Spatiotemporal decoupling of littoral and lacustrine geosmin dynamics: Implications for early warning in drinking water reservoirs

Supplementary Material

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Summary: 11 pages, 9 figures and 1 table.

Fig. S1

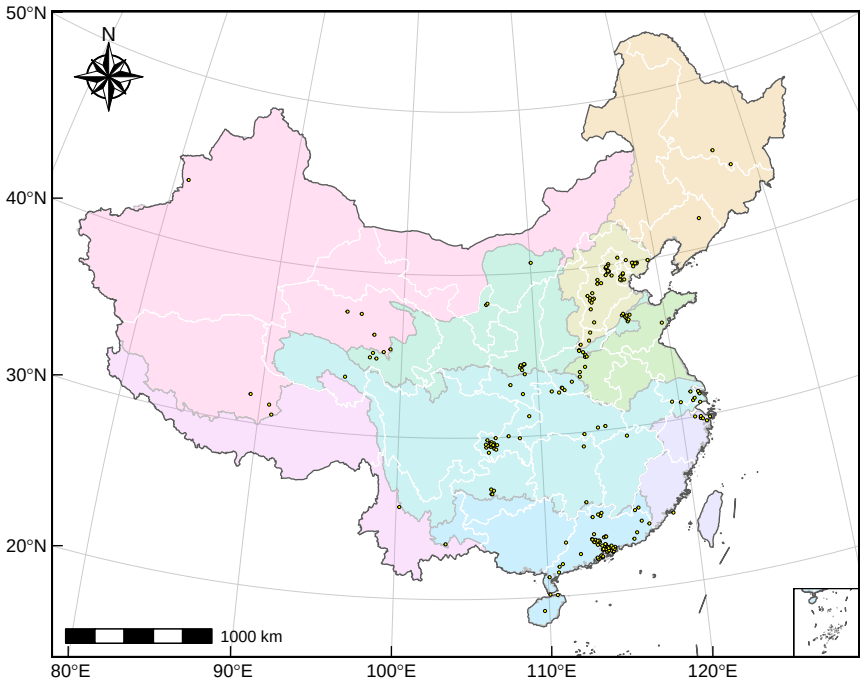

Fig. S1: Geographic distribution of sampling sites for the national geosmin survey in China.

Fig. S2

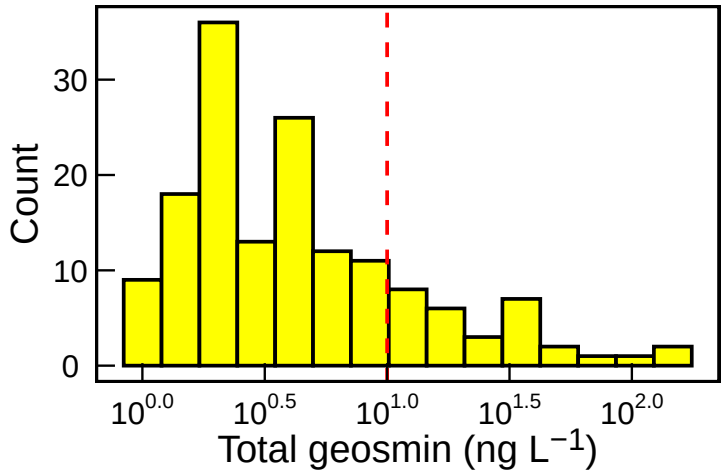

Fig. S2: Frequency distribution of geosmin concentrations from the national survey.

