

# Functional and Taxonomic Structure of Soil Algoflora Relevant to Irrigated Agroecosystems of Quva District, Uzbekistan: Regional Quantitative Synthesis and A Paired Soil-Monitoring Framework

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## Abstract

*Photosynthetic microorganisms in agricultural soils may contribute to organic matter production, extracellular polymer formation and nutrient transformations, but their functional significance cannot be inferred from a taxonomic inventory alone. This quantitative secondary synthesis examines the relevant regional evidence and develops an analysis-ready soil–algoflora monitoring framework for the irrigated agroecosystems of Quva district, Uzbekistan. Historical Fergana Valley observations comprising 159 reported algal species and infraspecific taxa were reanalysed by seven morphological categories and by a six-division × five-soil-type table. Coccoid forms represented 63 taxa (39.62%) and simple filaments 51 (32.08%), together accounting for 71.70% of the regional list. Regional soil-type inventories ranged between 63 and 109 taxa, with notable differences in the proportional representation of cyanobacteria and green algae. Literature-reported algal abundance was 19.0–60.0 thousand cells per gram of soil overall, while ranges for individual broad groups were also documented. These endpoints are literature ranges, not uncertainty intervals, and cannot be combined to estimate simultaneous community structure. No Quva-specific paired biological and physicochemical samples were identified in the datasets analysed; thus no novel species records or correlation coefficients for Quva are claimed. Building on critical literature about algal exopolysaccharides, photosynthetic carbon assimilation and nitrogen-related pathways, we specify which measured variables, experimental units and statistical procedures are required to examine possible relationships between algal traits, salinity, organic carbon and nutrient status. The contribution is an auditable numerical reference and an explicitly testable framework for original research in irrigated Quva soils.*

**Keywords:** Soil phototrophs; algal morphotypes; Quva district; irrigated agriculture; extracellular polysaccharides; soil chemistry; literature-based quantitative analysis; ecological monitoring.

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## 1. Introduction

The biological quality of cultivated soil is shaped by an intricate network of organisms that respond to light, water, nutrients, disturbance and plant cover. Among these organisms, cyanobacteria and eukaryotic microalgae are distinct because they are capable of photosynthesis and can occupy the upper soil surface, the

walls of macropores and transient aqueous microhabitats. Their ecological contributions include primary production and, in certain taxa and conditions, associations with nitrogen fixation, mineral mobilization and the synthesis of extracellular polymeric substances. Research reviews describe these mechanisms as promising elements of sustainable agriculture but

emphasize that strain identity, soil context and experimental verification determine the actual response (Abinandan et al., 2019; Ramakrishnan et al., 2023; Joseph & Ray, 2024).

Irrigated agricultural fields are fundamentally different from undisturbed habitats. Irrigation pulses alter water-filled pore space and temporarily activate phototrophic communities, while drying can concentrate soluble salts and change the osmotic environment. Cultivation changes the structure of the surface, fertilizer addition can alter nutrient limitation, and crop canopy development restricts the light reaching photosynthetic soil organisms. Consequently, the presence of a taxon in a regional catalogue does not prove that it is actively growing in a particular Quva field. A functional claim, such as enhancement of organic carbon or soil aggregation, requires measured processes and an appropriate counterfactual comparison.

Quva district in Fergana Region is a relevant setting for investigating managed irrigated soils, including cultivated fields and perennial cropping systems. Nevertheless, public agronomic descriptions of the district cannot replace a biological survey. A technical distinction is essential: district-level environmental context describes where future observations could occur; regional algal statistics describe published species lists across the broader valley; and experimental evidence from elsewhere suggests possible mechanisms. These types of evidence can inform each other, but they cannot be joined into a statistical association without common sample identifiers, dates, depths and methods.

The Fergana Valley offers a substantial regional algological starting point. Tukhtaboeva (2019) reported 159 species and infraspecific taxa in a historical system of six divisions, seven morphological growth forms and several soil categories. The same source provides published ranges of algal cell density expressed as thousands of cells per gram of soil. Because the inventory reports aggregate counts, it is particularly suitable for clear descriptive recalculation and for assessing the taxonomic breadth that field identification would have to cover. Yet no publicly verified sample-level dataset from the Quva district was supplied to this analysis, and the regional figures should not be misrepresented as new results from Quva.

The ecological interpretation of an algal morphological form is conditional. Coccoid organisms, simple filaments and motile cells differ in shape and growth strategy, but

a morphotype is not a functional gene assay, nor does its species count measure its contribution to nutrient cycling. Even the term 'dominance' can mislead: a group with many named taxa may contribute a small share of total live biomass at a specific moment. Separating taxon richness, abundance, biomass and functional activity should therefore precede any model that links microbial properties to soil fertility.

International studies of biological soil crusts show that selected cyanobacterial communities can influence aggregation and erosion susceptibility, partly through extracellular polymer production (Rossi et al., 2022; Garcia-Pichel, 2023). Agricultural application is more complex because ploughing, irrigation and harvest operations change the microhabitat repeatedly. Reviews of inoculant technologies also highlight scale-up, strain viability and inconsistent outcomes as key challenges (Ramakrishnan et al., 2023). These observations justify experimental hypotheses but not automatic extrapolation of a positive fertility effect to every irrigated soil.

