

Overview of the distribution and adaptation of a bloomforming cyanobacterium *Raphidiopsis raciborskii*: integrating genomics, toxicity, and ecophysiology*

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Abstract Raphidiopsis raciborskii is a notorious bloom-forming and filamentous cyanobacterium that has been extensively investigated into its toxicity, phylogeny, and spreading potential. Studies have demonstrated that this species has spanned different climates from tropical zones to temperate regions, suggesting that R. raciborskii is becoming a cosmopolitan species in freshwater systems around the world. In fact, it has been proposed that several characteristics of R. raciborskii may explain its spread and dominance. In particular, R. raciborskii is known to display a high extent of physiological plasticity regarding nutrients, light regimes, and temperatures. Moreover, this species illustrates different ecotypes with distinct environmental requirements. Here, we present an overview of R. raciborskii's global distribution and adaptation strategy based on the recent findings from genome variance, toxicity, and ecophysiology. The expansion of its geographical distribution can be linked to its genome, toxicity, and ecophysiology. The variable genes are mainly associated with the stress response, phage defense, DNA repair, cell cycle control, and membrane transport, illustrating the species' adaptability in response to changing environments. In fact, the species shows rapid adaptability to low and/or variable nutrient availability, especially changing phosphorus availability. Moreover, the variabilities of strains within the population extend their flexibility to adapt and acclimate to ambient environment. In addition, cylindrospermopsins (CYN) appear to have a potential biological role in facilitating theirs dominance or bloom. These strategies of R. raciborskii make it a challenge to manage in a freshwater system, reflecting the management of its bloom from further evidence of the complex ecophysiology, toxicity, and genome of this species.

Keyword: distribution; ecophysiology; genome variance; Raphidiopsis raciborskii; toxicity

1 INTRODUCTION

Raphidiopsis raciborskii (basonym Cylindrospermopsis raciborskii; Aguilera et al., 2018) is a solitary, planktonic, and filamentous diazotrophic cyanobacterium belonging to the order Nostocales. Because it has two terminal heterocysts, R. raciborskii was originally described as Anabaena raciborskii Wołoszyńska from the samples collected in Java, Indonesia, in 1912 (Wołoszyńska, 1912). Original observations were limited to the Indo-Malayan realm, so R. raciborskii was considered to be a tropical species. However, an increasing number of reports have been made from every continent except

Antarctica (Padisák, 1997; Sinha et al., 2012) that *R. raciborskii* forms bloom in approximately 18% of freshwater lakes, reservoirs, and rivers (Xiao et al., 2020a). These results make it reasonable to assume that *R. raciborskii* is an invasive species (Padisák, 1997; Briand et al., 2004; Antunes et al., 2015).

Apart from its dispersal potential, *R. raciborskii* has attracted scientific interest due to its association

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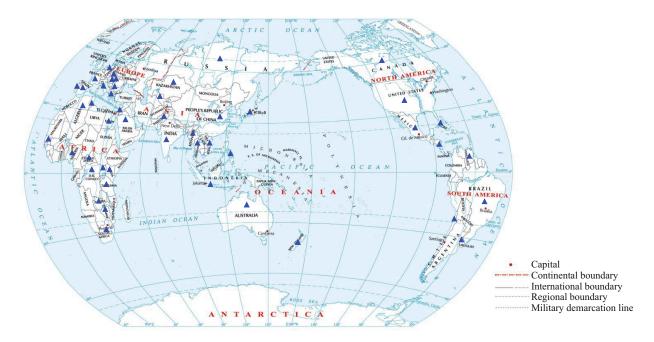


Fig.1 The global geographic distribution of Raphidiopsis raciborski

Data are obtained from Padisák, 1997; Sinha et al., 2012; Antunes et al., 2015; Panou et al., 2018; Sidelev et al., 2020; Yang et al., 2021. Map review No. GS(2016)2958. The blue triangles stand for the countries and regions where *R. raciborskii* was observed.

with toxic effects. The cyanotoxin alkaloid cylindrospermopsin (CYN) was first identified by Ohtani et al. (1992) isolated from *R. raciborskii*, after which more CYN variants were found (Li et al., 2001; Rzymski and Poniedziałek, 2014; Wimmer et al., 2014). Recently, some strains of *R. raciborskii* have also been found that can produce other toxins, including alkaloid saxitoxin (STX; Lagos et al., 1999; Zingone and Enevoldsen, 2000; Neilan et al., 2003; Miotto et al., 2017) and lipophilic congeners of phorbol 12-myristate 13-acetate (PMA; Rzymski et al., 2017).

Several studies have highlighted the distinctive features of this species that aid its succession and dominance. For example, laboratory studies have observed that R. raciborskii can utilize all kinds of different nitrogen sources (Harris and Baxter, 1996; Moisander et al., 2012; Ammar et al., 2014) and a high uptake affinity and storage capacity for phosphorus (Isvánovics et al., 2000; Posselt et al., 2009; Wu et al., 2009; Xiao et al., 2020a), as well as can thrive in a wide range of light intensities (Padisák and Istvánovics, 1997; Padisák and Reynolds, 1998; Briand et al., 2002; Pierangelini et al., 2014). Therefore, information on the ecology, phylogeography, and toxicology of this species has been reviewed (Padisák and Istvánovics, 1997; Griffiths and Saker, 2003; Antunes et al., 2015; Burford et al., 2016, 2018). However, as interest in R. raciborskii has increased,

some issues regarding its phylogeography, molecular selection, and ecophysiological adaptation have been questioned. Here, the latest proposals on its distribution and adaptation through the integration of genomics, toxicity, and ecophysiology are discussed. As well, managing implications for *R. raciborskii* are also presented according to new insights into the success of this species in different environments.