Fig. S3

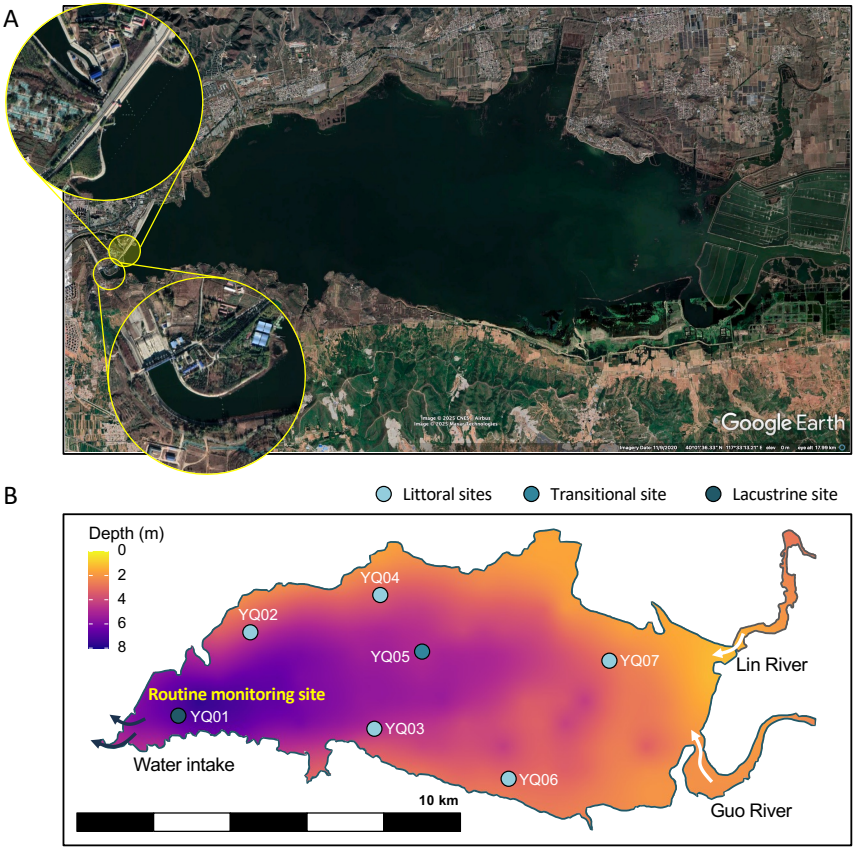

Fig. S3: Study site overview: YQ Reservoir. (A) Satellite image and (B) bathymetric map with locations of sampling stations.

Fig. S4

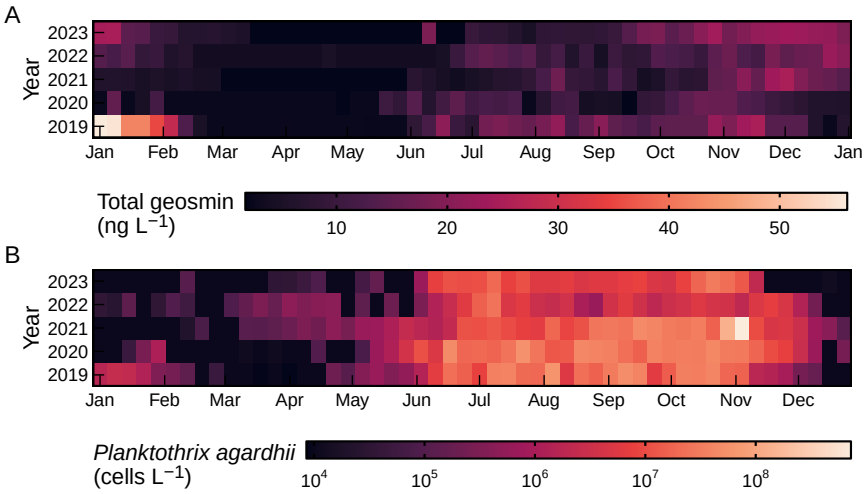

Fig. S4: Temporal dynamics of geosmin concentration and *Planktothrix agardhii* abundance in YQ Reservoir.

