroplast DNA markers, including both the coding and non-coding regions, revealed that the sample from Oo-ike pond is distinguishable from those from other Japanese specimens, although they are genetically very similar.

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#### Introduction

The genus *Lamprothamnium* J. Groves (Charales, Charophyceae) is characterized by ecorticated thalli, unforked whorled branchlets, stipulodes occurring directly below the branchlets, and one tier of coronal cells (cronula) in the oogonia (Wood 1965; Imahori and Kasaki 1977; Bryant and Stewart 2011; Casanova 2013). In most

species, the male organs (antheridia) are positioned above the female reproductive organs (oogonia). This genus usually develops spherical bulbils on the rhizoidal filaments, inhabits brackish to saline water environments, and has an almost cosmopolitan distribution (Wood 1965; García and Casanova 2003). Within the genus, 20 extant taxa have been described (Groves 1916; Ophel 1947; Corillion 1957; Wood 1965; de Donterberg 1984; García and Casanova 2003; Schubert and Blindow 2003; Casanova 2013).

*Lamprothamnium succinctum* (A. Braun) R. D. Wood is characterized by irregularly developed stipulodes and the occasional positioning of oogonia above antheridia (Wood 1965). Moreover, its members are distributed widely from tropical to temperate regions, including East Asia (Allen 1887; Groves 1919; Zaneveld 1940; Kasaki 1964; Wood 1965; Guerlesquin et al 1987; Choi and Kim

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1997; Casanova 2013). In Japan, this species was recorded only in two localities, i.e. Lake Hachiro-gata (Akita Prefecture) and Oo-ike pond (Deba-jima Island, Tokushima prefecture) (Imahori 1963; Kasaki 1964). However, recent field surveys revealed that this species has become extinct in Lake Hachiro-gata because of the reclamation of the lake (Imahori and Kasaki 1977; Watanabe et al 2005). Consequently, *L. succinctum* was listed as a "critically endangered species (CR+EN)" in the Japanese Red List of Ministry of the Environment, Japan (MOEJ 2019), and the remaining viable populations of this species inhabiting in Oo-ike pond were protected as a natural monument designated by the government in 1972. In addition, individuals of this species collected at Oo-ike pond were cultured and are maintained in the Microbial Culture Collection at the National Institute for Environmental Studies (MCC-NIES, Tsukuba, Japan), for *ex situ* conservation.

Recent scanning electron microscopy (SEM) and molecular phylogenetic studies have shown that the morphology of the fully mature oospores is a reliable character for elucidating the specieslevel taxonomy of the charalean taxa (John and Moore 1987; John et al 1990; Leitch 1990; Ray et al 2001; Sakayama et al 2002; Sakayama et al 2004; Sakayama et al 2005; Casanova 2005, 2009; Sakayama 2008; Sakayama et al 2009; Urbaniak 2011a, 2011b; Perez et al 2014, 2015; Sakayama et al 2015; Perez et al 2017). However, the oospore morphology of Japanese *L. succinctum* has not been studied at the SEM level, and only two specimens of this species have been analyzed based on molecular phylogeny (Sakayama et al 2009; Perez et al 2017). More recently, Casanova (2013) pointed out that *L. succinctum* sensu R. D. Wood (1965) might include several species based on detailed morphological analyses. Therefore, the examination of the detailed morphology of fully mature specimens and genetic analyses are necessary to clarify the taxonomic status of Japanese specimens of *L. succinctum*.

During our recent field surveys, we identified five new localities of *L. succinctum* inhabitation in Japan. In this study, we determined the morphology of the vegetative thalli and the fine oospore structures of *L. succinctum* using newly collected fully matured specimens. In addition, we conducted genetic analyses of the chloroplast *rbcL* DNA sequences and of the intergenic spacer (IGS) region located between the *atp*B and *rbcL* genes (*atpB-rbcL* IGS) in Japanese specimens of *L. succinctum*, to elucidate their phylogenetic relationships and genetic differences.

