

**Agrivoltaic Panel Shading Influences Soil Nutrient Dynamics and Microbial Community Structure
in a Wheat-Cultivated Field**

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Abstract

Agrivoltaic systems (AV), which combine photovoltaic panels with crop cultivation, represent a dual land-use strategy to address food and energy security challenges under growing population pressures. However, the effects of AV systems on soil biogeochemical processes and microbial communities remain insufficiently characterized. This study investigated the effects of AV trackers with varying Ground Coverage Ratios (GCR) on soil physico-chemical properties, and microbial community composition and diversity. Field experiments were conducted in a wheat-cultivated field using two AV configurations: standard (STV1, GCR = 13%) and extended (STV2, GCR = 41%) trackers, compared to a full-sun control (CI). Soil chemical analysis revealed significant increases in organic carbon, total nitrogen, Olsen phosphorus, and exchangeable calcium, potassium, and magnesium under STV2 relative to STV1 and the control. Elemental profiles showed marked enrichment in elements, under STV2 compared to both STV1 and CI. Amplicon sequencing of the 16S rRNA and ITS1 regions revealed reduced bacterial and fungal diversity under STV2. Significant taxonomic shifts in bacterial and fungal communities were also observed at both phylum and genus levels relative to the control. These findings suggest that extended shading from STV2 altered soil chemical properties while restructuring microbial communities, reducing diversity and favoring copiotrophic taxa. Overall, the results underscore the central role of agrivoltaic design, specifically shading intensity and GCR, in shaping belowground processes with critical implications for soil health and the long-term agroecological sustainability of dual land-use energy-food systems.

Keywords: agrivoltaics; soil properties; microbial diversity; soil microorganisms; ground coverage ratio

Introduction

Global agriculture systems are facing increasing challenges, including resource constraints, climate variability, pressure on land use, and the growing vulnerability of energy markets. Ensuring long-term sustainability and resilience requires innovative strategies integrating food and energy production while minimizing environmental impact.

Within this context, renewable energy development has emerged as a key strategy for ensuring long-term energy security [1]. Among emerging approaches, agrivoltaics (AV), a land-sharing system that combines photovoltaic energy generation with crop cultivation, has attracted significant attention for its potential to optimize land use, increase system productivity, and reduce environmental impacts [2,3]. The physical presence of photovoltaic (PV) panels influences local microclimatic conditions by modifying solar radiation flux, wind speed, and even air temperature beneath the structures [4-6]. Shading also alters rainfall patterns, concentrating water at panel edges and generating heterogeneous soil water distribution and localized water storage [6-8]. By lowering potential evaporation directly under panels, these systems reduce drought stress, enhance soil water availability, and limit water loss in arid climates [9-11]. In addition, appropriate shading can decrease evapotranspiration by reducing stomatal opening, thereby improving crop water-use efficiency, although species-specific responses remain evident. PV panels buffer soil temperature fluctuations: they cool the soil during hot daytime conditions while reducing nighttime cooling in autumn and winter, with reported variations of up to 10 °C compared to open-field soil [6,9].

Such regulation of soil temperature and moisture, combined with increased relative humidity under panels [2,12], has been shown to enhance crop performance under heat and drought stress, by reducing heat stress, increasing water-use efficiency, and, in some cases, stabilizing yields under adverse climatic conditions [8,10,13]. However, crop responses vary with species, management practices, and panel configuration. Evidence from vegetable systems highlighted variability: in lettuce, the most frequently studied species, shading has produced outcomes ranging from substantial yield reductions to marked increases, often depending on season and variety [14,15]. Tomatoes likewise show contrasting responses, with some trials reporting reduced fruit set under diminished light, while others highlight improved fruit size and physiological adaptation under partial shade [13,16]. Cereals were less investigated: maize has demonstrated tolerance to moderate shading, with slight yield gains under low panel density due to reduced evaporative losses, but sharp declines at higher coverage [17]. Wheat showed contradictory results as well: increases in vegetative biomass have been observed, but grain yields often decline, particularly in terms of grain weight [2,18].

The same microclimatic modifications that improve crop performance also influence soil biological functioning, particularly the activity and composition of microbial communities. Soil microorganisms dynamically respond to shifts in temperature, moisture, and root exudation patterns, which are shaped by AV design and shading [19-21]. In fact, panel-induced heterogeneity generates diverse soil microhabitats that are crucial for sustaining microbial diversity [22]. Panels alter key abiotic factors, thereby restructuring microbial biomass, richness, and composition [23,24]. For example, shading can increase total microbial biomass by 20–30%, while reducing alpha diversity indices due to the decline of light-dependent taxa and the competitive release of shade-adapted groups [24,25]. Beyond microclimate, panel coverage also affects nutrient dynamics, with C and N storage decreasing by up to 61% and 50%, respectively, resulting in cascading effects on microbial functional groups. These effects include increases in Proteobacteria and reductions in Acidobacteria [26,27].

Existing studies often report contrasting results, as crop and soil responses are shaped not only by species and local environmental conditions, but also by the design of the AV installation itself [23,28]. Different technological solutions have been developed to integrate photovoltaic power generation and crop cultivation. Interspersed PV arrays place panels between crop rows, whereas overhead systems can either be greenhouse-mounted, replacing part of the transparent cover, or stilt-mounted above open-field crops [29]. Panels may be static or dynamic, the latter adjusting their tilt to balance energy generation with crop light requirements [9]. Moreover, the ground coverage ratio (GCR), the proportion of soil surface occupied by PV modules relative to the total cultivated area, has emerged as a key parameter linking energy output and agricultural productivity [30]. Increasing GCR generally enhances energy yield but can negatively affect crop performance by reducing light availability [30]. However, while the relationship between GCR and crop yield has been explored, its implications for soil physical, chemical, and biological functioning remain largely overlooked. This knowledge gap is particularly critical for temperate cereal-based agroecosystems, where soil health is essential for long-term productivity.

This study investigates the impact of different agrivoltaic (AV) ground coverage ratios on soil properties and microbial communities in a wheat-based system in Northern Italy. The research

specifically aims to evaluate: (i) how AV ground coverage ratios can influence soil physico-chemical characteristics and (ii) whether AV installations alter the structure composition of microbial communities as an agroecosystem service. Addressing these aspects provides insights into the potential of AV systems to sustain not only energy generation and crop yield, but also the long-term integrity and health of soils.