Fig. S5

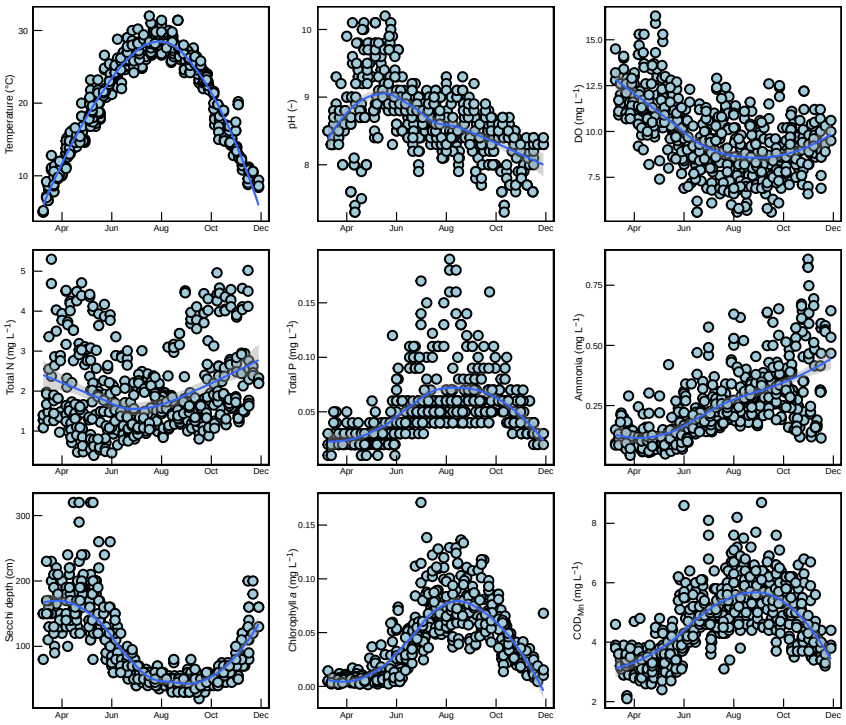

Fig. S5: Limnochemical characteristics of littoral zone in YQ Reservoir.

Fig. S6

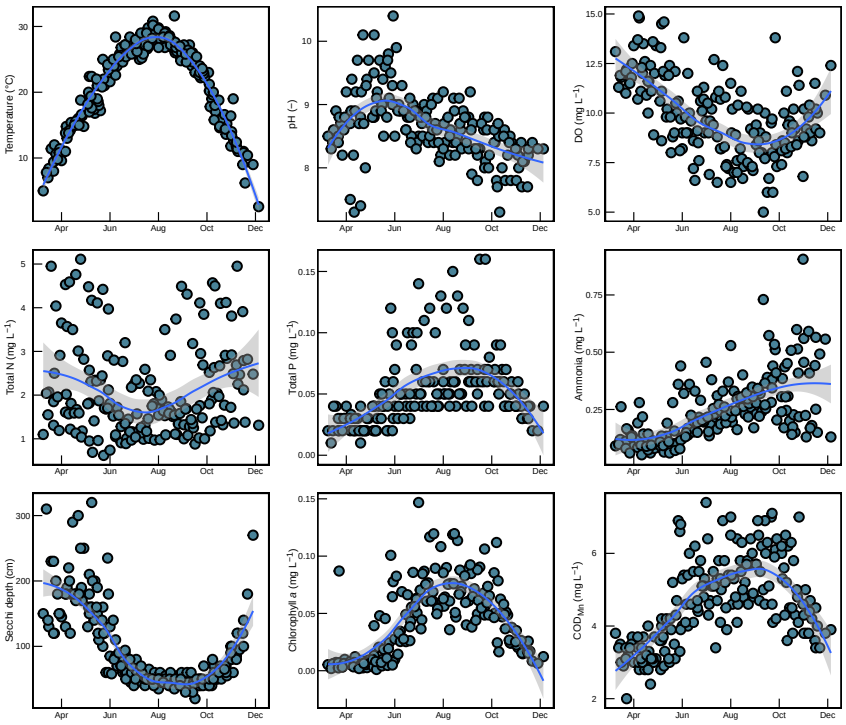

Fig. S6: Limnochemical characteristics of transitional zone in YQ Reservoir.

Fig. S7

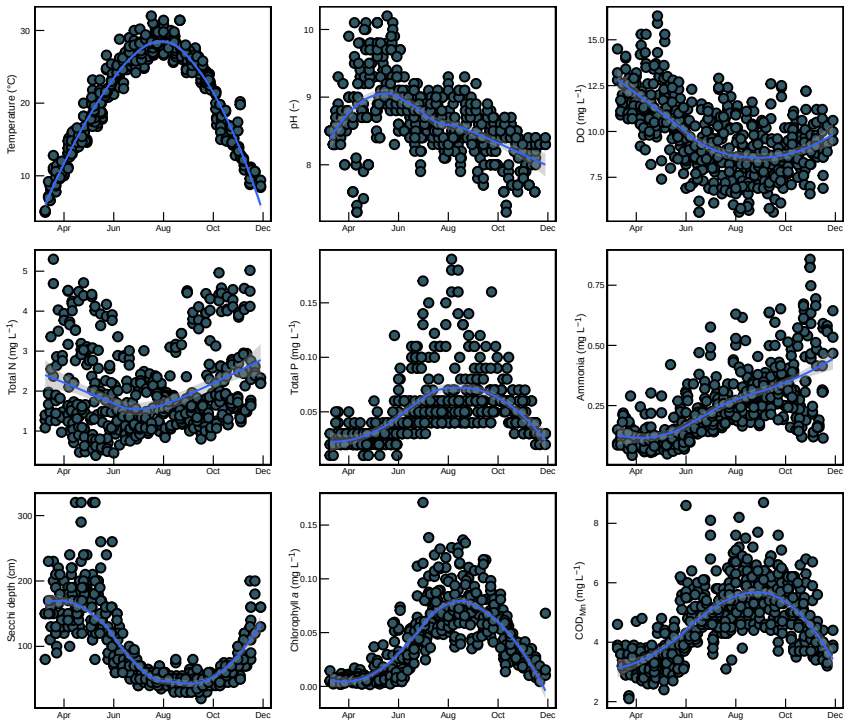

Fig. S7: Limnochemical characteristics of lacustrine zone in YQ Reservoir.