The objectives of the present paper are to reconstruct and quantify the published regional morphotype spectrum; tabulate between-soil taxonomic differences without conflating them with Quva observations; evaluate the correct meaning of published algal abundance ranges; and construct a rigorous field-to-laboratory framework that could test associations of algal abundance and function with measured moisture, salinity, pH, soil organic carbon and nutrients. The resulting manuscript is a quantitative secondary analysis and methodological synthesis, not an empirical report of newly collected Quva samples.

## 2. Methods

### 2.1. Source corpus, extraction rules and taxonomic treatment

The central numerical source was the open dissertation abstract by Tukhtaboeva (2019), which provides an aggregated soil-algal inventory for five soil types of the Fergana Valley. The primary extracted datasets were (1) six division-level taxon counts; (2) seven morphotype counts; (3) a table crossing six historical divisions with five regional soil categories; and (4) four literature cell-density ranges. Historical names and numeric values were preserved to ensure that the tabulations remain auditable against the original document. Some of these names are no longer the preferred terminology in contemporary classification, and therefore the group

labels are descriptive of the historical source rather than new taxonomic determinations.

Review literature was selected to cover functional and methodological topics relevant to field monitoring: the ecological and biotechnological potential of soil microalgae, biological soil crust microbiology, experimental cyanobacterial inoculation, and the limitations of inferring activity from taxon presence (Abinandan et al., 2019; Rossi et al., 2022; Garcia-Pichel, 2023; Joseph & Ray, 2024). Regional soil studies were consulted to establish environmental plausibility for including pH, carbon and saline chemistry among potential explanatory variables, but they were not recoded as Quva district laboratory values. No invented geographic sample coordinates or dates are used.

The three source levels must remain distinct during analysis. A compilation of species from the valley supports a statement about historical regional occurrence. A review article supports a statement about processes documented in other systems. A prospective field protocol supports a statement about what needs to be measured in Quva. None of these alone can produce a local species inventory or effect size. In particular, an average of regional taxon counts is not the expected species richness in a new Quva field: species accumulation depends on effort, habitat diversity and detection probability.

## 2.2. Descriptive analysis of morphological and taxonomic structure

The seven morphotype categories were treated as mutually exclusive classes reported in the historical table, giving total  $N = 159$ . Each category share was

calculated as  $100 \times n_k/N$ . A simple concentration ratio was calculated for the two numerically largest categories,  $CR2 = (n_{(1)} + n_{(2)})/N \times 100$ . CR2 describes concentration of taxon counts among form categories and must not be interpreted as an ecosystem diversity index. We did not estimate abundance-weighted Shannon or Simpson indices because the original dataset provides no species-level counts per Quva sample.

For the soil-type  $\times$  division matrix, rows correspond to Cyanophyta, Bacillariophyta, Xanthophyta, Cryptophyta, Euglenophyta and Chlorophyta; columns correspond to light-gray, typical-gray, dark-gray, typical-brown and light-brown soil types. We extracted each source count, checked each column total against the published soil-type richness, and calculated the percentage of each division relative to its column total. Because taxa may occur across several soil types, the total over the matrix is larger than the 159-taxonomy union. The matrix therefore should not be used to calculate a total number of independent species records without duplication information.

Where the source gives cell-density ranges, these are displayed as interval segments with correctly labelled endpoints and units. A minimum and maximum do not identify sample size, standard error or replication structure; they are not 95% confidence intervals and cannot support hypothesis tests by themselves. Group-specific ranges may originate from different samples than the total range, and neither summation of minima nor summation of maxima is biologically justified. No regression between cell density and a soil attribute was attempted because corresponding paired values were not available.

**Table 1. Morphotype categories as reported in the regional inventory.**

| Morphotype                 | Reported taxa | Recalculated share (%) |
|----------------------------|---------------|------------------------|
| Monad                      | 18            | 11.32                  |
| Hemimonad                  | 3             | 1.89                   |
| Coccoid                    | 63            | 39.62                  |
| Sarcinoid                  | 5             | 3.14                   |
| Simple filament            | 51            | 32.08                  |
| Unequal-thickness filament | 17            | 10.69                  |
| Siphonal                   | 2             | 1.26                   |
| Total                      | 159           | 100.00                 |

