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Chemical and volatile composition, and microbial communities in edible purple flowers (*Torenia fournieri* F. Lind.) cultivated in different organic systems

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ABSTRACT

Edible flowers have been widely consumed fresh in drinks, salads, desserts and salty dishes. This study evaluated the color parameters, chemical composition (phenolics, sugars, organic acids), volatiles compounds and microbiota (bacterial and fungal communities) in edible purple flowers (*Torenia fournieri* F. Lind.) cultivated in biocompost and traditional organic systems. Torenia flowers cultivated in biocompost had high ($p < 0.05$) contents of anthocyanins (cyanidin 3,5-diglucoside, delphinidin 3-glucoside), flavonols (quercitin 3-glycoside, myricetin and rutin), sugars (rhamnose and glucose), organic acids (citric and succinic), aldehydes (hexanal, *cis*-2-hexenal and *trans*-2-hexenal), and alcohols (*trans*-2-hexenol and 3-ethyl-4-methylpentan-1-ol). Flowers cultivated in biocompost showed higher ($p < 0.05$) abundance *Cyanobacteria* and *Basidiomycota* bacterial and fungal phyla, respectively, than flowers cultivated in traditional system. The high abundance of *Oxyphotobacteria* and *Dothideomycetes* classes, *Acetobacterales* and *Cladosporiales* orders, *Oxyphotobacteriaceae* and *Cladosporiaceae* families, and *Raoultella* and *Cladosporium* genera characterized torenia flowers cultivated in biocompost. The cultivation system influenced the torenia flowers microbiota and composition, primarily due to environmental response and enhanced uptake of nutrients. Our findings indicate that cultivation of torenia using the agro-industrial based-biocompost improves bioactive and volatiles contents in more purple and fruity flavored flowers, rendering flowers more attractive for consumption.

1. Introduction

Edible flowers are a growing trend in the food industry due to consumers' demand for comfort foods, which arose emotions through aromas, formats, flavors, colors, and textures (Barros et al., 2020). Sensory properties and potential health benefits directly influence the decision to ingest edible flowers in salty or sweet food dishes. The awareness of the benefits of bioactive compounds found in edible flowers has further boosted the commercial value of these products (Morais et al., 2020; Skrajda-Brdak, Dąbrowski, & Konopka, 2020). Drying, crystallization and freezing technologies have been used to extend the postharvest shelf life of flowers (Mariutti et al., 2021).

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Although, colorful fresh raw flowers are preferred among chefs and consumers.

Torenia (*Torenia fournieri* F. Lind.) stands out among the edible flowers consumed fresh due to its delicate aspect, velvety texture and slightly sweet flavor (Morais et al., 2020). It is native from Asia and widely cultivated in tropical and subtropical climates (Janarny, Gunathilake, & Ranaweera, 2021). Torenia has purple, violet, pink or white flowers and it is appreciated in salads, savory dishes containing meat and fish, soups, drinks, and desserts (Morais et al., 2020). Purple torenia has caught the scientific community's attention in the last decade because its bioactive compounds (e.g., phenolics, organic acids) present biological activities such as antioxidant, anti-inflammatory, anticarcinogenic (Morais et al., 2020; Skrajda-Brdak, Dąbrowski, & Konopka, 2020).

The cultivation of edible flowers for food purposes is traditionally performed in organic systems. Organic fertilizers are classified according to the raw organic materials in their composition, which are generally rich in slow-releasing organic nitrogen (N). Animal manure is the most used organic fertilizer to provide nutrients such as phosphorus and potassium during flower cultivation (Aiysha & Latif, 2019). A sustainable and low-cost alternative for flower cultivation is biocompost as organic fertilizer. The biocompost is obtained from the aerobic composting of organic residues from agro-industrial waste. Composting is a biological method used to treat agro-industrial organic residues for producing biofertilizers with relatively low air and water pollution (Pergola et al., 2018). Furthermore, the biocompost generated can improve the physicochemical and biological characteristics in the soil, making it suitable for food cultivation (Zhang et al., 2020). Biocompost derived from fruits and vegetable residues decreases environmental problems related to waste management and, depending on residues composition, can serve as a source of phytochemical compounds, carbon, and other nutrients for the cultivation of edible flowers (Ganesh, Sridhar, & Vishali, 2022; Tratsch, Ceretta, Silva, Ferreira, & Brunetto, 2019).