#### Material and methods

The localities at which sample collections were performed are shown in Figure 1 and Table 1. The methods used for field collection, culture, light microscopy (LM), and SEM were all according to those reported by Sakayama et al (2002, 2004, 2009, 2015) and Kato et al (2008), with the following modifications: filtered seawater was diluted to a salinity of approximately 10‰ and used to prepare the brackish soil–water medium for the Charales (B-SWC). The pressed specimens were deposited at the Herbarium, Department of Botany, National Science Museum (TNS), Tsukuba, Japan.

The extraction of total DNA, amplification of DNA by polymerase chain reaction (PCR), direct sequencing of the PCR products, and phylogenetic analyses were conducted as described previously (Sakayama et al 2002; Sakayama et al 2006; Kato et al 2008), with



Figure 1. Map of the localities where the Japanese specimens of *Lamprothamnium succinctum* were collected for this study (open circles, A–F). The closed circle (Lake Hachiro-gata, Akita Prefecture) indicates the locality at which this species has become extinct. For detailed information on these localities, see Table 1.

Collection and strain/specimen information			rbcL		atpB-rbcL IGS	
Collection site <sup>a</sup>	Collection date	Strain/specimen designation	Accession number	Source	Accession number	Source
Pond at Nonoshima Island, Shiogama, Miyagi (A)	2012/10/5	MYG006/TNS-AL 213317	LC536055	This study	LC536062	This study
Pond at Niihama, Ichikawa,	2007/6/29	SK166/TNS-AL 213318	LC536056	This study	LC536063	This study
Chiba (B)	2008/5/24	-/TNS-AL 213319	LC536057	This study	LC536064	This study
Jaga-ike Pond at Minami,	2003/12/14	-/TNS-AL 213320	LC536058	This study	LC536065	This study
Kaifu, Tokushima (C)	2004/6/14	KGK1947/NY01089138	KX431014	Perez et al (2017)	-	-
Oo-ike pond, Deba-jima Island, Muki, Tokushima (D)	-	S038/TNS-AL 213321	AB440262	Sakayama et al (2009)	LC536066	This study
Pond at Uranouchi	2006/9/20	-/TNS-AL 213322	-	-	-	-
Nishibun, Susaki, Kochi (E)	2012/8/28	EHM117/TNS-AL 213323	LC536059	This study	LC536067	This study
Pond at Kume-jima Island,	2006/5/13	SK164/TNS-AL 213324	LC536060	This study	LC536068	This study
Kume-jima, Okinawa (F)	2012/9/3	KMJM002/TNS-AL 213325	LC536061	This study	LC536069	This study
	2018/5/26	S399/TNS-AL 213326	-	-	-	-

Table 1. Sources of the specimens of Lamprothamnium succinctum used in this study.

<sup>a</sup> The characters placed in parentheses after the collection site indicate the localities shown in Figure 1.

the exception of the use of the four primers designed by us for the *atpB-rbcL* IGS (Table 2).