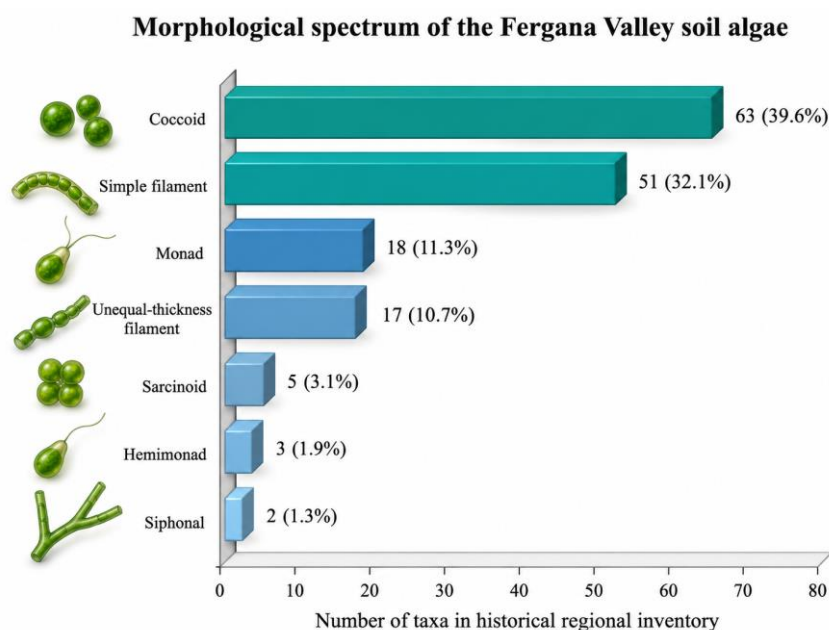


**Figure 1. Historical taxon richness by morphology (valley-wide); these are neither Quva counts nor biomass shares.**

### 2.3. Measurement architecture for evaluating soil–algae relations

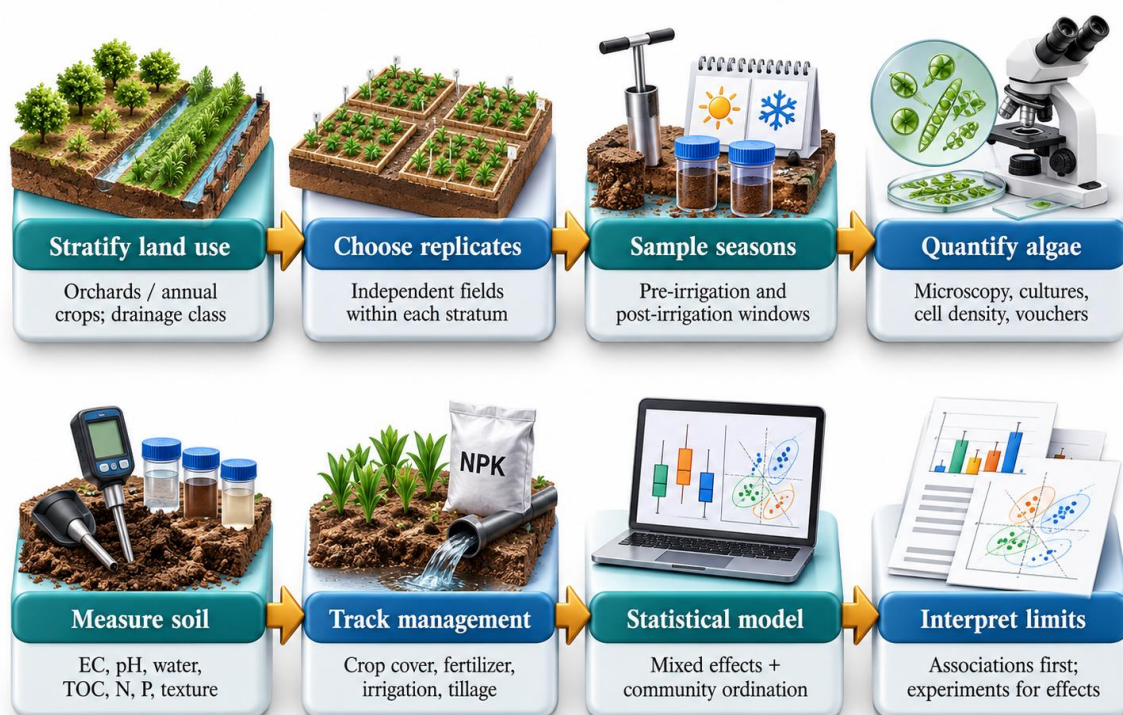
A future study in Quva should begin with a stratified selection of independent fields, distinguishing crop cover, soil unit, management regime and salinity class. Each selected field requires a permanent identifier, georeferenced location, sampling permission and records of irrigation and fertilization. Sampling must represent relevant vertical differences: the illuminated upper 0–5 cm is appropriate for surface phototrophs, whereas deeper intervals require separate interpretation because light availability declines strongly. Surface vegetation, residue and bare-soil proportion should be recorded as site covariates rather than ignored.

The biological sampling unit should be a standardized mass or area of soil acquired at a stated depth and time. Microscopy should generate species-by-sample occurrence and abundance matrices with clear identification certainty and vouchers. When feasible, pigments, microscopy cell counts and molecular sequencing offer complementary views of active or potentially present phototrophs, although their outputs are not directly interchangeable. A sequence read proportion is not a cell-density measurement, and a culture-derived taxon list is biased by growth media. Species lists should use current accepted nomenclature with source synonym identifiers for historical comparisons.

Soil chemistry should be measured on aliquots from the same sampling unit and immediately linked by a unique key. Priority fields include gravimetric moisture or volumetric water content, pH in a specified soil:solution ratio, EC, soluble salts, TOC, mineral or total nitrogen, available phosphorus and soil texture. Secondary indicators such as aggregate stability, microbial respiration and nutrient mineralization may be introduced to test function, provided sufficient replication. Recent wetting history is essential: days since irrigation and rainfall before sampling help separate hydrologic pulses from broad calendar seasonality.