2 DISTRIBUTION

Raphidiopsis raciborskii was first identified by Wołoszyńska (1912) in 1899-1900 from samples taken from the lakes in Java, Indonesia. In Europe, R. raciborskii was first observed in Lake Kastoria, Greece (Skuja, 1937), and later in Hungary (Padisák, 1997). In Africa, R. raciborskii was recorded in detail in Lake Victoria by Komárek and Kling (1991) and was probably first detected in 1938 by Huber-Pestalozzi (1938). Additionally, this species was first reported in America in 1955 (Prescott and Andrews, 1955), in Australia in 1979 (Hawkins et al., 1985), and in the Middle East in 1998 (Zohary, 2004). To date, an increasing number of observations have localized this species in rivers, lakes, reservoirs, and shallow waters in the northern and southern hemispheres (Fig.1). This species has been found, for example, in Spain (Romo and Miracle, 1994), Thailand (Li et al., 2001), New Zealand (Stirling and Quilliam, 2001), Germany (Fastner et al., 2003), Japan (Chonudomkul

et al., 2004; Zarenezhad et al., 2012), Brazil (Soto-Liebe et al., 2010; Stucken et al., 2010), Poland (Kokociński et al., 2010), Italy (Messineo et al., 2010), Russia (Vinogradska, 1974; Babanazarova et al., 2015; Sidelev et al., 2020), Vietnam (Dao et al., 2010; Nguyen et al., 2017), USA (Yilmaz and Phlips, 2011), and Myanmar (Ballot et al., 2020; Swe et al., 2021). In China, R. raciborskii was first reported in a fish pond in Kunming, Yunnan, in 2006 (Wu et al., 2011); thereafter, this species was found to be present in freshwater bodies in Guangdong (Lei et al., 2014; Yu et al., 2014), Hubei (Wu et al., 2011, Jiang et al., 2014), Shanghai (Wu et al., 2011), Guizhou (Chen et al., 2011), Jiangsu (Wu et al., 2012a), Taiwan (Yamamoto and Shiah, 2012), Fujian (Lv et al., 2013; Jiang et al., 2014; Tan et al., 2021), Beijing (Xie et al., 2018), Sichuang (Tao et al., 2016), Shangdong (Wang, 2019), Chongqing (Zhang, 2019), and Zhejiang (Chao et al., 2021).

2.1 Phylogeography and dispersal route

Several hypotheses have been proposed to explain the origin and dispersal routes of R. raciborskii from tropical/subtropical zones to northern latitudes. The "radiation center" hypothesis was proposed by Padisák (1997) only based on the high diversity and salinity tolerance characteristics of R. raciborskii. Padisák and Istvánovics (1997) suggested that two radiation centers, Africa as the primary center and Australia as the secondary center, were responsible for expansion in Central America and Asia, respectively. Two possible routes, such as an oceanic route to the America by migratory birds or by unintentional human activities and a continental route to Central Asia and then to European by river course or by birds, are thought to explain the expansion of R. raciborskii from Australia to temperate regions (Padisák and Istvánovics, 1997; Moreira et al., 2011).

Another "refuge" hypothesis for the current geographic distribution was proffered by Gugger et al. (2005) based on a phylogeographic study. They found that three clusters of *R. raciborskii* strains were grouped: (i) America, (ii) Europe, and (iii) Africa and Australia using the 16S–23S internally transcribed spacer (ITS1) sequences. Therefore, they suggested that recent spread of *R. raciborskii* across the Americas and Europe occurred from restricted warm refuge areas rather than through intercontinental exchanges. Wood et al. (2014) indicated that cryptic akinetes of *R. raciborskii* were already present in lake sediment layers in New Zealand long before

they were discovered as phytoplankton in 2003. A similar finding was found in the Blanca subtropical lagoon (De La Escalera et al., 2014). However, the refuge hypothesis has been repeatedly challenged as significant genetic differences were found in strains of *R. raciborskii* from southern Europe (Spain, Greece, and Italy) and northern Europe (Germany, Hungary, and Russia) (Cirés et al., 2014; Panou et al., 2018; Sidelev et al., 2020).

Later, a new hypothesis was raised by Haande et al. (2008) and Moreira et al. (2015) through the phylogeographic analysis of strains from all five continents based on three genetic markers, 16S rRNA gene, 16S–23S rRNA larger fragment (ITS-L), and RNA polymerase (*rpoC1*). They postulated that the primary evolutionary center of *R. raciborskii* was the tropical area of America, from where this species spread to the African continent, followed by Australia, Asia, and Europe. The hypothesis was supported by recent studies which indicated that strains from Spain, Greece, Italy, Tunisia, Russia, and New Zealand are more genetically similar to strains from the Americas (Cirés et al., 2014; Wood et al., 2014; Panou et al., 2018).