For molecular phylogenetic analyses, we used a data matrix containing 1,194 base pairs (bp) of unambiguously aligned rbcL gene sequences [corresponding to nucleotides 31 to 1224 of the rbcL gene of Chara vulgaris L.; Accession No. NC\_008097 (Turmel et al 2006)] from nine specimens of L. succinctum, as well as 19 species from the genera Chara L., Lamprothamnium, Nitellopsis Hy, and Lychnothamnus (Rupr.) Leonh. (Table 1, Appendix A; TreeBASE accession number S26033). Two species of the genera Nitellopsis and Lychnothamnus were selected as an outgroup because recent phylogenetic studies demonstrated that the tribe Chareae (Chara, Lamprothamnium, Lychnothamnus, and Nitellopsis) is monophyletic, where a clade comprising of species of genera Nitellopsis and Lychnothamnus is sister to a clade comprising of species of genera Chara and Lamprothamnium (McCourt et al 1996; McCourt et al 1999: Sakavama et al 2002: Sakavama et al 2004: Sakavama 2008; Sakayama et al 2009; Perez et al 2014; Perez et al 2017). The aligned dataset was subjected to the Bayesian inference (BI) method using MrBayes 3.2.6 (Ronquist and Huelsenbeck 2003). Kakusan4 (Tanabe 2011) was used to identify the sequence evolution model that fitted the dataset. The criteria used for model selection were Bayesian Information Criterion (BIC4) for BI analyses and corrected Akaike's Information Criterion (AICc4) for maximum likelihood (ML) analyses. The substitution models used for each codon position of the *rbcL* gene in the BI analyses were HKY85 + I (first codon position), JC69 (second codon position), and GTR + I (third codon position), which were selected by Kakusan4. BI analyses were performed using MrBayes 3.2.6, as previously described (Nakada and Nozaki 2009). The parameters of the substitution models for each codon position were unlinked. The Markov chain Monte Carlo iteration process was stopped at 1,000,000 generations. The first 25% of generations were discarded as burn-in, whereas the remaining trees were used to calculate a 50% majority-rule tree and to determine the posterior probabilities of individual branches. The average standard deviations of the split frequencies were below 0.01, indicating convergence of the iterations. ML analyses were performed with 1.000 bootstrap replications (Felsenstein 1985) using RAxML v. 8.2.10 (Stamatakis 2014), and the GTR + G model (selected by Kakusan4) was used for each codon position. Maximum-parsimony analyses were performed with 1,000 bootstrap replications (using a heuristic search with the

stepwise addition of 10 random replications using the tree-bisection—reconnection branch-swapping algorithm) using PAUP\* 4.0b10 (Swofford 2002).

#### Results

#### Morphological observations

The thalli of the present specimens of L. succinctum were monoecious, bright to dark green, and up to 40 cm high. The axes were up to 440 µm in diameter, the internodes were up to ca. 4.5 cm long, and cortical cells were absent (Figure 2A). The stipulodes were developed, grew downward, were placed opposite the branchlets in one tier, and were up to ca. 900 µm long and ca. 110 µm in diameter (their length varied) (Figure 2B). Whorls comprised 6–8 branchlets that were up to ca. 4 cm long, lacked cortical cells, and were composed of three or four (or five) segments (Figure 2A). The terminal segments of branchlets were oneor two-celled, were elongated, and were up to ca. 2 cm long (Figure 2A). The branchlets exhibited one or two bracteoles that were up to ca. 810 µm long and included two or three bract cells that were weakly or well developed and up to ca. 650 µm long (Figure 2A and 2C). The bulbils were spherical and up to ca. 900 µm in diameter and were arranged in clusters of 1 to 4 units attached to the rhizoidal filaments (Figure 2D). The oogonia and antheridia were usually sejoined (rarely conjoined) and formed at the basal two-branchlet nodes and at the base of the whorl (Figure 2C). The oogonia were bright yellow, up to ca. 890 µm long (excluding coronula), up to ca. 550  $\mu$ m wide, and had 9–11 convolutions; the coronula were ca. 80–110 µm long and 130–160 µm wide (Figure 2C). Finally, the antheridia were orange and 360-460 μm in diameter (Figure 2C). These vegetative and reproductive characters were essentially consistent with those included in previous descriptions of Japanese specimens (Kasaki 1964; Imahori and Kasaki 1977).

In the present study, the oospore morphology of Japanese specimens of *L. succinctum* was examined using SEM for the first time. The oospores were dark-brown to black colored and ellipsoid in shape, and had 9–11 spiral ridges (Figure 3A). Moreover, they were ca.  $550-680 \mu m$  long, ca.  $280-360 \mu m$  wide, and up to 74  $\mu m$  across the fossa (Figure 3A). The spiral ridges were weakly developed and lacked ribbon-like structures (Figures 3A and 3B). The

**Table 2.** Primers used for the amplification and sequencing of the full-length *atpB-rbcL* IGS performed in the present study.