In a repeated seasonal design, field identity is the experimental cluster, with sampling visits nested within fields and technical subsamples within each visit. A site-level random effect can account for baseline heterogeneity in cell-density or richness models. Differential detection should be addressed by recording counting effort and repeating samples when practical. For multivariate composition, ordination coupled with constrained permutation can assess the associations of community structure with moisture, EC and management while respecting the blocked design. The validity of any fitted model should be checked against the actual distribution, replication level, confounders and collinearity.

## Proposed paired-measurement design in Quva



This is a prospective design, not a completed field campaign.

**Figure 2. Prospective Quva sampling and analysis workflow; diagram specifies methodological requirements rather than completed experimental operations.**

### 3. Results

#### 3.1. Regional morphological composition and concentration

The seven form categories in the historical regional inventory total 159 taxa. Coccoid forms are the most numerous with 63 taxa (39.62%), followed by simple filaments with 51 (32.08%), monad forms with 18 (11.32%), filaments of unequal thickness with 17 (10.69%), sarcinoid forms with 5 (3.14%), hemimonad forms with 3 (1.89%) and siphonal forms with 2 (1.26%). Together, coccoid and simple-filamentous categories comprise 114 taxa or 71.70% of the source list. The profile is strongly unequal among form classes, but the percentages describe the distribution of names across morphological classes rather than the relative numbers of living cells in a soil sample.

The concentration ratio  $CR_2 = 71.70\%$  is a reproducible descriptor of the historical inventory and can help direct

laboratory expertise. In practical terms, microscopic preparation and identification procedures must cope with both compact unicellular forms and filaments. However, this indicator says nothing about their relative photosynthetic productivity, polymer release or nitrogen fixation rates. There are multiple possible relationships between form and function; one morphological class can contain taxa with distinct physiological strategies.

The two smallest reported categories—siphonal and hemimonad—together comprise five taxa, or 3.14% of the inventory. Their low richness should not be interpreted as ecological insignificance without abundance and activity observations. Rarely listed groups may be under-detected because of low persistence in a given preparation or different habitat specialization. Moreover, taxonomic counts are shaped by the scope of historical identification methods. The re-analysis thus characterizes the reporting structure of a past study rather than claiming functional dominance in Quva.

## A testable soil-algal interaction model

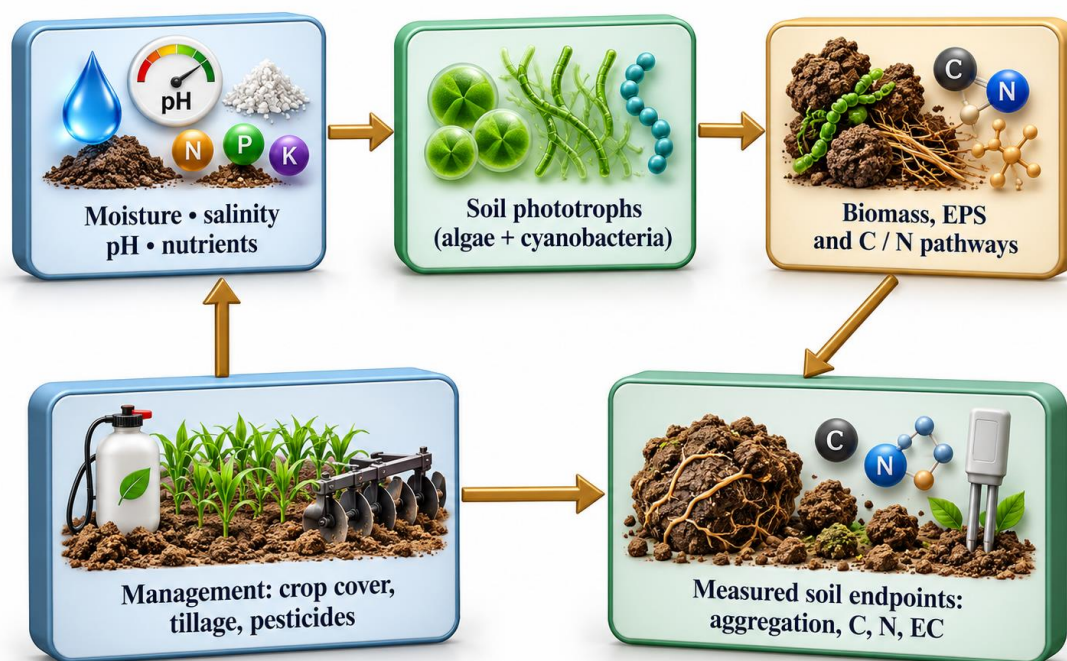


Figure 3. Qualitative mechanisms and confounders relevant to soil–algal research. Arrows represent literature-based hypotheses, not effects measured in Quva.