Materials and Methods

Study area

The study area is located in Borgo Virgilio (Mantova Province, northern Italy; N 45°05.40', E 10°47.30') and hosts the agrivoltaic system investigated in this study. The system was installed in 2011. The system spans a total surface area of 11.42 hectares, of which 13% (1.30 hectares) is shaded. The photovoltaic system has a nominal capacity of 2150.4 kW and consists of 768 dual-axis trackers (BIAXIAL TRACKERS 3D-T1.0) supporting 7680 polycrystalline silicon (Poly) panels, each rated at 280 Wp. The installed power density is approximately 188 kWp/ha. The dual-axis tracking system automatically adjusts the panels' inclination angles in response to the sun's position, optimizing solar energy capture. The primary (central) axis rotates from 50° (morning) to 140° (afternoon), passing through 90° (horizontal), while the secondary axis shifts from an initial position of 90° (flat) up to 135°-140°, and down to 50° by evening. Regarding structural specifications, the maximum clearance beneath the panels in their safety position is 4.5 m. In contrast, the minimum ground clearance at the panels' maximum inclination is approximately 3.20 m [31].

The crop cultivated in the portion of the field considered for this study was Durum wheat (*Triticum durum* Desf.) Levante (Syngenta Italia, Milano, Italy); seeds were sown at a density of 350 seeds m⁻². The crop previously cultivated was Italian ryegrass (it was mechanically destroyed by ploughing). Pre-sowing harrowing was performed one week prior to sowing on October 20th, 2023, using a combined row seeder (Nina 250-400, Maschio Gaspardo, Campodarsego, Padova, Italy). Fertilization rates were 100 kg N ha⁻¹ and 40 kg K ha⁻¹, adjusted based on soil chemical analysis. No irrigation was applied.

According to Soil Taxonomy, the soil is classified as Typic Calciustepts, fine-silty, mixed, mesic (Soil Survey Staff, 2022), corresponding to an Endocalcaric Calcisol (Siltic, Hypereutric) in the WRB system (IUSS Working Group WRB, 2022).

During the study period (March–July 2024), the mean air temperature was 15.1 °C, total rainfall was 815 mm, mean relative humidity was 83.3%, and average global solar radiation was 1618 W m⁻². The site typically receives 1800-2000 hours of sunlight per year.

Soil Sampling and Experimental Design

Soil was sampled under two agrivoltaic (AV) configurations: extended trackers (STV2) and standard trackers (STV1), and in a full-sun control (CI) condition. Ground cover ratio (GCR) was 41% (STV2) and 13% (STV1).

For each condition, three plot replicates were selected, and five sub-samples per plot were collected from the 0–30 cm layer using a manual auger. Sub-samples were homogenized into a composite sample (~1 kg), which was then split into 3 technical replicates, for a total of 9 replicates per condition (**Fig S1**). The 9 plots considered, three for each experimental condition, were randomly

distributed along an inter-row corridor designated for the experiment. Each plot had a surface area of 12x12 m, for a total tested area of 1.296 m².

Sampling was performed twice with the same sampling design: at the wheat early vegetative stage – March 10th (T1), and at the harvest stage - July 2nd (T2), 2024. Soil samples were air-dried and sieved at 2 mm for analysis.

Soil physico-chemical and elemental analyses

The particle size distribution (PSD) was determined for each soil sample using laser diffraction analysis, with Mastersizer 2000 (Malvern Panalytical, Malvern, United Kingdom). Soil pH was measured potentiometrically using a glass electrode in a suspension of soil and ultra-pure water following a standardized ratio of 1:2.5 (w/v). The same suspension was used to measure electrical conductivity (EC). To quantify the total nitrogen (N_{tot}) and total carbon (C_{tot}) contents, samples were subjected to dry combustion analysis using an Elementar Vario MACRO CNS analyzer (Elementar Analysensysteme GmbH, Hanau, Germany). Organic carbon (C_{org}) was specifically assessed by combustion with the Skalar PrimacsSNC–100 analyzer (Skalar Analytical BV, Breda, The Netherlands), after removal of inorganic carbon fractions. The plant-available phosphorus (P) concentration was determined using the Olsen P extraction method [32], suitable for soils with neutral to alkaline pH.

Exchangeable bases (Ca²⁺, Mg²⁺, K⁺, Na⁺) were extracted using 1 M ammonium acetate at pH 7.0. Then, the elemental composition was determined by inductively coupled plasma optical emission spectrometry (ICP–OES), using a Spectro Arcos MV instrument (Spectro Ametek, Kleve, Germany).

Total soil DNA extraction, 16S and ITS metabarcoding

Total genomic DNA was extracted from 250 mg of air-dried soil using the DNeasy PowerSoil Pro Kit (Qiagen GmbH, Hilden, Germany), according to the manufacturer's protocol. Final elution was performed with nuclease-free, autoclaved double-distilled water (ddH₂O). DNA concentration was quantified using a Qubit Flex fluorometer (Thermo Fisher Scientific, Carlsbad, CA, USA) in combination with the Qubit 1x dsDNA High Sensitivity Assay Kit (Thermo Fisher Scientific), enabling accurate quantification of low-concentration DNA samples.

DNA samples were processed and sequenced at Novogene (Germany) for 16S and ITS rDNA metabarcoding. Briefly, the V4–V5 hypervariable regions of the 16S rRNA gene were amplified using the primer pair GTGCCAGCMGCCGCGGTAA (forward) and CCGTCAATTCCTTTGAGTTT (reverse), while the ITS1 region was amplified using primers CTTGGTCATTAGAGGAAGTAA (forward) and GCTGCGTTCTTCATCGATGC (reverse). Short-reads sequencing was performed on the Illumina NovaSeq platform to generate 2 × 250 bp paired-end reads.