Depending on the cultivation system, flower species produce substances from the primary and secondary metabolism that allow adaptation and survival (Canarini, Kaiser, Merchant, Richter, & Wanek, 2019). Organic acids and sugars are primary metabolites that strongly influence the taste balance and sensorial acceptance of flowers foods by consumers (Fernandes, Ramalhosa, Pereira, Saraiva, & Casal, 2020). Phenolics are secondary metabolites classified according to their structure in phenolic acids, stilbenes and flavonoids (flavonols, flavanones, flavonols and anthocyanins). They impact the color, astringency, and oxidative stability of flowers (Morais et al., 2020). On the other hand, the volatiles emitted by flowers are low molecular weight secondary metabolites represented mainly by terpenes, esters, alcohols, carbonyls and hydrocarbons compounds. Volatile compounds give unique flavor characteristics to each flower, which are essential in food perception by consumers (Najar et al., 2019).

Furthermore, the indigenous microbial communities influence floral metabolites such as emitted volatiles (Fernandes et al., 2019). On the other hand, the metabolites composition defines the visitation of insects, birds, pollinators, which activate the plant's metabolism and at the same time they are vectors of bacteria and fungi contributing with the microbial abundance in flowers (Morris, Frixione, Burkert, Dinsdale, & Vannette, 2020; Gaube, Junker, & Keller, 2021). Bacteria from *Proteobacteria* phylum and fungi from *Ascomycota* and *Basidiomycota* phyla are the main microbial communities in edible flowers, but the microbiome varies depending on the cultivation system (Gaube, Junker, & Keller, 2021). As far as the authors know, no prior studies evaluated the influence of the cultivation system on microbiota and metabolites in edible torenia flowers.

Therefore, the objective of this study was to evaluate the color parameters and primary and secondary metabolites, namely, sugars, organic acids, phenolics and volatiles in torenia flowers cultivated in organic (traditional) and biocompost systems. The bacterial and fungal communities in flowers were evaluated using metabarcoding (16S and 18S rRNA) sequencing. Soil quality parameters in both systems were also determined.

2. Materials and methods

2.1. Cultivation systems and soil chemical characterization

Torenia fournieri F. Lind. (torenia) flowers were cultivated during four weeks (cultivation period for commercial maturity) in a field experiment at Agricultural Supply and Services of Paraíba state (Paraíba, Brazil) following the guidelines of the Brazilian Legislation Decree 52/2021 (Anon, 2021) and Food and Agriculture Organization (FAO, 2018) for organic cultivation.

Four flowerbeds (2 m × 1 m) separated by a distance of 1 m were included in each experiment. Thirty-day seedlings were arranged in double rows with a distance of 30 cm. A 40 cm distance was kept between the rows. The system was maintained under drip irrigation in a black shading screen (50 % UV block).

For traditional organic cultivation, an animal organic fertilizer (manure) certified by the Brazilian Ministry of Agriculture, Livestock and Supply was acquired from a local store. The biocompost was supplied by the Agricultural Supply and Services of Paraíba state. It was prepared through an aerobic composting step with rotation of windrow, carried out for 120 days of maturation at 45 °C, using whole fruits (mango, passion fruit, melon, watermelon, banana, pineapple, papaya and tomato) and vegetables (pepper, eggplant, chayote, potato, pumpkin, kale, chard, lettuce, cauliflower and onion) resulting from food waste in the distribution chain. The organic fertilizer and the biocompost comply with the guidelines for organic production (Anonymouns, 2020; Anonymouns, 2021).

Samples of soil with animal manure and biocompost fertilizers were collected, air-dried on-site and stored in sealed plastic bags. Soil pH was determined with a soil/solution ratio of 1:2 in deionized water. The extraction for analysis of phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg) and aluminum (Al) in soil samples was carried out according to the methodology adopted by Mugo et al. (2020) with minor modifications. Ten mL of Mehlich-1 solution (0.0125 M H_2SO_4 + 0.025 M HCl) were added to 5 g of soil, followed by titration to determine Al, Ca, Mg and optical density reading in a UV–vis spectrophotometer for the determination of P and K (Khadka et al., 2019).

2.2. Color analysis in flowers

The color parameters L* (lightness), a* (redness), b* (blueness), C* (chroma), and h (hue angle) were determined in three different points of ten flowers in each sample using a digital colorimeter (KONICA MINOLTA, Chroma Meter CR-400, Osaka, Japan) following the CIELab scale. (Fernandes et al., 2018).