### 3.2. Taxonomic heterogeneity across historical regional soil classes

The transcribed  $6 \times 5$  matrix reproduces column totals of 63, 67, 104, 108 and 109 taxa for the five soil types, providing an internal quality-control check. Within light-gray soils, Cyanophyta accounts for 29 listed taxa and Chlorophyta for 22; within typical-gray soils, the corresponding counts are 25 and 27. In dark-gray soils the counts are 34 and 42, respectively, while typical-brown soils have 30 and 46 and light-brown soils have 34 and 44. These figures indicate that the rank ordering of the two large divisions differs across the published soil-type lists.

The proportional calculations reinforce this descriptive contrast. In the light-gray soil column, the cyanobacterial share is  $29/63 = 46.03\%$ , whereas the green-algal share is  $22/63 = 34.92\%$ . In the typical-brown column, the cyanobacterial share is  $30/108 = 27.78\%$  and the chlorophyte share is  $46/108 = 42.59\%$ . The approximately 18-percentage-point lower cyanobacterial share between these two columns is a difference in historical taxonomic composition, not a measured

ecological effect of soil color or salinity. Sampling differences and environmental contrasts cannot be separated with the available aggregates.

Bacillariophyta counts also vary: 7, 7, 12, 16 and 14 taxa across the five columns. Xanthophyta counts are 5, 8, 12, 15 and 16. Cryptophyta occurs as one reported taxon only in dark-gray soils, while Euglenophyta is absent from two columns and represented by three, one and one taxa in the remaining three. These small cells are informative for laboratory completeness, but zero in an historical summary must not be asserted to demonstrate local ecological absence without a comparable sampling effort and detection sensitivity.

Figure 4 displays the exact published counts, and Figure 5 displays their within-column proportional recalculations. Together they show how taxonomic comparisons change depending on whether absolute richness or compositional share is emphasized. A field study in Quva would require species-level sample records to test turnover, nestedness or shared taxa, because aggregate division counts do not provide species identity across columns.

**Table 2. Published regional taxa by historical division and soil class; not a Quva sample matrix.**

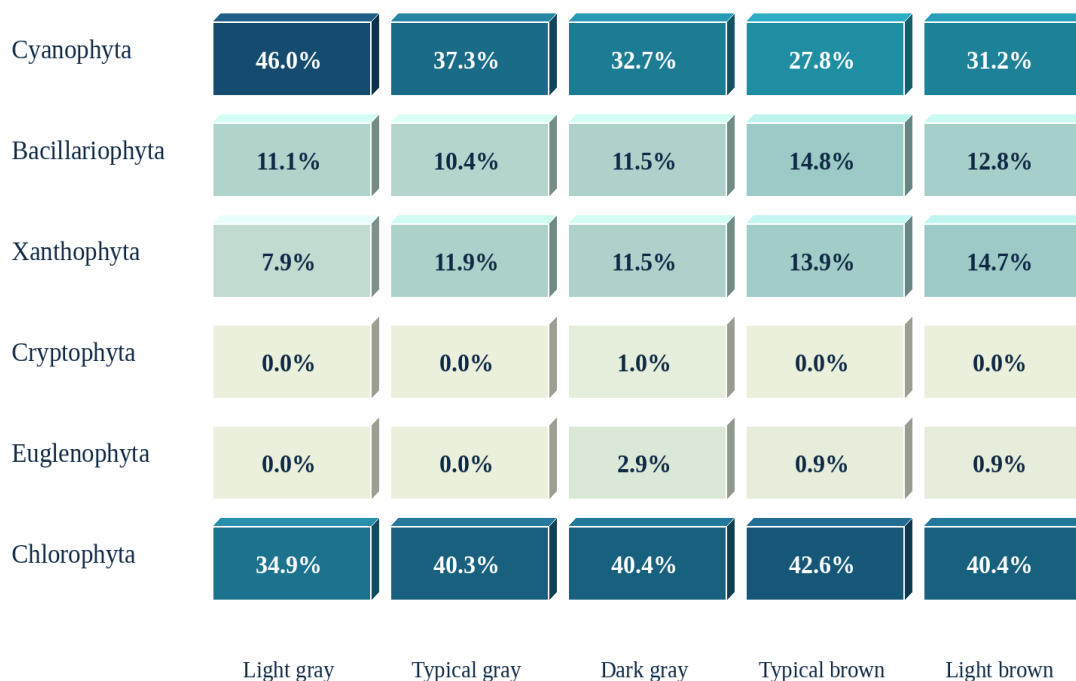
| Division        | Light gray | Typical gray | Dark gray | Typical brown | Light brown |
|-----------------|------------|--------------|-----------|---------------|-------------|
| Cyanophyta      | 29         | 25           | 34        | 30            | 34          |
| Bacillariophyta | 7          | 7            | 12        | 16            | 14          |
| Xanthophyta     | 5          | 8            | 12        | 15            | 16          |
| Cryptophyta     | 0          | 0            | 1         | 0             | 0           |
| Euglenophyta    | 0          | 0            | 3         | 1             | 1           |
| Chlorophyta     | 22         | 27           | 42        | 46            | 44          |
| Total           | 63         | 67           | 104       | 108           | 109         |

### Literature-only group × soil-class count matrix

**Figure 4. Count heatmap for five historical regional soil classes; values are taxa, not cell abundance.**

## Within-soil-class algal division shares (%)

Derived from historical regional lists; percentages within each soil-type column



Source: Tukhtaboeva (2019); regional reference only, not Quva field data.