Data analysis for 16s and ITS metabarcoding

Preliminary raw data processing was performed at Novogene UK using the company's proprietary standard pipeline based on Illumina raw reads for quality screening, tag filtration and chimera removal to obtain clean data. Cleaned reads were further denoised and dereplicated into amplicon sequence variants (ASVs) using DADA2 [33]. Representative ASV sequences were taxonomically classified using QIIME2 classify sklearn plugin [34] with SILVA 138.1 database for bacterial 16S [35] and UNITE v9.0 database for fungal ITS [36]. ASVs and their respective count tables were used to compute diversity indices and relative abundance profiles, to perform sample clustering, and to conduct other statistical analyses. Microbiome data analyses were performed

198 using MicrobiomeAnalyst 2.0, with data normalization using Cumulative Sum Scaling (CCS) [37,38].
199 The suite was used to obtain alpha-diversity metrics, species composition, and beta-diversity
200 estimation. Alpha diversity at the genus level was calculated using Chao1, Shannon, and Simpson
201 indices. Beta diversity of microbial communities at the genus level was assessed using Principal
202 Coordinate Analysis (PCoA) based on Bray-Curtis distances, followed by Permutational Multivariate
203 Analysis of Variance (PERMANOVA) to test for significant difference in sample clustering ($p < 0.05$).
204 Linear Discriminant Analysis Effect Size (LEfSe) was performed to identify potential biomarkers at the
205 genus level, with an LDA score threshold of 2.0 [39]. Data visualisation was conducted using SRplot
206 [40].

207 **Statistical analyses**

208 Data from three experimental conditions ($n = 9$ replicates per condition) were analyzed to
209 assess statistical differences. A one-way analysis of variance (ANOVA) was performed, and when
210 significant differences were detected ($p < 0.01$), pairwise comparisons were conducted using Tukey's
211 Honestly Significant Difference (HSD) post-hoc test. Statistical significance was set at $p < 0.01$. This
212 analytical pipeline was applied to evaluate differences in soil physico-chemical properties, elemental
213 composition, and genus- and phylum-level abundances, at both time points.

214 Differences in alpha-diversity among conditions were assessed using the non-parametric
215 Kruskal–Wallis test. Statistical significance was indicated as follows: ns (not significant), * p -value $<$
216 0.1, ** p -value < 0.05 , *** p -value < 0.01 .

217 A multivariate Canonical Correspondence Analysis (CCA) was conducted to assess the
218 microbial communities concerning physico-chemical and elemental composition as environmental
219 variables. CCA plots were constructed using Statistica v13.5 (TIBCO Software Inc.), using Scaling Type
220 2 to ensure accurate interpretation of compositional gradients.

221 **Results**

222 **Soil physico-chemical profiles**

223 Stable soil characteristics (clay, silt, sand content, and pH) did not exhibit significant variation
224 across the different agrivoltaic (AV) configurations and the control (**Table 1**).

225 Soil total nitrogen (N_{tot}) and soil organic carbon (C_{org}) differed significantly among treatments
226 ($p < 0.01$): N_{tot} being 26% higher in STV2 than in STV1 and 34% higher than in CI; and C_{org} being 21%
227 higher, on average, in STV2 than in STV1 and CI. Conversely, total carbon (C_{tot}) content in STV2 was
228 markedly lower, with reductions of 26% in STV1 and 30% in CI. C/N ratio decreased significantly in
229 STV2 with respect to CI (-10%). DM did not show a tendency; however, it was 1% lower in STV1 than
230 CI, and this difference was significant. Olsen phosphorus (Olsen P) was more than double in STV2
231 compared to STV1 (+102%) and 60% higher relative to CI. Electrical conductivity (EC) increased under
232 STV2 compared to both STV1 and CI (+15% and +24%, respectively) (**Table 1**).

233 Regarding exchangeable bases, STV2 consistently displayed elevated levels of key cations:
234 exchangeable calcium (Ca^{2+}) was 11% and 24% higher than in STV1 and CI, respectively; potassium
235 (K^+) increased by 52% compared to STV1 and by 78% relative to CI; and magnesium (Mg^{2+}) appears
236 higher by 27% and 32% in comparison to STV1 and CI, respectively (**Table 1**).

237 **Table 1 Physical and chemical properties across different conditions.** Values are expressed as mean
238 $\pm$ standard error (n = 9). CI: control; STV1: standard trackers; STV2: extended trackers. Different
239 letters indicate a statistically significant difference in the post-hoc test ($p < 0.01$).

Parameter	CI	STV1	STV2
Clay (%)	31.78 $\pm$ 0.68 a	31.57 $\pm$ 0.75 a	31.57 $\pm$ 0.59 a
Silt (%)	29.80 $\pm$ 0.49 a	30.91 $\pm$ 0.62 a	30.68 $\pm$ 0.67 a
Sand (%)	38.41 $\pm$ 1.02 a	37.52 $\pm$ 0.68 a	37.74 $\pm$ 0.59 a
N _{tot} (%)	0.10 $\pm$ 0.01 b	0.10 $\pm$ 0.01 b	0.13 $\pm$ 0.00 a
C _{tot} (%)	3.92 $\pm$ 0.26 a	3.74 $\pm$ 0.16 a	2.76 $\pm$ 0.09 b
C _{org} (%)	0.96 $\pm$ 0.04 b	0.98 $\pm$ 0.05 b	1.17 $\pm$ 0.01 a
C/N	10.06 $\pm$ 0.23 a	9.63 $\pm$ 0.26 ab	9.03 $\pm$ 0.12 b
DM	97.02 $\pm$ 0.28 a	96.09 $\pm$ 0.12 b	96.17 $\pm$ 0.12 ab
Olsen P (mg/kg)	16.78 $\pm$ 2.97 b	13.31 $\pm$ 1.94 b	26.87 $\pm$ 0.54 a
pH	8.34 $\pm$ 0.02 a	8.44 $\pm$ 0.03 a	8.43 $\pm$ 0.03 a
EC (mS/cm)	176.56 $\pm$ 2.74 b	173.61 $\pm$ 3.16 b	198.86 $\pm$ 3.35 a
Ca exch. (mg/kg)	3131.97 $\pm$ 92.51 b	3488.06 $\pm$ 64.90 b	3884.48 $\pm$ 85.60 a
K exch. (mg/kg)	102.85 $\pm$ 10.52 c	119.96 $\pm$ 11.07 b	182.60 $\pm$ 11.27 a
Mg exch. (mg/kg)	178.87 $\pm$ 13.15 c	185.36 $\pm$ 11.32 b	235.35 $\pm$ 6.14 a
Na exch. (mg/kg)	16.43 $\pm$ 0.53 a	12.03 $\pm$ 0.85 b	17.69 $\pm$ 0.53 a
N _{tot} = total nitrogen; C _{tot} = total carbon; C _{org} = organic carbon; DM = dry matter; Olsen P = Olsen phosphorus; EC = electrical conductivity; Ca exch. = exchangeable calcium; K exch. = exchangeable potassium; Mg exch. = exchangeable magnesium; Na exch. = exchangeable sodium.			