2.3. Analyses of phenolics, organic acids and sugars in torenia flowers

Phenolics were extracted using methanol and sonication following procedures described by Morais et al. (2020). Flowers samples macerated were mixed with methanol (1:5, w/v), homogenized using a vortex by 2 min and the pH was reduced to 2 by adding 0.1 mol/L HCl. The extracts were centrifuged (4500 × g for 15 min, 25 °C), and the supernatant was filtered through a 0.45 μm membrane (Millipore Co., Bedford, MA). A 20 μL-aliquot was injected into the chromatograph as Padilha et al. (2017) described. Phenolics were separated using a Zorbax C18 pre-column (12.6 × 4.6 mm, 5 μm) and a Zorbax Eclipse Plus RP-C18 column (100 × 4.6 mm, 3.5 μm). The column temperature was maintained constant at 35 °C. Acidified (pH 2) water; phase A) and acidified methanol (phase B) were used as mobile phases. The flow rate was kept at 0.8 mL/min. Data acquisitions from DAD were processed using OpenLAB CDS ChemStation EditionTM software (Agilent

Technologies).

Organic acids and sugars were extracted using 4.5 % metaphosphoric acid (1:10, v/v) according to Lockowandt et al. (2019). The extract obtained was centrifuged at (4000 × g, 15 min, 4 °C) and the supernatant was filtered through a 0.45 μm membrane (Millipore Co., Bedford, MA). The analyses were done using an Agilent Hi-Plex H column (7.7 × 300 mm, 8 μm) and H_2SO_4 4 M in ultrapure water as a mobile phase (flow rate 0.5 mL/min).

Analyses were done using a High-Performance Liquid Chromatography (HPLC) using an Agilent chromatography equipment (model 1260 Infinity LC, Agilent Technologies, USA) coupled to a diode array detector (DAD) and a refractive index detector (DIR). Organic acids were carried out by DAD at 210 nm and sugars by RID. The retention times of peaks (phenolic, sugars and organic acids) were compared with external standards (Sigma Aldrich, St. Louis, USA). The quantification was based on calibration curves ($R^2 \geq 0.998$) following validated methods (Coelho et al., 2018; Padilha et al., 2017). The spectral purity of peaks was checked through the Threshold tool.

2.4. Determination of volatiles in torenia flowers

The volatile fraction was extracted through Headspace solid-phase microextraction (HS-SPME) following procedures previously described by Fernandes et al. (2019), with minor modifications. First, fresh ground flowers (4 g) were introduced in a 20 mL vial and mixed with 5 mL of ultrapure water and 1 μL of internal standard (butyl acetate 33 μg/mL). The vial was immediately sealed with a PTFE/Silicone septum and placed in a bath at 36 °C (mouth temperature) for 60 min to ensure the headspace balance. Then a 50/30 μm divinylbenzene/carboxen/polydimethylsiloxane (DVB/Car/PDMS) fiber was exposed to the sample headspace for 60 min for volatiles sorption. Later, thermal desorption of the volatile compounds and fiber coating reconditioning were performed in the injection port of the chromatography system for 5 min at 230 °C. A blank system containing no flowers was run as a control.

Chromatography analyses were performed according to the method described by Marchioni et al. (2020), with some modifications. An Agilent® Technologies gas chromatograph (7890B model) coupled to a mass spectrometer (5977B model; Little Falls, ME, USA) was used to analyze the volatiles. The fiber was manually exposed into the injection port, operating in splitless mode. Helium (analytical purity of 99.9999 %, White Martins, Pernambuco, Brazil) was used as carrier gas at a flow rate of 1.0 mL/min. The analytes separation was carried out on a VF-5MS (30 m × 0.25 mm; 0.25 μm of thickness film) column. The column oven temperatures were: 50 °C for 1 min; 3 °C/min until 100 °C; 20 °C/min until 250 °C hold for 2 min. The GC/MS interface and ion source temperatures were set at 250 °C and 230 °C, respectively. Mass spectrometry detector was operated in electron ionization mode at 70 eV, and the single quadrupoles mass analyzer scanning from *m/z* 40 to 350 at 4.44 scans/s. The SPME data were acquired and analyzed using Mass Hunter software (Agilent®, Version 10.0, 2008). The linear retention index (LRI) was calculated for each volatile compound using the retention times of a homologous series of C8-C20 *n*-alkanes. The volatile compounds that presented spectral similarity with those of the NIST/EPA/NIH Mass Spectral Database library (Version 2.2 2014) exhibiting the Match coefficients > 600 and RMatch > 700 and similarity with the NIST LRI were considered identified. Volatile amounts were calculated by the ratio of each individual base ion peak area to the area of the internal standard base ion peak and converted to mass equivalents on the basis of the internal standard mass added, expressed in μg/100 g flower.