**Figure 5. Share of each historical division within each reported soil-class list, recalculated from the same table.**

### 3.3. Published cell-density intervals and inferential limits

The regional literature reports total algae between 19.0 and 60.0 thousand cells per gram of soil. The broad grouping labelled Cyanophyta spans 5.4–30.8 thousand cells g<sup>-1</sup>; Chlorophyta and Xanthophyta combined span 10.5–35.2 thousand cells g<sup>-1</sup>; and Bacillariophyta spans 5.1–30.0 thousand cells g<sup>-1</sup>. These ranges were originally presented as observational envelopes from the wider Fergana Valley and are not calibrated to the depth, season, land use or field identities required for Quva. The endpoints cannot be transformed into a mean or variance without additional sample information.

Numerically, the overall interval width is 41.0 thousand cells g<sup>-1</sup>. The individual broad-group interval widths are 25.4, 24.7 and 24.9 thousand cells g<sup>-1</sup>, respectively. This re-expression makes the heterogeneity visible, but does not constitute a treatment contrast. Since the minima and

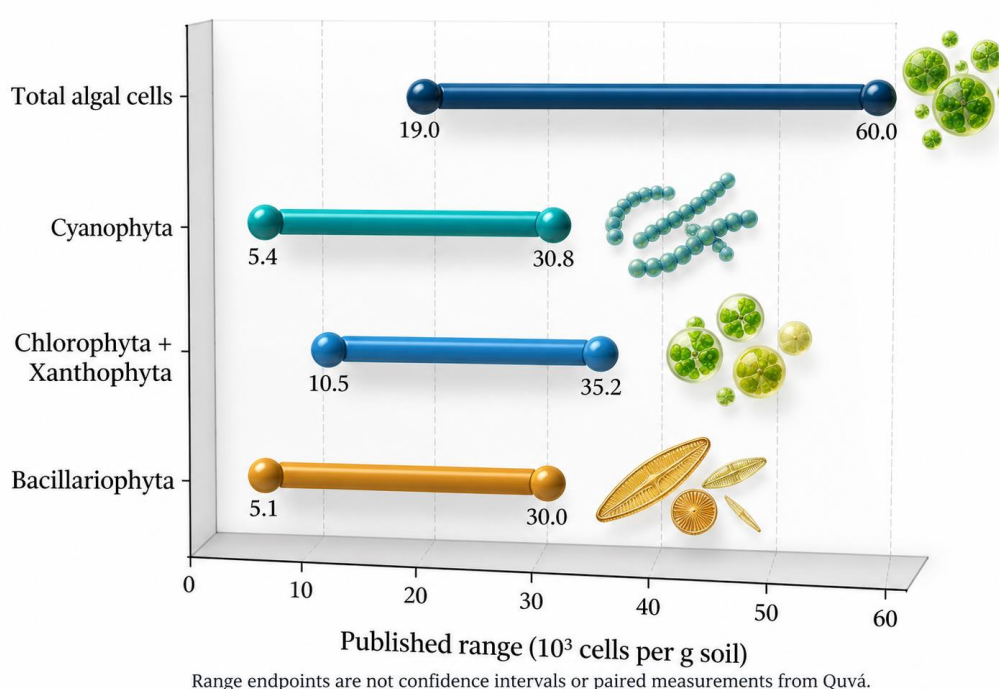
maxima for different groups may refer to different sites and occasions, adding their endpoints would generate a physically meaningless synthetic total. Nor is the difference between the largest and smallest endpoints an observed seasonal amplitude. Figure 6 intentionally uses interval segments instead of uncertainty whiskers or conventional boxplots because quartiles and replicates are unknown.

No measured Quva pH–cell-density or EC–cell-density pairs were identified among the sources assembled for this synthesis. Hence neither Pearson nor Spearman coefficients, regression slopes, significance levels or local functional effect sizes can be responsibly stated. This distinction affects interpretation even if physiologically plausible mechanisms are well documented elsewhere: mechanistic plausibility is not a substitute for site-specific experimental evidence.

**Table 3.** Valley-wide literature abundance intervals; endpoints are neither seasonally paired nor Quva-specific.

| Algal grouping            | Minimum | Maximum | Interval width | Unit                                  |
|---------------------------|---------|---------|----------------|---------------------------------------|
| Total algae               | 19.0    | 60.0    | 41.0           | 10 <sup>3</sup> cells g <sup>-1</sup> |
| Cyanophyta                | 5.4     | 30.8    | 25.4           | 10 <sup>3</sup> cells g <sup>-1</sup> |
| Chlorophyta + Xanthophyta | 10.5    | 35.2    | 24.7           | 10 <sup>3</sup> cells g <sup>-1</sup> |
| Bacillariophyta           | 5.1     | 30.0    | 24.9           | 10 <sup>3</sup> cells g <sup>-1</sup> |

### Historical regional algal cell-density envelopes

**Figure 6.** Literature-reported regional cell-density envelopes; horizontal segments show ranges rather than confidence intervals.