240
241 Elemental composition showed significant changes in elemental concentrations across CI,
242 STV1, and STV2, with STV2 exhibiting the highest enrichment for most elements. One-way ANOVA
243 followed by Tukey's HSD test identified statistically significant increases in 23 out of the 26 measured
244 elements in STV2 compared to both CI and STV1 (**Table 2**). On average, STV2 showed a 24% increase
245 in elemental concentrations relative to both CI and STV1. The most notable increases were observed
246 for copper (+46% vs CI; +39% vs STV1), potassium (+30%; +29%), molybdenum (+33%; +36%), zinc
247 (+32%; +34%), and lead (+34%; +32%). In contrast, calcium, magnesium, and strontium
248 concentrations were significantly reduced in STV2 (Ca: -43% vs CI; Mg: -18%; Sr: -30%).

249 Principal Coordinate Analysis (PCoA; **Fig 1**) showed that STV2 samples clustered separately
250 along PC1, which explained 74% of the variance. In contrast, STV1 and CI samples showed partial
251 overlaps, indicating more similar soil profiles (**Fig 1**).

252 **Table 2 Elemental composition of soils across different conditions.** Values are expressed as mean $\pm$
253 standard error (n = 9). CI: control; STV1: standard trackers; STV2: extended trackers. Different letters
254 indicate a statistically significant difference according to the post-hoc test ($p < 0.01$).

Parameter (mg/kg)	CI	STV1	STV2
Al	28824.97 $\pm$ 1779.44 b	30366.15 $\pm$ 1392.92 b	38857.50 $\pm$ 396.43 a
As	8.97 $\pm$ 0.46 b	9.39 $\pm$ 0.37 b	11.27 $\pm$ 0.1 a
B	17.90 $\pm$ 1.08 b	18.60 $\pm$ 0.91 b	23.25 $\pm$ 0.12 a
Ba	131.56 $\pm$ 7.07 b	137.41 $\pm$ 5.43 b	173.59 $\pm$ 1.71 a
Be	0.96 $\pm$ 0.05 b	1.01 $\pm$ 0.04 b	1.27 $\pm$ 0.01 a
Ca	96353.09 $\pm$ 7473.99 a	89179.39 $\pm$ 6942.84 a	53456.21 $\pm$ 3086.78 b
Cd	0.19 $\pm$ 0.01 b	0.19 $\pm$ 0.01 b	0.23 $\pm$ 0.00 a
Co	8.65 $\pm$ 0.45 b	9.11 $\pm$ 0.36 b	11.00 $\pm$ 0.12 a
Cr	40.48 $\pm$ 2.17 b	42.66 $\pm$ 1.75 b	53.23 $\pm$ 0.51 a
Cu	23.79 $\pm$ 2.54 b	26.85 $\pm$ 3.08 b	37.27 $\pm$ 0.40 a
Fe	19014.43 $\pm$ 1133.90 b	19938.86 $\pm$ 848.69 b	25348.42 $\pm$ 272.66 a

K	6029.93 ± 356.46 b	6354.32 ± 288.67 b	8195.15 ± 92.76 a
Li	26.21 ± 1.35 b	27.76 ± 1.07 b	33.69 ± 0.21 a
Mg	15277.28 ± 442.19 a	14648.3 ± 505.32 a	12521.72 ± 72.45 b
Mn	467.47 ± 22.18 b	496.56 ± 18.89 b	599.46 ± 9.25 a
Mo	0.79 ± 0.04 b	0.80 ± 0.03 b	1.09 ± 0.05 a
Na	473.72 ± 8.44 b	475.67 ± 5.89 b	529.72 ± 7.26 a
Ni	25.46 ± 1.52 b	26.63 ± 1.10 b	33.13 ± 0.31 a
P	634.32 ± 41.05 b	652.07 ± 29.31 b	837.18 ± 10.11 a
Pb	13.49 ± 1.207 b	14.66 ± 1.02 b	19.35 ± 0.11 a
S	238.89 ± 8.27 b	246.04 ± 6.69 b	280.53 ± 2.81 a
Sn	4.19 ± 0.16 b	4.40 ± 0.09 b	4.97 ± 0.05 a
Sr	150.45 ± 7.68 a	142.83 ± 7.18 a	103.40 ± 3.06 b
Ti	1022.48 ± 38.46 b	1051.16 ± 22.56 b	1201.06 ± 27.03 a
V	50.30 ± 2.37 b	52.38 ± 1.77 b	63.80 ± 0.47 a
Zn	51.55 ± 3.87 b	50.97 ± 2.71 b	68.15 ± 0.30 a

Fig 1 Principal coordinate analysis (PCoA) of soil characteristics based on physico-chemical and elemental composition. Shapes represent samples, colored by experimental conditions (STV2, STV1, CI). Axes show the percentage of variance explained by each principal coordinate.

Microbial community structure

To assess the independent and interactive effects of condition and sampling time on microbial composition, the two-way PERMANOVA was performed on the 30 most abundant Taxa using the Bray-Curtis Method with 9999 permutations. For the bacterial community, sampling time had a significant influence ($p = 0.0006$), but neither the conditions nor the Interaction between factors were observed (**Table S1**). In contrast, for the fungal community, although both factors were also statistically significant ($p = 0.0001$), there was no significance for the Interaction of factors (**Table S2**).

Microbial alpha diversity was influenced by both experimental condition and sampling time, with distinct patterns observed for bacterial and fungal communities.