2.5. 16S rRNA and 18S rRNA metabarcoding sequencing in torenia flowers

For high-throughput sequencing analyses, DNA extraction was performed using a MoBio Power Food DNA isolation kit, Mobio Laboratories Inc., USA, following the manufacturer's procedures and quantification in a fluorimeter. Bacteria were identified by sequencing amplicons of the 16S rRNA V3/V4 region using the 341F (CCTACGGGRSGCAGCAG) (Wang & Qian, 2009) and 806R (GGACTACHVGGGTWTCTAAT) (Caporaso et al., 2012) primers. The amplification of the 18S rRNA region was done using the primers 528F (GCGGTAATTCCAGCTCCAA) and 706R (AATCCRAGAATTTCACCTCT) (Cheung, Au, Chu, Kwan, & Wong, 2010; Mangot et al., 2013). The 16S rRNA and 18S rRNA libraries were sequenced using the MiSeq Sequencing System (Illumina Inc., USA) with the V2 kit, 300 Cycles. Library multiplexing, clustering and sequencing reactions were performed using the Nextera XTindex kit (Illumina, USA) on a MiSeq platform (Canani et al., 2017). The bioinformatics data analysis started with data quality of the initial sequences of 16S rRNA V3/V4 performed in the FASTQC. Subsequently, the low-quality sequences and chimera were removed using Trimmomatic (0.36) and UCHIME2 (Edgar, Haas, Clemente, Quince, & Knight, 2011), respectively. After that, the remaining sequences were used to assignment of the taxonomy in Quantitative Insights into Microbial Ecology (QIIME version 1.9.0) software (Caporaso et al., 2010a, 2010b). The access to the taxonomic annotation was done through the bacterial 16 S rRNA SILVA 132 database (Quast et al., 2013; Yilmaz et al., 2014). Regarding 18S rRNA, the resulting sequences that presented 100 % identity were clustered and used for taxonomic assignment, using a 18S rRNA sequences database (NeoRef, Neoprospecta Microbiome Technologies, Brazil).

2.6. Statistical analysis

Two independent experiments (two biological replicates) were performed. All analyzes were performed in triplicate and results were expressed as mean ± standard deviation. Analysis of variance (ANOVA) was used to determine significant differences at a level of 5 % of significance, followed by Student's *t*-test.

3. Results

3.1. Chemical parameters in soil samples with biocompost and traditional fertilizer

The soil with biocompost system had higher ($p < 0.05$) pH than the soil of the traditional system (7.1 ± 0.02 and 6.6 ± 0.02, respectively). Higher ($p < 0.05$) concentrations of K and Ca (0.19 ± 0.01 and 9.2 ± 0.02 cmolc/dm^3, respectively) were verified in soil with biocompost than in traditional system (0.14 ± 0.02 and 6.3 ± 0.02 cmolc/dm^3, respectively) (Table S1). In contrast, soil of the traditional system presented higher ($p < 0.05$) Mg concentration (1.5 ± 0.02 *vs* 0.8 ± 0.01 cmolc/dm^3, respectively; Table S1) than soil with biocompost. The concentration of P was > 40 mg/dm^3 in soil samples of both systems ($p \geq 0.05$; Table S1). Al was not detected in soil samples, regardless of the system. The evaluated samples with biocompost and traditional systems comply with the quality parameters established by the Normative Instruction 61/2020 of the Brazilian Ministry of Agriculture, Livestock and Supply, which establishes the minimum levels of nutrients for organic production (Anon, 2020).

3.2. Color parameters in flowers

Lightness (L*) was the only color parameters without difference between flowers cultivated in biocompost (39.78 ± 0.12) and traditional system (40.19 ± 1.12; $p \geq 0.05$). Torenia flowers cultivated in biocompost system presented higher chroma (C* 15.07 ± 0.22) and redness (a* 10.70 ± 0.41) than flowers cultivated in traditional system (12.79 ± 1.25 and 7.20 ± 0.50, respectively). In contrast, torenia cultivated in traditional system had higher blueness (b* −8.62 ± 0.24) and hue angle (h: 316.70 ± 0.73) values than flowers cultivated in biocompost (-10.59 ± 0.73 and 311.7 ± 0.40; $p < 0.05$).

3.3. Phenolics, organic acids, sugars in torenia flowers

Anthocyanins and flavonols were the major classes identified in torenia flowers, regardless of the cultivation system. The contents of each phenolic compound in flowers varied ($p < 0.05$) with the cultivation system (Table 1).