### 3.4. Synthesis of measurable endpoints and priority evidence gaps

The quantified results identify two kinds of information that can be carried forward without overstatement. First, the morphotype and taxonomic group distributions determine the breadth of species identification needed for a field inventory. Second, the historical abundance ranges indicate an order of magnitude for planning microscopy, soil-extraction volumes and counting effort. Neither offers estimates of current mean abundance in Quva. The required bridge between algal ecology and soil chemistry is a dataset where every biological record is linked to measured edaphic attributes and management metadata.

For a defensible monitoring endpoint, the numerator and denominator must be defined. Richness should be expressed as taxa detected per standardized sampling effort; cell density as cells per gram of dry soil; chlorophyll measurements by extraction method and dry mass or area; and functional rates with appropriate units and controls. Nutrient or structural changes should be reported in the same plots over time or in randomized experiments. A broad label such as 'improved fertility' is insufficient unless a prespecified measurable variable changes beyond sampling and analytical uncertainty.

A data structure capable of answering the dissertation topic would have one primary row per field  $\times$  date  $\times$  soil depth, with nested tables for species detections and

technical laboratory replicates. Unique identifiers are more valuable for this objective than additional descriptive charts disconnected from raw samples. Metadata should include coordinate reference, irrigation date, crop cover, sample transport and identification

certainty. This infrastructure would allow the morphological fractions, cell-density means and soil-property models to be recalculated transparently in subsequent publications.

**Table 4. Quva measurement and analytical matrix proposed for original research; all rows are design specifications.**

| Question             | Paired measurements                      | Unit / outcome                  | Appropriate analysis                |
|----------------------|------------------------------------------|---------------------------------|-------------------------------------|
| Seasonal abundance   | Algal cells, date, days since irrigation | Cells g <sup>-1</sup> dry soil  | Mixed-effects count / density model |
| Edaphic association  | Algae, EC, pH, moisture, TOC             | Matched field × date × depth    | Multivariable association model     |
| Taxon turnover       | Species-by-sample occurrences            | Presence / frequency            | Ordination and blocked permutation  |
| Functional mechanism | EPS, aggregate stability, nitrogen flux  | Measured response with controls | Randomized test where feasible      |
| Detection quality    | Voucher, replicate ID, count volume      | Laboratory QC indicators        | Measurement error / coverage review |

## 4. Discussion

### 4.1. How to interpret morphology without confusing richness and function

A major implication of the regional re-analysis is that morphological structure is an informative but incomplete ecological proxy. High numbers of coccoid and simple-filamentous taxa suggest that monitoring should accommodate multiple growth architectures, but the number of taxa in each class cannot establish a class-specific rate of carbon fixation, nitrogen acquisition or extracellular polymer synthesis. Those functions are phylogenetically and environmentally variable. Interpretation must therefore proceed from an observed taxonomic pattern to a testable mechanism and only then to field measurement.

The role of extracellular polymeric substances (EPS) illustrates this difference. Laboratory and restoration studies have shown that selected cyanobacteria can produce polymers contributing to the cohesion of soil particles and the formation of biocrusts (Rossi et al., 2022). In cultivated soils, however, the persistence of such polymers depends on disturbance and hydration regimes. It is not valid to multiply a count of filamentous taxa by a literature polymer-production coefficient to obtain field soil stability. Direct characterization of aggregate stability, EPS quantity and a control treatment is needed to identify whether a functional change occurred.

The taxonomic mix also illustrates why a broad label such as 'soil algae' can mask very different life histories. Some organisms remain viable through extended drying, others require persistent water films; some fix atmospheric nitrogen under suitable conditions whereas many do not. Differential sensitivity to pH and salt ions may alter observed communities, but without measured exposure histories the resulting local response cannot be predicted reliably. A descriptive taxon inventory should therefore remain the first stage of functional monitoring, not its endpoint.

### 4.2. Interactions of soil moisture, salinity, carbon and crop management

Moisture regulates the duration of active metabolism in terrestrial photosynthetic microorganisms. Under irrigation a moist soil surface can temporarily support growth, yet crop cover may simultaneously reduce illumination. The effect of an irrigation event is thus not necessarily monotonic. Too little water can suppress photosynthetic activity, while waterlogging, low light or other unfavorable conditions can also limit certain organisms. Realistic field analysis requires measuring moisture rather than assuming that more irrigation always produces more algae.

Salinity likewise operates through multiple coupled pathways. EC is an integrative index of soluble ions, but it does not distinguish specific ionic toxicity from osmotic stress. Soil texture and evaporation can concentrate salts near the surface, while drainage and

timing of irrigation determine the residence time of saline water films. The environmental literature on Central Fergana demonstrates why saline chemistry should be included in the regional research agenda (Turdaliev et al., 2023; Koriyev et al., 2025). Nonetheless, these publications are not paired measurements of Quva phototrophs and salts. Any Quva-specific statement must await sampling in that district.

Organic carbon is both a possible ecological endpoint and a source of confounding. Photosynthetic microbes may contribute carbonaceous biomass and extracellular organic substances, but vegetation residues, fertilizer, manure and soil formation frequently dominate carbon variability in managed fields. A positive correlation between algal abundance and TOC could arise because both respond to favorable moisture, not because algae caused an increase in TOC. Conversely, crop shading can reduce algal visibility in a field with high carbon stocks. Statistical adjustment for management and soil class is useful for interpreting such associations, but a causal conclusion is stronger when supported by a controlled intervention.