Although various hypotheses have been raised to explain the spread of R. raciborskii, there is a lack of high-quality paleontological evidence to support each hypothesis (Padisák et al., 2016; Kokociński et al., 2017). Sidelev et al. (2020) suggested that close genetic relatedness between the southern European, Tunisian, and American strains, as well as between the African and Australian strains, may be the result of the ancient origin of the species inhabiting the continents, rather than new transport in some cases through birds, insects, humans, or rivers in some cases. Recently, however, Vico et al. (2020) showed Central Africa as the primary center of distribution based on the analysis of 354 orthologous genes from all available genomes and ITS sequences. A nested clade analysis (NCA; Posada et al., 2006) was performed to test the phylogeography of 96 strains of R. raciborskii from different continents in our laboratory (Fig.2). Our results revealed that these strains isolated from Uganda, Senegal, and Australia formed a tight cluster, confirming the result of Padisák and Istvánovics (1997) and Vico et al. (2020). It suggests that R. raciborskii can spread from the tropical zone to temperate and northern regions (Padisák and Istvánovics, 1997). However, closer relationships between some Chinese strains and other strains (e.g. European and American strains) were also noted in our results. It suggests that

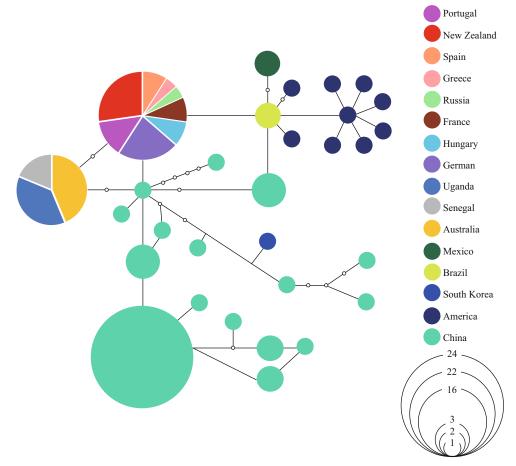


Fig.2 A nested clade analysis (NCA) of *nif* gene for 96 strains of *R. raciborskii* isolated from different continents

Some genes data are from NCBI: https://www.ncbi.nlm.nih.gov.

the biogeography of *R. raciborskii* has become even more confused with the increasing studies of more strains being isolated from around the world.

2.2 Toxicity and dispersal route

The cyanotoxin cylindrospermopsin (CYN) first became known in scientific documents as the "Palm Island Mystery Disease," which occurred in 1979 on Palm Island, Australia. One hundred forty-eight persons were hospitalized with severe symptoms of anorexia, vomiting, and tender livers after consumption of cyanobacterial bloom water treated with copper sulfate (Byth, 1980; Ohtani et al., 1992). Another implication of *R. raciborskii* in the poisoning was in northern Queensland, Australia, 13 cattle died in 1992 after drinking from a water source with a heavy cyanobacterial bloom (Thomas et al., 1998).

A novel structure for CYN was proposed by Ohtani et al. (1992). To date, four different CYN variants, 7-epicylindrospermopsin (7-epi-CYN), 7-deoxy-cylindrospermopsin (7-deoxy-CYN),

7-deoxy-desulfo-cylindrospermopsin, and 7-deoxydesulfo-12-acetyl-cylindrospermopsin, have been described (Norris et al., 1999; Banker et al., 2000; Rzymski and Poniedziałek, 2014; Wimmer et al., 2014). Their novel structures, chemical properties, and toxicological effects and occurrences have been extensively reviewed (see reviews by De La Cruz et al., 2013; Burford et al., 2016; Adamski et al., 2020; Yang et al., 2021). Moreover, R. raciborskii can also produce neurotoxic STX and its analogs (i.e., neo-STX, gonyautoxins 2 and 3 [GTX-2 and GTX-3], decarbamoyl STX [dc-STX], and decarbamoylneo-saxitoxin [dc-neo-STX]), collectively known as paralytic shellfish toxins (PST) (Lagos et al., 1999; Li et al., 2001; Griffiths and Saker, 2003; Molica et al., 2005; Soto-Liebe et al., 2010). A 43-kb cyr gene cluster (Stucken et al., 2014) and a 35-kb stx gene cluster (Kellmann et al., 2008) were responsible for the production of CYN and STX, respectively. Recently, another toxic compound, polymethoxy-1-alkene (PMA) was reported from strains isolated from North America (Rzymski et al., 2017).

Most studies on the dispersal route of R. raciborskii are based on molecular genetic markers (i.e., 16S rRNA, ITS, PC-IGS, nifH, and rpoC1), and did not consider the phenotypes and genotypes of their toxicity (Vico et al., 2020). Studies have shown that R. raciborskii's ability to produce toxins appears to show a geographic pattern. For example, CYNs isolated from Australia, New Zealand, and Asia can be produced (Hawkins et al., 1997; Saker et al., 2003; Wood and Stirling, 2003; Chonudomkul et al., 2004; Jiang et al., 2014; Lu et al., 2021), while the South American strains are associated with STX producers (Lagos et al., 1999; Antunes et al., 2015). In contrast, strains from Africa, Europe, and North America are neither PST nor CYN- producers (Fastner et al., 2003; Neilan et al., 2003; Kellmann et al., 2006; Yılmaz et al., 2008; Mowe et al., 2015). Vico et al. (2020) found that the strains analyzed were divided into two clades, one with the South American strains (mostly PSP-producers) and another with the non-toxic strains isolated from Europe and Sun-Saharan Africa and CYN-producers isolated from Oceania. A similar result was also reported by Jiang et al. (2020), who indicated that Clade IV included all PST-producing strains, while CYN-producing strains were divided into two clusters, Clade II and Clade V.