Designations	Sequence (5' to 3')	Position	Source
CH-atpB-R1	AGACCATCAGTAGCACTCATAG	248-227 <sup>b</sup>	Kato et al (2008)
CHAR-RR-5 <sup>a</sup>	GCTAAAATGTCAGTATCTTTAG	113–92 <sup>c</sup>	Kato et al (2008)
Cb_atpB_R84-63	AACAGGTCCAATAATTTGAGTA	84–63 <sup>b</sup>	This study
Ls_IGS-F23	ATCAATGGTATATATGAATTTGAA	436–459 <sup>d</sup>	This study
Ls_IGS-R14 <sup>a</sup>	AGTTTCTTTATATTGAAAAGCATGA	619–595 <sup>d</sup>	This study
CH_rbcL_R65-44 <sup>a</sup>	AATCTGTAATCTTTTACCCCTG	65–44 <sup>c</sup>	This study

IGS, intergenic spacer.

<sup>a</sup> Reverse primer.

<sup>b</sup> Coordinate number from the *atpB* gene of *Chara vulgaris* (Turmel et al 2006).

<sup>c</sup> Coordinate number from the *rbcL* gene of *C. vulgaris* (Turmel et al 2006).

<sup>d</sup> Coordinate number from the *atpB-rbcL* IGS of *Lamprothamnium succinctum* (strain S038).

oospore wall ornamentations were granulate, as observed using LM (Figure 3D). Under SEM, it was observed that the fossa wall had an irregular granulate pattern (Figure 3B); the granules rarely had a pore at the apex and were ca.  $0.3-2.7 \mu m$  in diameter (Figure 3C).

#### Molecular phylogeny and genetic variations

The *rbcL* DNA sequences (1,194 bp) of our seven Japanese specimens of *L. succinctum* were identical to the previously published sequences of the specimens from Oo-ike pond (strain S038) and Jaga-ike pond (KGK1947) (Figure 4, Table 1). The Japanese specimens of *L. succinctum* formed a robust clade with three other species of *Lamprothamnium* [*L. papulosum* (Wallroth) J. Groves, *L. macropogon* (A. Braun) Ophel, and *L. heraldii* Adr. García & Casanova]. In our *rbcL* phylogeny, the phylogenetic position of the genus



**Figure 2.** Thalli of *Lamprothamnium succinctum* collected from Ichikawa, Chiba, Japan: A, apical part of a thallus consisting of a main axis and whorled branchlets; B, node of the main axis, from which whorled branchlets (above) and developed stipulodes (below) occur; C, node of the main axis, showing whorled branchlets with antheridia and bracteoles/ bract cells, as well as oogonia that formed on the inside of the base of the whorl (OO: oogonia, AN: antheridia); D, white spherical bulbils attached to the rhizoidal filaments. <scale bar: 1 mm (A–D)>.



**Figure 3.** Oospores of *Lamprothamnium succinctum* collected from Ichikawa, Chiba, Japan: A, overall appearance of an oospore, as imaged using scanning electron microscopy (SEM), showing 9 or 10 flanged spiral ridges on the surface, and fossa walls between the spiral ridges; B, part of the fossa wall, as imaged using SEM, showing an irregular granulate ornamentation; C, detail of the fossa wall, as imaged using SEM, showing large and minute granules on its surface; D, part of the fossa wall, as imaged using light microscopy, showing an irregular granulate pattern. <scale bar: 300 μm (A); 50 μm (B and D); 10 μm (C)>.

*Lamprothamnium* was not clearly supported. This finding was similar to that reported previously (McCourt et al 1999; Sakayama et al 2009; Perez et al 2014; Perez et al 2017). Based on the full-length sequences of the *atpB-rbcL* IGS (1,065 bp), two haplotypes were detected within the eight specimens of *L. succinctum* examined in the present study, in which a single-nucleotide variant was found in the *atpB-rbcL* IGS sequences of the S038 strain (from Oo-ike pond, Deba-jima Island) (Appendix B).

#### Systematic accounts

## *Lamprothamnium succinctum* (A. Braun) R. D. Wood (Figures 2, 3)

Lamprothamnium succinctum (A. Braun) R. D. Wood, Taxon 11: 15, 1962 (Wood 1962).—Chara succincta A. Braun in Asch., Oesterr. Bot. Zeitschr. 28: 257, 1878 (Ascherson 1878).