Available nitrogen and phosphorus also have bidirectional relationships with phototrophic communities. Dissolved nutrients can regulate growth; certain organisms alter nutrient transformations; and fertilizers change nutrient supply independently of algal processes. Reviews describe biostimulant and biofertilizer potential, but the outcome depends on strain selection and field conditions (Nawaz et al., 2024; Ramakrishnan et al., 2023). For Quva, it would be premature to make a fertilizer-saving recommendation from a morphological inventory. A field study should quantify nutrient dynamics and crop responses with preplanned controls and realistic agronomic endpoints.

#### **4.3. Models, replication and safeguards against false precision**

Appropriate modelling begins with the sampling hierarchy. Repeated visits to the same field are not independent rows for an ordinary cross-sectional regression. Individual microscope counts from one soil homogenate are technical replicates rather than field-level experimental units. A mixed-effects model may include field as a random term, season and measured EC as fixed effects, and additional covariates justified by the design. Statistical assumptions should be assessed with residual diagnostics, including overdispersion and zero

inflation where appropriate. Effect estimates with uncertainty are preferable to p-values alone.

Taxonomic richness and abundance demand careful treatment of detection. When the same specimen could be classified differently across visits, apparent turnover can be a taxonomic artifact. Culture and sequencing methods differ in sensitivity and compositional bias; protocol changes should be avoided in a seasonal series or explicitly calibrated. The 2024 northern Fergana study applying combined morphological and molecular approaches illustrates why methodological transparency is necessary for interpreting terrestrial algal diversity (Tukhtaboeva et al., 2024). Where samples are geographically separated, recording field identities and effort supports defensible comparisons.

The distinction between observational association and intervention effect is especially important for the dissertation's proposed relationship between algoflora and soil properties. A significant correlation between richness and carbon does not identify the direction of causation. Randomized microcosm or field inoculation studies, sham controls and measurements before and after treatment would provide stronger evidence for an influence of a selected algal assemblage. If such experiments are not feasible, the appropriate scholarly language is 'association', 'co-variation' or 'environmental relationship', with unmeasured confounding discussed transparently.

Another practical risk is false precision arising from public raster products. SoilGrids or global reanalysis layers can supply landscape-scale environmental context, but a gridded pixel does not replace laboratory pH or soil EC from the same sample used for algae. Pixel size, prediction uncertainty, sensing date and land-cover mixture limit such substitutions. Secondary geospatial layers can assist in planning strata or describing broad gradients but should be treated as contextual covariates with explicit spatial uncertainty, not as experimentally paired soil chemistry.

#### **4.4. Distinguishing this Quva synthesis from the Yozyovon research question**

The two district-focused manuscripts address different scientific questions. The Yozyovon manuscript uses measured published soil profiles to quantify environmental heterogeneity and establish salinity-aware seasonal sampling priorities. The present Quva synthesis instead concentrates on morphological and functional

interpretation of the regional algal literature and on the quantitative design required to link algal activity with soil chemical and structural properties. Although both refer to the same historical Fergana Valley taxonomic baseline, they recalculate and visualize different components and ask distinct follow-up questions. They are not presented as two independent biological field campaigns based on duplicated regional observations.

The shared regional baseline must be explicitly cited wherever used. Claims of novelty should be restricted to the transparent restructuring of evidence, calculation of descriptive proportions and specification of an auditable measurement framework. Species totals that originally appeared in Tukhtaboeva (2019) remain that author's published data. Any future paper reporting new Quva results must identify the sampling year, number of independent fields, crop/soil context, laboratory method and specimens, enabling differentiation from historical valley-wide reports.

The present study is limited by the absence of a Quva-specific sample-level dataset containing algal species, biomass, cell abundance and matched chemical measurements. The historical morphotype counts do not represent ecological biomass fractions. The cell-density ranges are not repeated-measures or confidence intervals, and soil-class comparisons lack uniform sampling-effort metadata. These constraints rule out local correlations, causal effects, and time-trend plots. They do not prevent a useful methodological synthesis, provided the limitations are stated in the title, abstract, captions and conclusions.

## 5. Conclusions

Quantitative secondary analysis of the historical Fergana Valley inventory indicates 63 coccoid and 51 simple-filamentous taxa, jointly 71.70% of 159 reported taxa. Division-by-soil-class tables demonstrate heterogeneity in historical taxonomic representation, and literature-reported total algal cell densities range from 19.0 to 60.0 thousand cells per gram of soil. These statistics are regional reference values, not new measurements from Quva district.

For original Quva research, the decisive requirement is a georeferenced dataset pairing taxonomic observations and cell densities with moisture, EC, pH, organic carbon, nutrients, crop cover and irrigation timing on replicated fields and dates. Such information will support legitimate tests of relationships between environmental variation

and algae; a direct influence of algae on soil fertility or stability additionally requires controlled experimental evidence. The present manuscript is accordingly a reproducible quantitative synthesis and research framework that should be submitted and classified as such, not as a completed Quva experiment.

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