Nevertheless, partial sequences of cyr genes are determined in American non-CYN producing strains (Piccini et al., 2011) and in PST-producing strains from Brazil (Hoff-Risseti et al., 2013). Recently, Vico et al. (2020) found that the partial genes of cvrA, cvrB, and cvrC are present again in the strains isolated from South America. Meanwhile, Yilmaz and Phlips (2011) found that cyr genes exhibit more exchange changes within North American strains of CYN-producing Aphanizomenon (Chrysosporum) ovalisporum than between species. A hypothesis raised by Vico et al. (2020), is therefore that (i) non-toxic R. raciborskii spread early from tropical Africa as the primary evolutionary center to North Africa, North America, and Mediterranean Europe; (ii) a secondary evolutionary event was involved to acquire the cluster for CYN synthesis. These CYNproducing species spread warm climates across sub-Saharan Africa, Oceania, and South America. Later, the populations in South America somehow lost the cyr cluster and acquired the stx cluster through horizontal gene transfer, then the STXproducing species migrated to North America. In fact, the secondary evolutionary event mentioned by Vico et al. (2020) was the result of a phylogenetic

analysis based on the ribosomal ITS of the species. Moreover, the estimated divergence time calculated for *Raphidioposis* may coincide with the time when Gondwana was split into Oceania and the South American continent. However, strains isolated from North America, Europe, Africa, and the Middle East have not been reported to produce CYN (Neilan et al., 2003; Yılmaz et al., 2008; Alster et al., 2010), which does not support this secondary evolutionary evidence that African strains are a source of the CYN gene cluster.

Recently, Jiang et al. (2020) found that strains of R. raciborskii isolated from China (i.e., CHAB3409, CHAB3422, and CHAB3426) produce STX, neo-STX, and dc-STX, and these strains and American strains have been clustered into different clades, further supporting the recent intercontinental spread events of toxic R. raciborskii (Antunes et al., 2015), but not the geographic origin of the strains. In fact, other cyanobacterial genera, including Chrysosporum, Aphanizomenon, Anabaena, Umezakia, Microseira, and Oscillatoria, have been reported to produce CYN (Rzymski and Poniedziałek, 2014). Hence, a complex history of acquisition and loss in the cyr gene cluster may be associated with its intra- and intergenomic transfers (Jiang et al., 2014, 2020; Burford et al., 2016). Similarly, Moustafa et al. (2009) also suggested that STX is a common ancestral trait of R. raciborskii strains. Therefore, to answer these questions, additional genomic data from these diverse lineages, including closely related toxic and non-toxic strains, are needed.

Based on the literature and our NCA analysis (Fig.2), we partially agree with Padisák's early hypothesis of the tropical region as the evolutionary center of R. raciborskii, but do not support the finding of Africa and Australia as the primary and secondary centers, and the high genetic and toxic diversity of Chinese strains indicates a high heterogeneity of the R. raciborskii population (Cirés et al., 2014; Moreira et al., 2015; Panou et al., 2018). Willis et al. (2018) also suggested that R. raciborskii exhibits high plasticity due to frequent gain or loss of genes. These reflect that the ability of R. raciborskii to produce toxins may not be a geographical pattern but the result of environmental responses and adaptations (Willis et al., 2019; Jiang et al., 2020). Therefore, a larger number of strains with different toxicity are required to test the comprehensive biogeography of this species, as previously suggested (Cirés et al., 2014).

Table 1 Genome assembly and toxins statistics in R. raciborskii strains

	GanDank aggar-1-1-					1 IV. rucioorskii sti ams
Strain	GenBank assembly or accession No.	Size (Mb)	GC (%)	Coding sequence CDS	Origin	Toxicology (reference)
N8	GCA_018139025.1	3.9	40.1	3 261	China	Non-toxin (Chen and Lei, unpublished)
Cr2010	GCA_003367075.1	3.6	40.2	3 023	USA	- (Martin et al., unpublished)
CS-505	GCA_001676585.1	4.2	40.3	3 537	Australia	Cylindrospermopsin (Stucken et al., 2010)
GIHE 2018	GCA_006523545.1	3.6	40.2	3 073	Korea	Non-toxin (Jeong et al., 2020)
CENA302	GCA_002027345.1	3.5	40.1	3 037	Brazil	Saxitoxin (Abreu et al., 2018)
MVCC14	GCA_001858125.1	3.6	40.1	3 130	Uruguay	Saxitoxin (Vico et al., 2020)
CENA303	GCA_002114155.1	3.4	40.3	2 987	Brazil	Saxitoxin (Abreu et al., 2018)
MVCC19	GCA_012583295.1	3.5	40.1	3 022	Uruguay	Saxitoxin (Vico et al., 2020)
ITEP-A1	GCA_001586755.1	3.6	40.1	3 185	Brazil	Saxitoxin and Cylindrospermopsin (Lorenzi et al., 2016)
S01	GCA_002893285.1	3.8	40.3	3 343	Australia	Cylindrospermopsin (Willis et al., 2018)
S06	GCA_002893245.1	3.9	40.3	3 415	Australia	Cylindrospermopsin (Willis et al., 2018)
C04	GCA_002893145.1	4.0	40.3	3 437	Australia	Cylindrospermopsin (Willis et al., 2018)
C03	GCA_002893155.1	4.0	40.3	3 466	Australia	Cylindrospermopsin (Willis et al., 2018)
S05	GCA_002893265.1	3.9	40.3	3 387	Australia	Cylindrospermopsin (Willis et al., 2018)
C07	GCA_002893125.1	4.0	40.3	3 465	Australia	Cylindrospermopsin (Willis et al., 2018)
CS-508	GCA_001858115.1	3.6	40.2	3 052	Australia	Non-toxin, (Fuentes-Valdés et al., 2018)
S07	GCA_002893205.1	3.9	40.3	3 398	Australia	Cylindrospermopsin (Willis et al., 2018)
CYRF	GCA_002321945.1	4.2	40.2	2 791	Brazil	- (Hoffmann et al., unpublished)
S10	GCA_002893215.1	3.9	40.3	3 405	Australia	Cylindrospermopsin (Willis et al., 2018)
S14	GCA_002893185.1	3.9	40.3	3 427	Australia	Cylindrospermopsin (Willis et al., 2018)
CS-506_A	GCA_013867415.1	3.8	40.5	2 637	Australia	Cylindrospermopsin (Sinha et al., 2014)
KL1	GCA_015708265.1	3.7	40	3 115	USA	- (Martin et al., unpublished)
CYLP	GCA_002321935.1	4.0	40	0	Brazil	- (Hoffmann et al., unpublished)
LB2897	GCA_012583345.1	2.7	39.9	1 702	Uruguay	Saxitoxin (Vico et al., 2020)