Diagnosis. Lamprothamnium succinctum is similar to L. hansenii (C. Sond.) Corill. and L. tasmanicum (A. Braun) Casanova in having monoecious thalli without foxtail-like apices, in which whorled branchlets are not inflated (Wood 1965; Casanova 2013). However, L. succinctum can be distinguished clearly from L. hansenii by the size of stipulodes (irregular in size and up to 1,000 µm long in L. succinctum, and uniform in size and well developed in L. hansenii) and the position and arrangement of reproductive organs [usually sejoined (when conjoined, oogonium are positioned above or beside antheridium) and formed at the base of the whorl in L. succinctum, and conjoined (oogonium are positioned below antheridium) and not formed at the base of the whorl in L. hansenii], and also distinguished clearly from L. tasmanicum by the oospore wall ornamentation (irregular glanulate in L. succinctum and smooth to roughened in L. tasmanicum) and the position and arrangement of reproductive organs [usually sejoined (or rarely conjoined) in L. succinctum, and uniformly sejoined in *L. tasmanicum*].

*Distribution.* Japan (Imahori 1963; Kasaki 1964), Egypt (Ascherson 1878), Libya (Compère 1986), Spain (Canary Islands) (Henríquez and Villalba 1995), Morocco (Muller et al 2017), Oman (Hussain et al 2003), Pakistan (Langangen and Leghari 2001), India (Dixit 1931; Khan 1980), China (Groves 1919; Ling et al 2000), Korea (Choi and Kim 1997), New Caledonia (Wood 1966), Mauritius (Allen 1887), and Bolivia (Guerlesquin 1981).

Japanese specimens examined in this study. TNS-AL 213317 (S. Kato, strain MYG006; collected by S. Kato and J. Yokoyama from Nonoshima Island, Miyagi); TNS-AL 213318 (S. Kato, strain SK166; collected by S. Kato, Y. Ito and N. Tanaka from Ichikawa, Chiba); TNS-AL 213319 (collected by H. Morishima from Ichikawa, Chiba); TNS-AL 213320 (collected by S. Kinoshita, A. Narita and M. Saji from Jaga-ike Pond, Tokushima); TNS-AL 213321 (H. Sakayama, strain S038; collected by E. Yoshida from Oo-ike pond, Deba-jima Island, Tokushima); TNS-AL 213322 (collected by Y. Ito and N. Tanaka from Susaki, Kochi); TNS-AL 213323 (S. Kato, strain EHM117; collected by S. Kato, S. Kobayashi and Y. Fujiwara from Susaki, Kochi); TNS-AL 213324 (S. Kato, strain SK164; collected by J. Tanaka from Kumejima Island, Okinawa); TNS-AL 213325 (S. Kato, strain KMJM002; collected by S. Kato and A. Higa from Kume-jima Island, Okinawa); TNS-AL 213326 (H. Sakayama, strain S399; collected by H. Sakayama and A. Higa from Kume-jima Island); MAK A12442, MAK A12443, MAK A12444, MAK A12445 and MAK A12446 (collected by K. Kato from Lake Hachiro-gata).

*Other specimen examined in this study.* MAK A20679 (collected by A. S. Hitchkock from Mauritius).

#### Discussion

Although the vegetative morphology is similar among the species of *Lamprothamnium*, they exhibit very marked differences in the arrangement of their reproductive organs and oospore characteristics (Wood 1965; García and Casanova 2003; García and Chivas 2004; Casanova 2013). In a monograph on Charales (Wood



**Figure 4.** The Bayesian phylogenetic tree based on the 1,194 bp of the *rbcL* DNA sequences of 20 operational taxonomic units (OTUs). Specimens with identical sequences were treated as a single OTU (Table 1, Appendix A). The characters annotated after the species name and the subsequent numbers in parentheses represent the strain/specimen names and the accession numbers on the GenBank database, respectively. The numbers placed above the branches indicate the posterior probabilities of Bayesian inference (BI, left) and the bootstrap values obtained from maximum likelihood (ML, right) analyses. The numbers placed below the branches indicate the bootstrap values obtained from a maximum-parsimony (MP) analysis. Only posterior probabilities  $\geq$  0.90 and bootstrap values  $\geq$  50% are shown. Branch lengths and the scale bar represent the expected number of nucleotide substitutions per site.