At T1, bacterial alpha diversity was significantly reduced in STV2. Specifically, Chao1 and Shannon indices were significantly lower in STV2 compared to the control (CI) ($p < 0.01$ and $p < 0.05$, respectively), and the Simpson index was significantly reduced relative to both CI ($p < 0.01$) and STV1 ($p < 0.05$) (**Fig 2A-C**). In contrast, no significant differences in bacterial alpha diversity were observed among conditions at T2 for any of the diversity indices considered (**Fig 2D-F**).

Fungal alpha diversity showed a different pattern. The Chao1 index did not differ significantly among conditions at either sampling time (**Fig 2G, 2J**). However, the Shannon index was significantly lower in STV2 compared to CI, at both T1 and T2 ($p < 0.05$) (**Fig 2H, 2K**). Similarly, the Simpson index was significantly lower in STV2 than in CI at T1 ($p < 0.05$), whereas no significant differences were observed at T2 (**Fig 2I, 2L**).

PCoA indicated treatment-related differences in both bacterial and fungal community structures at T1 and T2 (**Fig 3**). For the bacterial community, the conditions explained a significant portion of the observed variation in community composition at T1 ($p = 0.0146$, $R^2 = 0.23$) and T2 ($p = 0.0009$, $R^2 = 0.33$), with STV2 consistently differing from both STV1 and CI ($p < 0.01$). No significant differences were detected between STV1 and CI (**Fig 3A, 3B**). Similarly, in the fungal community

composition was significantly influenced by treatment, with condition explaining a substantial proportion of the variation at both time points ($p = 0.0006$; $R^2 = 0.39$ at T1 and $R^2 = 0.35$ at T2) (**Fig 3C, 3D**). All pairwise comparisons are statistically significant: STV2 vs STV1, STV2 vs CI ($p < 0.01$), and STV1 vs CI ($p < 0.05$).

Amplicon sequencing of 16S rRNA and ITS1 regions revealed taxonomically distinct bacterial and fungal communities, whose composition was significantly influenced by condition and sampling time.

Bacterial community composition at the phylum level was dominated by Actinobacteriota (51%), Proteobacteria (19%), Firmicutes (13%), and Acidobacteriota (5%) (**Fig 4A**). While the relative abundance of several dominant phyla, including Proteobacteria, Acidobacteriota, Planctomycota, Myxococcota, Chloroflexi, and Bacteroidota, remained relatively stable across conditions and sampling times (**Table S3**), other groups exhibited clear condition- and time-point-specific dynamics. Actinobacteriota increased significantly at T2 compared to T1 (+65%), whereas Firmicutes were consistently more abundant under the extended trackers (STV2), with this difference reaching statistical significance at T2 (+130%). In contrast, Nitrospirota showed higher relative abundance in the control (CI) at T1 but declined significantly at T2 (−50%).

At the genus level, bacterial communities were dominated by *Gaiella*, *Bacillus*, *Nocardioides*, and *Solirubrobacter*, collectively accounting for approximately 10%, 8%, and 6% of the total community, respectively (**Fig 4B**). All ten most abundant genera showed a significant increase from T1 to T2 time points, with an average relative abundance rise of 77%. The most pronounced increases were observed for *Blastococcus* (+122%), *Streptomyces* (+132%), and *Pseudonocardia* (+133%). *Bacillus* was significantly more abundant in STV2 soils at both time points, with increases of +84% at T1 and +154% at T2. *Blastococcus*, *Microlunatus*, and *Microvirga* showed significant enrichment in STV2 soil at T2 only (+34%, +39%, and +58%, respectively; **Table S4**).

At the phylum level, fungal community composition was overwhelmingly dominated by Ascomycota, which accounted for approximately 90% of total sequences among all samples (**Fig 4C**). No statistically significant differences were detected in phylum-level fungal composition across conditions or sampling times (**Table S5**).

At a finer taxonomic resolution, the dominant fungal genera included *Fusarium* (17%), *Verticillium* (9%), *Striaticonidium* (4%), and *Sarocladium* (3%) (**Fig 4D**). Seasonal trends were evident, with genera such as *Fusarium*, *Verticillium*, *Stachybotrys*, *Furcasterigmium*, *Botryotrichum*, and *Chaetomium* increasing in abundance from T1 to T2 (+32% on average). In contrast, *Striaticonidium*, *Sarocladium*, *Neoschizothecium*, and *Chordomyces* decreased by an average of 59%. Although significant differences were detected among conditions for some genera, no consistent trend was observed. Notably, the intermediate configuration (STV1) did not consistently fall between the control (CI) and the extended trackers (STV2) in terms of genus abundance. Instead, the intermediate configuration (STV1) represented the condition under which peak values — either highest or lowest — were recorded for specific genera: *Striaticonidium* reached its statistically highest abundance, whereas *Botryotrichum* exhibited its lowest abundance under STV1, suggesting non-linear, condition-specific responses. Among the ten most abundant genera, *Stachybotrys*,

324 *Chordomyces*, *Furcasterigmium*, and *Chaetomium* did not exhibit significant variation among either
325 condition or sampling time (**Table S6**).

326 LEfSe analyses identified bacterial genera significantly associated with the different
327 conditions ($LDA > 2$, $FDR \leq 0.5$). *Bacillus* and *Blastococcus* emerged as biomarkers of the STV2 AV
328 configuration in both sampling times. At T1 and T2, *Lysobacter* and *Streptomyces* were identified as
329 biomarkers for the STV1 configuration, respectively (**Fig 5A, 5B**). The control showed *Nocardioides*
330 as biomarker, only at T2 (**Fig 5B**).

331 For Fungi, the LEfSe analyses identified biomarker genera only for STV1 and STV2, and only
332 at T2. Specifically, *Verticillium*, *Fusarium*, and *Stachylidium* were characteristic of the STV2 condition;
333 *Chordomyces* and *Talaromyces* were the most enriched genera in STV1 (**Fig 6**).

334 **Fig 2 Alpha diversity of microbial communities measured using Chao1, Shannon, and**
335 **Simpson indices.** Panels show bacterial diversity at the genus level under different agrivoltaic (AV)
336 configurations (STV2, STV1) and control (CI), at T1 (A–C) and T2 (D–F), and fungal diversity at T1 (**G–**
337 **I**) and T2 (**J–L**). Significance levels: ns (not significant), * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$ (Kruskal-
338 Wallis test). Boxplots represent median and interquartile ranges.