^{-:} unknown. Genomic data from NCBI: https://www.ncbi.nlm.nih.gov/.

3 ADAPTATION AND ACCLIMATION

3.1 Genome variations and adaptation

Based on ecological and genomic studies, new insights into the genomic adaptation of marine picocyanobacteria to the local environment have been provided (Kashtan et al., 2014; Larsson et al., 2014; Biller et al., 2015). However, due to the lack of balanced genomic samples, the genomic adaptation of cyanobacteria to a wide variety of environments is still poorly understood (Chen et al., 2021). The first R. raciborskii genome was sequenced from the toxigenic strain CS-505 (Stucken et al., 2010), followed shortly thereafter by those of CS-506 and CS-509 (Sinha et al., 2014). To our knowledge, only one R. raciborskii genome has been closed as late as 2021. However, several draft genomes isolated from different locations were subsequently sequenced. To date, 23 drafts and 1 closed genomes sequenced from

isolated strains from Australia, Brazil, United States, Uruguay, China, and Korea were available from NCBI (see Table 1 for detailed information). The average nucleotide identity (ANI) between strains was 0.997 6 (range 0.995 0–0.998 7, between genome pairs; Willis and Woodhouse, 2020).

Compared to other cyanobacteria (e.g., *Microcystis*, *Nostoc*, *Dolichospermum*, and *Aphanizomenon*), a smaller genome was found in *R. raciborskii* with a genome size of 3.74±0.24 Mb, 40.24%±0.15% G+C content, and 3 144±292.35 coding sequences (Table 1). Stucken et al. (2010) has suggested that a small genome found in *R. raciborskii* may be in the process of reducing superfluous functions. Typically, a downsizing of a genome is seen as an indication of an evolutionary adaptation strategy to different environments (Rocap et al., 2003; Shi and Falkowski, 2008; Larsson et al., 2011; Willis et al., 2018). It suggests that genome variants in *R. raciborskii* are

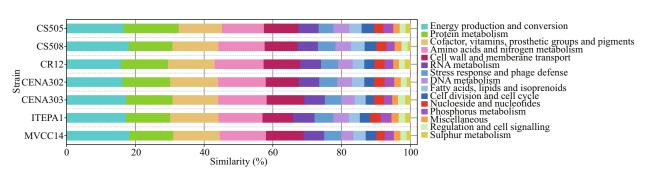


Fig.3 Comparison of strain-specific (or non-homologous) genes in Raphidiopsis raciborskii strains

Each layer represents a genome and each color of the layer indicates a subsystem. The values (%) show a similar percentage of the subsystem in the genome with *R. raciborskii* C04 strain (Genes data from Stucken et al., 2010; Abreu et al., 2018; Willis et al., 2018; Vico et al., 2020, and NCBI: https://www.ncbi.nlm.nih.gov/).

responsible for the global expansion into new habitats.

Willis et al. (2018) stated that the R. raciborskii pan-genome contains about 16% of R. raciborskii genome with 847 variables and 433 strain-specific orthologous groups, suggesting that there is greater genetic diversity in R. raciborskii strains. In addition, variation, arrangement, or shifting of genes are always found in R. raciborskii when seven strains of R. raciborskii are compared with the strain Raphidiopsis brookii D9 strain. These genes are involved in natural product biosynthesis, heterocyst glycolipid formation, nitrogen fixation, and toxin production. Similar results are reported by Abreu et al. (2018), who found variable genes involved in amino sugar metabolism, DNA modification, and carbohydrate biosynthesis. Shi and Falkowski (2008) suggested that selective pressures and evolution can affect the core and variable genes, resulting in strain variability in different environments (Kashtan et al., 2014).