Fig. S8

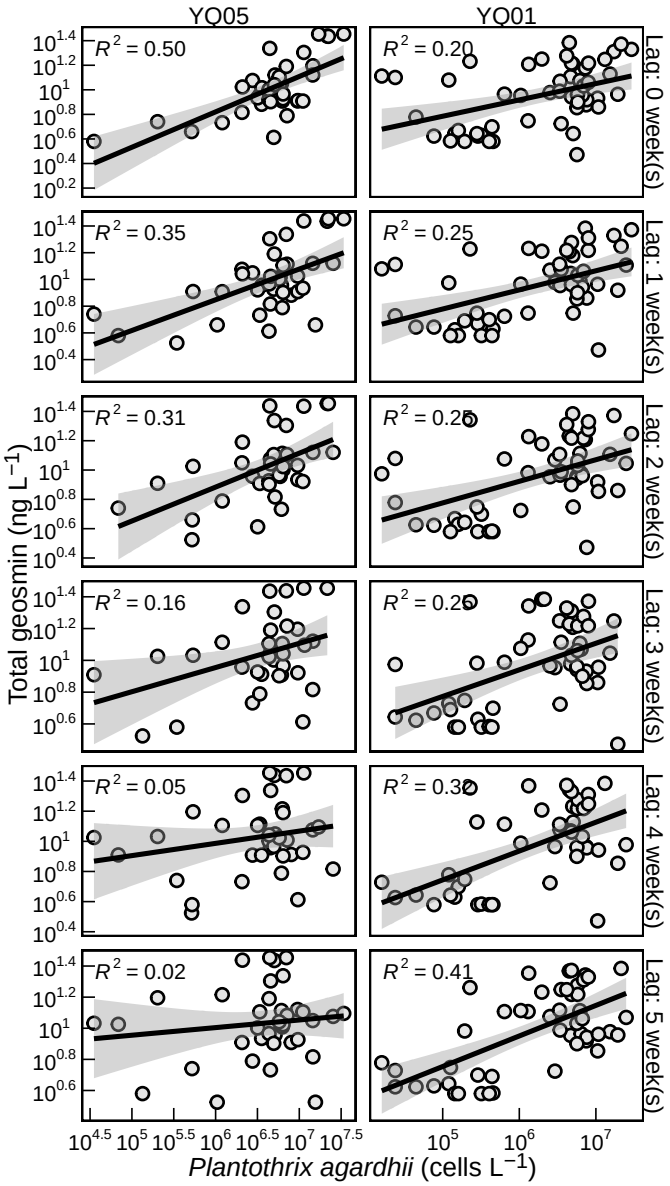

Fig. S8: Relationship between *Planktothrix agardhii* abundance and geosmin concentration at sites YQ05 (transitional) and YQ01 (lacustrine).