1965), the taxa of *Lamprothamnium* were classified into three species with eight infraspecific taxa, mainly based on vegetative and reproductive characteristics. Recently, Casanova (2013) analyzed a large number of Australian specimens of the genus and revised their taxonomic status, mainly based on reproductive and oospore characteristics. That author reported that the variation in the arrangement of reproductive organs is useful for delineating the monoecious species of the genus.

The thalli of the present specimens were identified as L. succinctum based on their vegetative and reproductive characteristics (Figure 2). Moreover, our SEM observations showed that the overall appearance and fossa wall patterns of oospores of Japanese L. succinctum are consistent with those of the specimens analyzed in previous studies (Frame 1977; García et al 2002; García and Chivas 2004) (Figure 3). In the thalli of Japanese specimens, the oogonia and antheridia were usually sejoined; the antheridia were solitary and formed at the basal two-branchlet nodes, whereas the oogonia were usually formed on the inside of the base of the whorl (Figure 2C). However, the present specimens were slightly different from the type material of *L. succinctum* collected in North Africa, because the type material has one or two oogonia both on the outside and the inside of the base of the whorl, and antheridia conjoined with oogonia on the branchlets (Casanova 2013). Wood (1962, 1965) selected the specimen collected in Mauritius as the neotype specimen, because the holotype specimen collected in North Africa was not found. Casanova (2013) pointed out that the North-African specimens are different from the specimens from Mauritius (Allen 1887; Wood and Imahori 1964) as well as the specimens from New Caledonia (Zaneveld 1940; Wood 1966). Therefore, for future taxonomic revisions, morphological and molecular analyses are needed to clarify the taxonomic status of L. succinctum using fully matured specimens from these localities as well as large numbers of specimens from various localities located worldwide.

We performed genetic analyses based on the *rbcL* and *atpB-rbcL* IGS sequences (Figure 4, Appendix B). Our *rbcL* phylogeny demonstrated that all of the Japanese specimens of *L. succinctum* had an identical *rbcL* DNA sequence and that this species formed a robust clade with three other species of *Lamprothamnium* (*L. papulosum, L. macropogon,* and *L. heraldii*) (Figure 4). Moreover, based on the *atpB-rbcL* IGS sequences of the eight Japanese specimens (Table 1), only two haplotypes (IGS-1 and IGS-2) differing by a single nucleotide were identified, with the *L. succinctum* sample from Oo-ike pond (strain S038) having a distinct haplotype compared with those from other Japanese specimens (Appendix B). Our results indicate that the degree of genetic divergence of Japanese *L. succinctum* is very low and that they are genetically very close to each other.

Our morphological and molecular analyses of Japanese specimens of *L. succinctum* revealed the detailed morphological characteristics and genetic differences among Japanese populations of this species. We only analyzed specimens collected in Japan because this study focused on the relationship among Japanese populations, although this species has been reported in many countries and morphological variations have been recognized within this species. Moreover, 20 extant taxa have been described for *Lamprothamnium*. Therefore, in future taxonomic studies, further morphological and molecular analyses of these taxa in a large number of specimens collected globally are needed to resolve their natural relationships.

Finally, in Japan, *L. succinctum* is listed as an endangered species and is protected by the government, because this species has been recorded only at two localities (Lake Hachiro-gata and Oo-ike pond) and has become extinct in one of them (Lake Hachiro-gata) (Watanabe et al 2005). In this study, however, we identified five new localities of this species in Japan. Therefore, further studies are needed to improve our understanding of the distribution and conservation status of this species.

#### **Declaration of Competing Interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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#### Appendix A. Supplementary data

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