A comparative genome analysis showed that strains of R. raciborskii contained a variety of strain-specific (or non-homologous) genes (Stucken et al., 2010; Sinha et al., 2014; Abreu et al., 2018). These genes are involved in energy production and conversion, stress response and phage defense, DNA repair and recombination, cell cycle control, and the nutrients transport and uptake (Fig.3), all of which are largely related to environmental response and adaptation. Moreover, the gene clusters associated with toxin production and heterocyst differentiation (i.e., hassallidin [hass], cylindrospermopsin [cyr], saxitoxin [sxt], heterocyte glycolipid [hgl], and nitrogen fixation [nif, fdxN, hesA and B, and feoaA]) also indicate phenotypic plasticity (Sinha et al., 2014; Abreu et al., 2018). Stucken et al. (2010) suggested that the absence or loss of the cyr cluster, rather than indicating mutations or partial deletions,

was associated with the absence of toxicity in some strains of R. raciborskii. However, several reports have found that some R. raciborskii strains retained the partial cyr cluster, i.e., cyrA, cyrB, or/and cyrC are still unable to produce CYN (Kellmann et al., 2006; Rasmussen et al., 2008; Hoff-Risseti et al., 2013). This supports that horizontal gene transfer or subsequent loss of the cyr gene is responsible for the acquisition of the cvr genes (Christiansen et al., 2008; Moustafa et al., 2009). Willis et al. (2018) has observed that 21 proteins, particularly those involved in sugar transport, phosphonate substrate binding, and CRISPR/Cas phage-defense systems, yield a greater copy number in the coiled compared to the straight morphotypes of R. raciborskii. Larsson et al. (2011) proposed that gene duplication can expand phenotype and adaptive behavior in cyanobacteria.

In short, comparative genomics provides new insights into the genotypic and phenotypic plasticity of the species R. raciborskii. A high proportion of variable strain-specific genes associated with environmental responses and adaptation, particularly in some key cellular processes (e.g., cell regulation, biosynthesis, and transport), are found in this species, reflecting that successful adaptation to specific habitat in R. raciborskii may allow the exploration of a wide range of environmental conditions. Furthermore, the co-existence of multiple strains within a R. raciborskii population in a single water sample can confer fitness advantages to this species in variable environments by eliciting their niche adaptation (Piccini et al., 2011; Willis et al., 2018). In addition, Abreu et al. (2018) found that the comparative genome analysis showed that the five South American genomes CENA302, CENA303, ITEP-A1, MVCC14, and D9 (Brazil and Uruguay) are slightly smaller and more conserved than the non-South American CS-505, CS-508, and CR12 (Australia and Singapore) genomes,

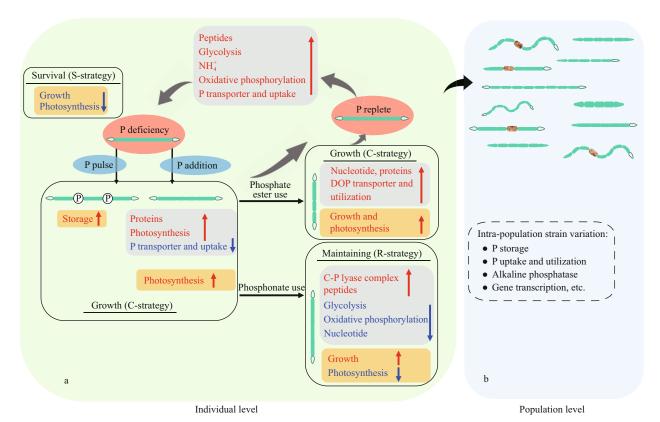


Fig.4 Diagram for the response to changing ambient phosphorus in Raphidiopsis raciborskii

Red texts: upregulated genes; blue texts: downregulated genes; gray and yellow squares: gene and physiological parameters, respectively (from Wu et al., 2012a; Bai et al., 2014; Willis et al., 2015, 2017; Burford et al., 2016; Xiao et al., 2020a; Shi et al., 2022).

suggesting that genomes from South America underwent gene loss events. However, due to the lack of genome sequences in European and African strains, no more precise conclusions can be drawn about the influence of the geographic environment on their genomic plasticity. Therefore, in order to explain the very different strategies for genomic organization and adaptation mechanisms in *R. raciborskii*, more strains from a range of habitats or regions needed to be sequenced and compared in the future.

3.2 Ecophysiology and adaptation

3.2.1 Phosphorus

Phosphorus is considered a key factor in the ecophysiology and dominance of *R. raciborskii*. A positive or negative correlation between *R. raciborskii* cell densities and phosphorus concentrations has been reported in field studies (Bonilla et al., 2012; Muhid et al., 2013; Soares et al., 2013a; Zhao et al., 2017). Several studies have illustrated that *R. raciborskii* has a high uptake affinity for dissolved inorganic phosphorus (Isvánovics et al., 2000; Wu et al., 2009) and a high phosphorus storage capacity (Posselt et al., 2009; Willis et al., 2017), as well as a superior

scavenger for dissolved organic phosphorus (Bai et al., 2014). Furthermore, both uptake and conversion of phosphorus were more effective in *R. raciborskii* than in *Microcystis aeruginosa* and *Aphanizomenon flos-aquae* (Wu et al., 2009). Therefore, these traits are favorable for the dominance of *R. raciborskii* populations (Isvánovics et al., 2000), which is supported by the results of Chislock et al. (2014), who indicated that *R. raciborskii* can dominate at different phosphorus concentrations.