Fig. S9

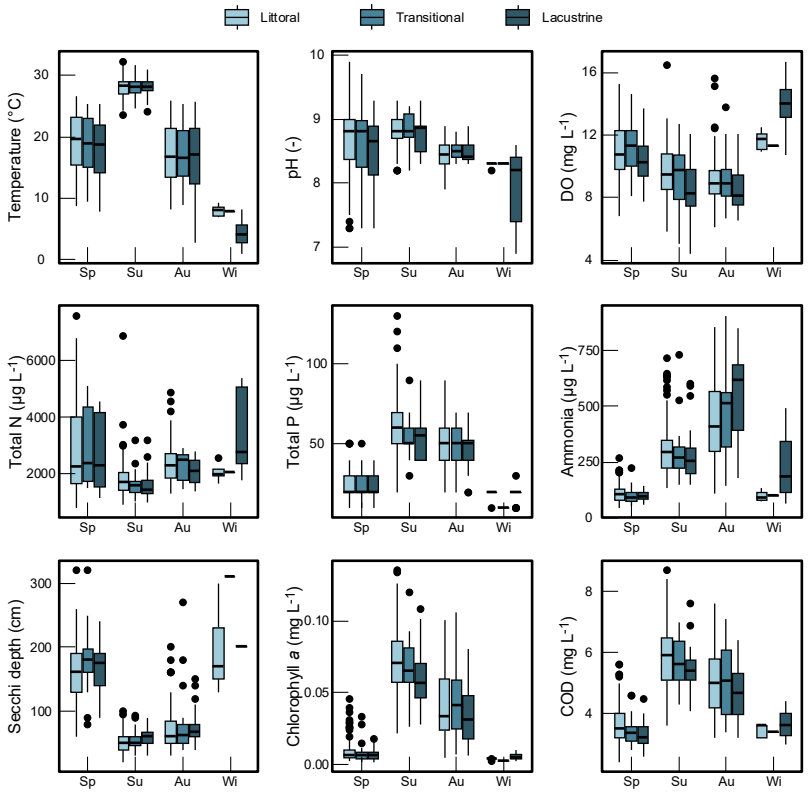

Fig. S9: Spatiotemporal variation of water quality parameters in YQ Reservoir. Comparison of physicochemical indicators across littoral, transitional, and lacustrine zones during spring, summer, autumn, and winter.

Table S1

BLASTn alignment of the sequence fragment OTU156/214-360 (S8_19530; length: 147 bp), amplified from environmental samples using functional primers, returned its highest similarity hits predominantly to *Planktothrix agardhii*. The top-ranking hits, including strains PCC7805, No.365, No.66, PCC7811, No.2A, and str. 7805, all exhibited consistent, high-quality alignment characteristics: 100% Query Cover and sequence identity (Per. ident) above 98%.

Similarly, BLASTn alignment of the sequence fragment OTU58/293–447 (S7_36548; length: 155 bp) yielded top matches primarily to *Aphanizomenon flos-aquae* (WILD-4 geoA gene for geosmin synthase, partial cds; accession LC739799.1), multiple *geoA* or putative geosmin synthase gene sequences from *Aphanizomenon gracile* (e.g., NRERC-027: OQ819013.1; CHAB2417: MK213950.1; WH-1: KP268488.1; NRERC-023: OQ819011.1; NRERC-022: OQ819010.1), and *Dolichospermum heterosporum* (TAC447; accession CP099464.1). All these top hits displayed remarkably consistent and strong alignment metrics (Query Cover = 99%, Per. ident = 100%, E-value = 3e−73), indicating that this sequence fragment is highly homologous to *geoA* sequences associated with *Aphanizomenon* and shows an equally perfect match with certain sequences from *Dolichospermum*.

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Sequencing fragments of water samples collect from YQ Reservoir

>OTU156/214-360 S8_19530
GTAATTTCTCTAATTTCCAACTTGTTCCATAAATTATGCCATCGTTAGTATAGCTGGTTT
TGTCATTAACATCCCCATTTAGAGGTAAATAGGCTAATAATCCTAGTTCATCGCCGACTA
AATGCCGATTCATGTCCTGTTTAATTT

>OTU58/293-447 S7_36548
CTGCCAATCCTGAAGTCCTTTGATGTAAAGGAGAACATTCACACGCTCTACTGGGTCTAC
TCCATACTCCTCAAAAAGGGAGGGCAACTCGGTGACAGCAGTGTTATCAAACTGATATAA
ACGGGAGTTGAGTAGTTCGTTAGTGAGGTTAGCCG
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OUT	Matched Species	Per. Ident (%)	Query Cover (%)	Accession
OUT156	*Planktothrix agardhii*	98.64	100%	LR882950.1
OUT156	*Planktothrix* sp.	92.52	100%	CP136572.1
OUT58	*Aphanizomenon flos-aquae*, *A. gracile*, *A.* cf. *flos-aquae*	100.00	99%	LC739799.1
OUT58	*Dolichospermum heterosporum*	100.00	99%	CP099464.1
OUT58	Uncultured cyanobacterium	100.00	92%	OR032742.1
OUT58	*Aphanizomenon gracile*, *Aphanizomenon* sp.	98.70-99.35	99%	OQ819012.1
OUT58	*Dolichospermum crassum*, *D. smithii*, *D. ucrainicum*, *D. planctonicum*	92.86-93.42	98-99%	LC739806.1

Table S1: BLASTn Annotation Results for *geoA* (Geosmin Synthase) Gene