339 **Fig 3 Principal Coordinates Analysis (PCoA) of community composition under AV**
340 **configurations (STV2, STV1) and control (CI).** Panels show bacterial (A, B) and fungal (C, D)
341 community composition at the genus level, at T1 (A, C) and T2 (B, D) sampling time points. Points
342 represent samples; ellipses (if present) indicate 95% confidence intervals per condition.

343 **Fig 4 Relative abundance of the 10 most dominant bacterial (A, B) and fungal (C, D) phyla**
344 **(A, C) and genera (B, D).** The figure shows microbial communities in soils under AV configurations
345 (STV2, STV1) and control (CI), at T1 and T2.

346 **Fig 5 Linear discriminant analysis effect size plots on Bacteria.** The analysis shows bacterial
347 genera significantly enriched in STV2 (red), STV1 (blue), and CI (green) conditions, at T1 (A), and T2
348 (B) ($LDA > 2$; $FDR \leq 0.5$).

349 **Fig 6 Linear discriminant analysis effect size plots on Fungi.** The analysis shows the top 15
350 fungal genera significantly enriched in STV2 (red) and STV1 (blue), at T2 ($LDA > 2$; $FDR < 0.1$).

351 Environmental structuring of microbial communities

352 To investigate the relationship between soil abiotic factors and microbial community
353 composition, Canonical Correspondence Analysis (CCA) was performed separately for bacterial and
354 fungal communities.

355 Bacterial communities exhibited moderate environmental structuring when constrained by
356 physico-chemical soil properties and elemental composition (**Fig 7A**). The CCA revealed that the first
357 two axes explained 57% of the constrained variation (CCA1: 45%, CCA2: 13%), corresponding to 22%
358 of the constrained inertia (**Table S7**), indicating moderate model fit but limited environmental
359 explanation of bacterial community variation. Bacterial assemblages showed partial separation
360 between CI and shaded soils (STV1, STV2) along CC1, suggesting that the presence of solar panels
361 influenced soil bacteria composition. The main environmental variables driving this pattern were

362 C_{org} , N_{tot} , P Olsen, EC, exchangeable cations which were positively correlated with the shaded plots,
363 STV2 in particular; C_{tot} , Mg, Sr, and Ca were correlated with the control; while parameters related to
364 soil texture and pH were not associated with either conditions. No clusterization related to the
365 sampling time was observed.

366 Fungal communities exhibited weak environmental structuring when constrained by physico-
367 chemical soil properties and elemental composition (**Fig 7B**). The first two CCA axes accounted for
368 38% of the constrained variance (CCA1: 25%, CCA2: 13%), corresponding to 14% of the total inertia
369 (**Table S8**). Overall, the clustering of samples from different conditions and sampling times was less
370 distinct than that observed for bacterial communities: only STV2 showed a cluster, which was mostly
371 driven by C_{org} , N_{tot} , P Olsen, EC, exchangeable cations. Again, no clusterization related to the sampling
372 time was observed.

373 **Fig 7 Canonical Correspondence Analysis (CCA) plots showing the relationships between**
374 **microbial communities and soil chemical-physical and elemental composition.** Soil bacterial (A)
375 and fungal (B) communities constrained by soil properties at two time-points: T1 (●), and T2 (◆), in
376 the different conditions: STV2, STV1, CI.

377 Discussion

378 Integrating photovoltaic systems into agricultural fields altered soil conditions and influenced
379 microbial community composition.

380 Differences in nitrogen and carbon dynamics across treatments indicate that AV shading may
381 alter the balance between mineralization and immobilization processes. The lower C/N ratio in STV2
382 soils suggests greater nitrogen retention than in CI and STV1 soil conditions. These trends likely
383 reflect shifts in organic matter decomposition and microbial turnover rates induced by the altered
384 vegetation and soil–water interactions beneath the panels. Although microclimatic parameters were
385 not measured, the lower dry matter content under panels implies greater soil moisture retention
386 (**Table 1**). These observations align with Luo et al., [41], who reported minimal effects on soil pH,
387 slight increases in N_{tot} , and significant enhancements in Olsen P and EC under AV systems. Luo et al.,
388 [41] focused on legume-based systems, with plants known for their nitrogen-fixing capabilities.
389 Interestingly, we observed a comparable increase in N_{tot} under wheat cultivation, suggesting that N
390 accumulation under AV systems may result from modulation of soil processes rather than from solely
391 biological fixation. The increases in available P, EC, and exchangeable base cations (Ca^{2+} , K^+ , Mg^{2+})
392 under STV2 further indicate enhanced nutrient retention and ion accumulation in shaded soils (**Table**
393 **1**). All plots were uniformly fertilized: thus, reduced exposure to direct rainfall beneath the panels
394 likely limited nutrient leaching, allowing fertilizers and dissolved ions to accumulate in the upper soil
395 layers. Such patterns could also reflect slower organic matter turnover under more humid, cooler
396 conditions, thereby favoring the persistence of soluble and exchangeable ions. Elemental profiling
397 further supported this pattern: STV2 soils were enriched in 23 out of 26 measured elements,
398 indicating increased accumulation of micronutrients and trace elements (**Table 2**). The enrichment
399 observed under STV2 likely reflects altered water–solute dynamics caused by panel shading [42]. In
400 the absence of direct precipitation, but under continued plant transpiration, water can be actively
401 drawn upward [43]. This process, well-documented in arid or covered soils, often leads to ion

402 accumulation in the upper soil horizon [44]. The observed increase in exchangeable Ca^{2+} and Mg^{2+} ,
403 without a corresponding rise in total Ca and Mg, supports this interpretation: nutrients are not
404 accumulating at depth, but rather concentrating in the biologically active zone. Interestingly, total
405 Ca in STV2 soil was markedly lower (53 g/kg) than in the control (96 g/kg) (**Table 2**). This suggests
406 that capillary transport may have promoted carbonate solubilization and CO_2 release. Changes in
407 exchangeable and total calcium may be linked to carbonate dissolution processes, but this
408 mechanism requires further verification [45]. This mechanism offers a plausible explanation for the
409 chemical data, though alternative hypotheses remain possible. Previous studies similarly reported
410 that shading and reduced wind speed under PV systems decrease soil evaporation and water loss
411 [13], while vegetative cover further limits water loss [46,47]. Moreover, vegetation under the panels
412 has been shown to lower soil surface temperatures [13]. Although we did not directly measure
413 moisture or temperature, the observed accumulation of C_{org} and nutrients in STV2 reinforces the
414 current understanding that moderated microclimatic conditions play a central role in enhancing soil
415 quality in AV systems [48]. Taken together, these observations suggest that the physico-chemical
416 changes in STV2 soils are not only the result of nutrient inputs or shading, but of dynamic water–
417 solute interactions modulated by vegetation and microclimate beneath the panels.