Physiological and molecular studies have suggested that *R. raciborskii* can evolve a variety strategies in response to environmental phosphorus (Fig.4a). Under phosphorus deficient conditions, strains show little metabolic activity to keep sustain themselves (i.e., "S-adapted strains"). In this environment, the growth and photosynthesis of these strains are significantly inhibited and the genes encoding photosynthesis and protein synthesis are markedly downregulated, while alkaline phosphatase and the genes encoding phosphate uptake and transport, ATP-consumption, and energy metabolism are markedly upregulated (Wu et al., 2012a; Bai et al., 2014; Willis et al., 2018; Shi et al., 2022). Under organic phosphate conditions, the strains showed a

rapid growth (i.e., "C-adapted strains or K-adapted strains"). In this state, rapid growth is noted, which is caused by a significant increase in genes encoding phosphate-specific transporters, alkaline phosphatase, and ribosomes (Bai et al., 2014; Willis et al., 2018; Shi et al., 2022). However, under phosphonate conditions (i.e., "R-adapted strains or r-adapted strains"), a slight inhibition of growth and photosynthesis is observed because alkaline phosphatase and the genes encoding carbon-phosphorus lyase, genetic information, and environmental information are dramatically upregulated (Willis et al., 2018; Shi et al., 2022). Additionally, since R. raciborskii has a high phosphorus storage capacity, pulsed additions of dissolved inorganic phosphorus are more favorable for the growth of this species compared to constant feeds of dissolved inorganic phosphorus (Posselt et al., 2009; Marinho et al., 2013; Amaral et al., 2014), referred to as "C-adapted strains or K-adapted strains" (Xiao et al., 2020a).

Recent studies have provided evidence that different strains in a R. raciborskii population exhibit significant differences in growth, storage, and molecular response to phosphorus concentrations and pulses (Fig.4b, Amaral et al., 2014; Willis et al., 2015, 2017, 2019; Guedes et al., 2019; Xiao et al., 2020a). For example, Xiao et al. (2020a) showed that phosphorus storage capacity can vary four-fold in six toxic strains of R. raciborskii. Willis et al. (2019) have also pointed out that gene copy number and expression patterns for phosphorus metabolism show differences between the coiled and straight R. raciborskii strains under phosphorus replete and deficiency conditions. This finding suggests that the intraspecific variability of R. raciborskii can lead to changes in the proportion of strains within a population (Burford et al., 2018). In addition, it has been suggested that R. raciborskii dominance can be promoted under both high and low nitrogen-to-phosphorus ratios (Posselt et al., 2009; Chislock et al., 2014).

Moreover, previous studies have confirmed that P availability can affect intracellular CYN concentration (Q_{CYNS}) or a shift in the proportion of toxic and nontoxic *R. raciborskii*. For example, Mohamed and AlShehri (2013) found that Q_{CYNS} of *R. raciborskii* cells was increased when P concentrations were higher in a Saudi lake. Burford et al. (2014) also indicated that the proportion of toxic *R. raciborskii* strains increases with increasing phosphorus availability, regardless of whether N was supplied using a mesocosm study. Lu et al. (2021) showed that phosphorus deficiency

stimulates *R. raciborskii* dominance by facilitating CYN-induced alkaline phosphatase secretion. A similar finding was reported by Bar-Yosef et al. (2010) in CYN-producing cyanobacteria, *Chrysosporum ovalisporum*. The results may indicate that CYN may be facilitated by the dominance of *R. raciborskii* under P deficiency.

3.2.2 Nitrogen

Raphidiopsis (Cylindrospermopsis) raciborskii was originally described as a Nostocales species with heterocytes, distinguished from other Raphidiopsis by its lack of heterocytes and nitrogen-fixing ability (Padisák, 1997). However, Abreu et al. (2018) found that the C. raciborskii strain CENA303 isolated from Brazil does not differentiate heterocytes due to the absence of nif and hgl gene clusters involved in nitrogen fixation and thick heterocyte glycolipid envelope formation, respectively. Therefore, Cylindrospermopsis and Raphidiopsis are considered to be a unifying genus, with Raphidiopsis using morphological, ultrastructural, physiological, and molecular approach (Aguilera et al., 2018). In general, nitrogen-fixing ability is often associated with an ecological advantage of R. raciborskii over non-nitrogen-fixing species (Harris and Baxter, 1996; Hadas et al., 2012). Studies have indicated that the terminal heterocyst cells of R. raciborskii can fix nitrogen, allowing this species to survive in low dissolved nitrogen environments (Harris and Baxter, 1996; Présing et al., 1996; Padisák and Istvánovice, 1997; McGregor and Fabbro, 2000; Spröber et al., 2003; Plominsky et al., 2013; Willis et al., 2016). However, a preference for different forms of dissolved nitrogen (i.e., ammonia, nitrate, and urea) has now been demonstrated in R. raciborskii (Hawkins et al., 2001; Saker and Neilan, 2001; Burford et al., 2006; Ammar et al., 2014; Figueredo et al., 2014; Yu et al., 2014). Ammar et al. (2014) showed that R. raciborskii can grow faster than the species *Planktothix agardhii*, a perennial biomass and phytoplankton community dominant in a Tunisian reservoir, at high ammonia concentrations. Dai et al. (2015) also found that the growth of R. raciborskii was significantly inhibited under conditions of low nitrogen (<0.5 mg/L).

The relationship between CYNs concentrations and nitrogen has led to conflicting conclusions. For example, Saker and Neilan (2001) found that the highest and lowest CYNs concentrations were determined in *R. raciborskii* grown in the absence of a fixed N source and ammonium, respectively.

Rigamonti et al. (2018) also indicated that a positive association between CYN production and nitrogen fixation was observed in R. raciborskii. In contrast, Vico et al. (2016) showed that nitrate availability is not related to the biosynthesis of saxitoxin and analogs in R. raciborskii. However, compared to nitrate uptake, nitrogen fixation is an inefficient and energetically expensive process (Shafik et al., 2001; Burford et al., 2006). Abreu et al. (2018) found that the non-nitrogenfixing strain R. raciborskii CENA303 lacks the nitrogen fixation (nif) and heterocyte glycolipid (hgl) gene clusters. Therefore, nitrogen availability can shift the proportion of toxic and non-toxic R. raciborskii and regulate the formation of R. raciborskii bloom. Switching between dissolved nitrogen assimilation and nitrogen fixation in R. raciborskii is an adaptive strategy to respond to fluctuations in environmental nitrogen (Moisander et al., 2012).

3.2.3 Other factor

Raphidiopsis raciborskii has shown a wide tolerance to different temperatures and light intensities. This species can grow at light intensities as low as tens to hundreds of µmol photons/(m²·s) (Saker et al., 1999; Shafik et al., 2001; Griffiths and Saker, 2003; Briand et al., 2004; Dyble et al., 2006; Mehnert et al., 2010; Yu et al., 2014). Field studies have shown that R. raciborskii can form blooms under low light intensity, which has advantages for its shade tolerance and light acclimatizaion (Padisák, 1997; Padisák and Reynolds, 1998; Briand et al., 2002; Mehnert et al., 2012). Moreover, stratified water column conditions are generally considered favorable for R. raciborskii, although it is typically dispersed throughout the water column (Bouvy et al., 1999, 2003; McGregor and Fabbro, 2000; Berger et al., 2006). This could be a factor contributing to the success of R. raciborskii (Antunes et al., 2015; Burford et al., 2016).

Raphidiopsis raciborskii also exhibits a wide tolerance to different temperatures (Briand et al., 2004; Chonudomkul et al., 2004; Everson et al., 2011; Bonilla et al., 2012). A model analysis revealed that R. raciborskii blooms can occur in the temperature range of 25 °C to 32 °C (Recknagel et al., 2014), suggesting that increasing temperature favor the bloom formation of this species (Soares et al., 2012). Studies have shown that rising temperatures are beneficial for the spread of R. raciborskii, as the akinete germination of this species is affected by early spring warming in temperate habitats (Padisák, 1997; Briand et al., 2002; Wiedner et al., 2007; Mehnert et

al., 2012; Yu et al., 2014). Saker and Neilan (2001) observed that temperate strains can produce more akinetes than those in tropical strains. These results suggest that the interplay between ecophysiology and genetic evolution may have an impact on the spread of *R. raciborskii*. A recent study also demonstrates that temperature and light have a synergistic effect on the growth rates of *R. raciborskii* (Kehoe et al., 2015; Xiao et al., 2020b).

In addition, the ecological performance and selection of *R. raciborskii* can also be influenced by anthropogenic CO₂ (Wu et al., 2012b; Pierangelini et al., 2014), pH (Bonilla et al., 2012; Holland et al., 2012), salinity (Moisander et al., 2012), allelopathy (Figueredo et al., 2007; Leão et al., 2009; Antunes et al., 2012; Mello et al., 2012), multiple disturbance (Yang et al., 2017), zooplankton (Soares et al., 2010; Bednarska et al., 2014), and other biotas (Sukenik et al., 2012; Bagatini et al., 2014; Guedes et al., 2019; Bai et al., 2020).

4 CONCLUSION AND IMPLICATION

The abundance of studies from around the world has provided our understanding of the biogeography, toxicity, genome, and ecophysiology of R. raciborskii. Considering all the evidence, the biogeography of this species is credited with an early spread from a tropical zone to temperate regions, while the scenario of refuge and secondary radiation centers has yet to be confirmed by exploring further strains from all continents or paleontological evidence. CYNproducing strains have been identified in a limited number of country, while a geographic spread of toxic strains or a complex history of acquisition and loss in the cyr or stx gene cluster is not excluded from the intra- and inter-genomic transfers based on current studies. Studies have shown that the production and export of CYN in R. raciborskii can be a functional strategy for competition with other phytoplankton. More direct evidence is still needed to support CYN's potential biological role to facilitate its dominance or bloom.

It is obvious that this species shows flexible adaptation strategies ("C-adapted, R-adapted, and S-adapted") in nutrient dynamics based on laboratory experiments, which are very crucial for their expansion behavior. However, field studies always indicate negative or positive effects of nitrogen or phosphorus on this species or its dominance, reflecting that an interaction of nitrogen or phosphorus is likely to be underestimated. Moreover, it is clear that genome

variation and ecotypes exist between co-occurring strains in a water sample. Therefore, supplementary reports on interaction effects, phenotypic differences, and population plasticity can be expected in this species. Furthermore, the impact of global climate change on the physiological resilience or existence of distinct ecotypes in this species remains unclear.

Overall, there is no doubt that rising temperatures can be associated with the spread and proliferation of this species. Moreover, flexible strategy and significant intra-population strain variation in nitrogen and phosphorus dynamics provide better resilience of a population under changing environmental nutrients. Therefore, controlling *R. raciborskii* bloom may not be achievable with a simple reduction in nitrogen or phosphorus loading, particularly in intermittent nutrient pulses and mixed water columns. Future efforts are essential for a comprehensive understanding of the ecophysiology of *R. raciborskii* in different scenarios in order to find an efficient means of the control.

5 DATA AVAILABILITY STATEMENT

The authors declare that all data supporting the findings of this study are available within the article. The raw data that support the findings of this study are available from the corresponding author upon reasonable request.

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