418 Thus, the improvements described cannot be attributed solely to shading. Rather, they
419 appear to result from the synergistic interaction among panel-induced environmental modification,
420 capillary-driven nutrient redistribution, and the ecological functions of vegetative cover, an
421 interaction intrinsic to the AV system as a whole. The higher ground coverage ratio (STV2) likely
422 enhanced nutrient retention and organic matter accumulation through the combined effects of
423 shading, moisture conservation, and vegetation feedback. These effects likely arise from improved
424 water retention, lower thermal stress, higher organic inputs, and upward nutrient movement,
425 collectively enhancing nutrient cycling and organic matter accumulation.

426 Bacterial diversity declined under STV2, largely due to the dominance of copiotrophic genera
427 such as *Bacillus*, which thrives in nutrient-enriched soils (**Fig 2A-C**). This reduction in alpha diversity
428 appears to be driven mainly by the marked increase in the genus *Bacillus* under STV2, which reduced
429 community evenness. Such nutrient-driven dominance patterns have been widely documented in
430 soil microbiomes, where shifts in resource availability alter both taxonomic composition and
431 functional potential [49]. The effect was more evident in Shannon and Simpson indices (dominance),
432 than in Chao1 (richness). The relative abundances of the ten most common genera (excluding
433 *Bacillus*) remained largely comparable across treatments, indicating that the decrease in diversity
434 stemmed from competitive dominance rather than the disappearance of rare taxa. *Bacillus* is a
435 copiotrophic and fast-growing genus that thrives in nutrient-rich environments [50]. Its proliferation
436 in STV2 soils is therefore consistent with the elevated levels of C_{org} , Olsen P, EC, and N_{tot} detected in
437 this treatment. The combination of enhanced nutrient availability and dense vegetation likely
438 favored opportunistic taxa capable of rapid resource exploitation, reducing overall evenness and
439 thereby lowering Shannon and Simpson diversity. At T2, although *Bacillus* remained more abundant
440 in STV2 compared to STV1 and CI, no significant decrease in alpha diversity was detected according
441 to any of the indices considered (**Fig 2D-F**). This may be due to the concurrent increase in
442 *Blastococcus*, *Microlunatus*, and *Microvirga*, which mitigated the dominance effect by enhancing the
443 community's evenness.

444 Fungal communities showed smaller diversity changes, remaining relatively stable across
445 treatments, consistent with their slower turnover and substrate dependence. This reduction in
446 evenness corresponded with an increased abundance of *Verticillium*, approximately twice that
447 observed in CI and about seven times higher than in STV1. While not all comparisons reached
448 statistical significance, this pattern suggests that fungal communities by larger panels may also
449 respond to nutrient enrichment through selective stimulation of a few opportunistic taxa. At T2, only
450 the Shannon index retained a similar trend (**Fig 2L–N**), possibly due to seasonal changes or shifts in
451 substrate availability.

452 Overall, the panel had a greater impact on ecological indices at T1 than T2, which may be
453 explained by the shorter shadows cast at T2 (summer), resulting in less pronounced microclimatic
454 differences. This temporal variability may reflect a stronger influence of stochastic processes and
455 dispersal dynamics on bacterial than on fungal assemblages [51]. These diversity patterns revealed
456 contrasting ecological behaviors between bacterial and fungal communities in response to AV-
457 induced environmental changes. Bacterial communities shifted markedly across seasons and
458 treatments (**Fig 3A, B**), reflecting rapid responses to environmental fluctuations and nutrient
459 dynamics, whereas fungal communities (**Fig 3C, D**) remained relatively stable, suggesting tighter
460 associations with persistent habitat features such as soil structure and organic matter pools [52-55].
461 This stability aligns with the broader view of fungi as key mediators that integrate biological and
462 physicochemical processes over longer temporal scales [56]. The reduction in microbial diversity
463 under STV2 is consistent with the ecological principle that high resource availability, particularly of
464 nutrients such as C, N, and P, can reduce microbial diversity by promoting competitive exclusion and
465 the dominance of a few fast-growing taxa [57,58].

466 LEfSe analysis revealed distinct microbial taxa significantly enriched in each condition,
467 indicating that AV configurations exert consistent selective pressures on soil microbial communities.
468 Across both bacterial and fungal datasets, STV2 consistently exhibited the highest number of
469 enriched taxa, suggesting a community shaped by strong deterministic selection linked to nutrient
470 redistribution beneath the panels.

471 In STV2 soils, *Bacillus* and *Blastococcus* emerged as recurrent biomarkers at both time points
472 (**Fig 5A, B**). Their prevalence reflects nutrient enrichment and microclimatic buffering under high
473 shade: *Bacillus*, a copiotrophic genus with plant growth-promoting traits [50,59], thrives in resource-
474 rich soils, while *Blastococcus*, typically stress-tolerant, likely benefits from metabolic versatility and
475 possible root-associated interactions [60]. STV1 was characterized by *Lysobacter* at T1 and
476 *Streptomyces* at T2, taxa associated with soil suppressiveness and organic matter turnover [61-63].
477 The alternating occurrence of these genera across seasons and treatments suggests a dynamic
478 response of bacterial communities to shifting resource and microclimatic conditions. Conversely,
479 *Nocardioides*, enriched under CI at T2, typifies adaptation to nutrient-poor, unshaded soils [64].

480 For fungi, significant enrichment occurred mainly at T1 (**Fig 6**). *Fusarium* and *Verticillium*
481 dominated under STV2, consistent with their preference for moist, nutrient-enriched habitats
482 (Klosterman et al., 2009; Hannula et al., 2022; Yan et al., 2023). These genera are common soilborne
483 taxa that can exploit shaded microsites with episodic increases in resource availability, especially
484 nitrogen and labile carbon [68-70]. Their enrichment under STV2 suggests that this configuration
485 fosters ecological conditions favoring the persistence of opportunistic taxa. Under moderate shading

486 (STV1), *Chordomyces* and *Talaromyces* prevailed. *Chordomyces* is generally classified as saprobic and
487 commonly isolated from soils [71]. *Talaromyces*, a well-known ubiquitous genus, is prolific in
488 producing secondary metabolites with broad biological activities and is studied for its biocontrol
489 potential [72,73]. Their presence under STV1 may reflect an environment characterized by moderate
490 shading and nutrient inputs, favoring fungi capable of metabolizing diverse substrates.

491 The Canonical Correspondence Analyses (CCA) revealed distinct patterns in the
492 environmental structuring of bacterial and fungal communities in response to soil physico-chemical
493 and elemental composition. The first canonical axis (CCA1) accounted for the majority of the
494 constrained variance. Accordingly, the interpretation of community-environment relationships was
495 primarily based on the distribution of samples and environmental vectors along CCA1. Sample
496 dispersion patterns varied, indicating that bacterial and fungal communities respond differently to
497 environmental gradients.

498 For bacteria, this suggests that a moderate proportion of community variation is structured
499 by the measured soil variables, indicating that specific environmental gradients play a non-negligible
500 role in shaping bacterial community patterns. This moderate structuring may reflect the ability of
501 specific bacterial taxa to respond to key physico-chemical drivers such as pH, nutrient availability,
502 and element concentrations, despite the overall compositional flexibility and rapid turnover of
503 bacterial communities. Unmeasured factors, such as micro-scale heterogeneity, root exudates, redox
504 conditions, and microbial interactions, may explain the remaining variation [74-78].

505 In contrast, fungal communities were only weakly structured by the same environmental
506 variables, with just 14% of the total inertia constrained by the CCA model. This suggests that
507 unmeasured or more stochastic factors, such as plant host identity, substrate availability, spatial
508 dispersal limitations, or legacy effects, may influence the fungal assemblages in this system. Fungi,
509 particularly mycorrhizal and saprotrophic taxa, are often expected to respond to edaphic gradients
510 [79]; however, in our study, the low explanatory power suggests that such relationships were not
511 captured, potentially due to landscape-level heterogeneity, functional redundancy, or the buffering
512 effect of filamentous growth habits.

513 These results demonstrate that AV management can modify soil nutrient profiles and
514 microbial community structure, even under uniform fertilization and crop management practices.
515 The STV2 configuration was characterized by higher concentrations of C_{org} , N_{tot} , available P, and
516 exchangeable cations, together with the enrichment of numerous trace elements. These changes
517 were accompanied by measurable shifts in microbial diversity and composition, most evident in the
518 bacterial assemblages. Bacterial communities exhibited clear seasonal and treatment-related
519 variability, whereas fungal assemblages remained comparatively stable across conditions and
520 sampling times. This contrast suggests that bacteria respond more rapidly to short-term changes in
521 soil properties, while fungi are influenced by more persistent edaphic factors such as substrate
522 quality and nutrient pools. However, CCA indicated that measured soil parameters explained only
523 part of the observed variation, suggesting that additional unmeasured factors, potentially biological
524 or spatial, contribute to shaping microbial assemblages. Collectively, these findings provide a
525 mechanistic framework for understanding how AV systems shape soil-microbe interactions, setting
526 the stage for broader evaluation across different designs and environments.

Conclusions

Our findings demonstrated that agrivoltaic system design, particularly ground coverage ratio (GCR), has a significant impact on soil biogeochemical properties and microbial community structure. The high-shade configuration (STV2, 41% GCR) enhanced soil fertility by increasing organic carbon, nutrient retention, and exchangeable cations. It also reduced microbial diversity, favoring copiotrophic taxa such as *Bacillus* and *Verticillium*. This may reflect a more selective and stable microenvironment that favors specialized microorganisms, especially fungal communities that showed resistance to seasonal fluctuations. While shifts in soil chemistry and microbial composition were generally aligned, their correspondence weakened at T2, possibly reflecting reduced shading influence. Overall, our results highlight that AV system design not only influences aboveground productivity and energy efficiency, but also regulates key belowground processes. Future research should employ functional metagenomics and trait-based modelling to determine whether AV-induced microbial shifts enhance or hinder ecosystem services such as carbon sequestration and pathogen suppression. Although these findings are specific to wheat-based systems in temperate climates, they underscore the importance of evaluating belowground impacts across diverse crop types and environmental conditions when designing agrivoltaic systems, to ensure both agronomic and ecological sustainability.

Supporting information

Figure S1. Scheme of soil sampling design.

Table S1. Results of two-way PERMANOVA based on Bray-Curtis dissimilarities for bacterial community structure.

Table S2. Results of two-way PERMANOVA based on Bray-Curtis dissimilarities for fungal community structure.

Table S3. Average total abundance of the 10 most abundant bacterial phyla.

Table S4. Average total abundance of the 10 most abundant bacterial genera.

Table S5. Average total abundance of the 10 most abundant fungal phyla.

Table S6. Average total abundance of the 10 most abundant fungal genera.

Table S7. Eigenvalues and explained variance from Canonical Correspondence Analysis (CCA) of soil physico-chemical and ionomic parameters constrained by bacterial profiles.

Table S8. Eigenvalues and explained variance from Canonical Correspondence Analysis (CCA) of soil physico-chemical and ionomic parameters constrained by fungal.

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Author contributions

CC: Investigation, Data curation, Writing – review & editing; FG: Investigation, Writing – original draft; SL: Writing – original draft; MC, DDTF, SR: Formal analysis; ADP, GC, AS: Supervision; AP: Project administration; CM: Project administration; PS: Conceptualization, Funding acquisition, Supervision, Investigation.

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