Torenia flowers cultivated in biocompost had higher ($p < 0.05$) contents of anthocyanins cyanidin 3,5-diglucoside and delphinidin 3-glucoside (55.09 and 17.69 μg/g, respectively), and flavonols quercitin 3-glycoside, myricetin and rutin (369.68, 310.17 and 6.85 μg/g, respectively). Torenia flowers cultivated in traditional system had higher ($p < 0.05$) contents of anthocyanins malvidin 3,5-diglucoside and pelargonidin 3,5-diglucoside (706.65 and 77.34 μg/g, respectively), and flavonol kaempferol 3-glucoside (547.70 μg/g) (Table 1).

Table 1
Phenolics, sugars, and organic acids in *Torenia fournieri* F. Lind. (torenia) cultivated in different systems.

Phenolics (μg/g)	**Compound**	**Biocompost**	**Traditional**
Anthocyanins	Delphinidin 3-glucoside	17.69 ± 0.46[a]	16.47 ± 0.60[b]
	Cyanidin 3,5-diglucoside	55.09 ± 0.37[a]	50.73 ± 0.21[b]
	Pelargonidin 3,5-diglucoside	54.31 ± 0.10[b]	77.34 ± 0.12[a]
	Malvidin 3,5-diglucoside	619.29 ± 0.26[b]	706.65 ± 0.34[a]
Flavonols	Myricetin	310.17 ± 0.66[a]	241.93 ± 0.59[b]
	Quercitin 3-glucoside	369.68 ± 0.54[a]	318.92 ± 0.21[b]
	Rutin	6.85 ± 0.27[a]	4.84 ± 0.90[b]
	Kaempferol 3-glucoside	370.09 ± 0.42[b]	547.70 ± 0.86[a]
Stilbenes	*cis*-Resveratrol	6.77 ± 0.16[a]	5.67 ± 0.29[b]
	trans-Resveratrol	66.71 ± 0.10[a]	57.35 ± 0.38[b]
Flavanones	Hesperidin	9.53 ± 0.20[b]	11.26 ± 0.41[a]
	Naringenin	3.20 ± 0.26[a]	2.53 ± 0.11[b]
Phenolic acids	Caftaric acid	14.54 ± 0.67 [a]	10.04 ± 0.78[b]
	Chlorogenic acid	39.92 ± 0.19[a]	34.04 ± 0.13[b]
	Caffeic acid	8.35 ± 0.55[a]	6.65 ± 0.21[b]
	ρ-Coumaric acid	3.42 ± 0.59[a]	3.07 ± 0.03[a]
	Gallic acid	0.68 ± 0.02[a]	0.42 ± 0.26[a]
	Syringic acid	4.29 ± 0.14[b]	5.07 ± 0.90[a]
Flavanols	Procyanidin B1	3.65 ± 0.13[a]	3.27 ± 0.24[a]
	Procyanidin B2	8.46 ± 0.16[a]	8.05 ± 0.59[a]
	Epigallocatechin gallate	18.57 ± 0.20[a]	14.17 ± 0.19[b]
	Epicatechin	4.36 ± 0.37[b]	5.09 ± 0.84[a]
	Epicatechin gallate	4.30 ± 0.01[a]	3.48 ± 0.16[b]
	Catechin	9.66 ± 0.18[a]	9.07 ± 0.67[a]
Sugars (mg/g)	Maltose	8.11 ± 0.19[a]	6.18 ± 0.09[b]
	Fructose	87.16 ± 0.10[b]	96.71 ± 0.74[a]
	Glucose	7.39 ± 0.09 [a]	<LOD
	Rhamnose	361.99 ± 0.11[a]	<LOD
Organic acids (mg/g)	Citric acid	23.56 ± 0.70[a]	15.79 ± 0.18[b]
	Acetic acid	2.42 ± 0.11[b]	4.73 ± 0.20[a]
	Succinic acid	8.36 ± 0.38[a]	7.38 ± 0.12[b]
	Formic acid	1.65 ± 0.77[a]	1.15 ± 0.25[a]
	Lactic acid	0.75 ± 0.10 [a]	<LOD

Different superscript lowercase letters in the same row denote difference ($p < 0.05$) among the same compounds or parameters in torenias of cultivates in diferent systems, based on Student's *t*-test. Values are expressed as the mean ± standard deviation. < LOD: below detection limit. LOD values were as follow: caftaric acid 0.09 mg/L, chlorogenic acid 0.11 mg/L, caffeic acid 0.01 mg/L, ρ-coumaric acid 0.10 mg/L, gallic acid 0.12 mg/L, syringic acid 0.08 mg/L, myricetin 0.05 mg/L, quercetin 0.11 mg/L, rutin 0.08 mg/L, kaempferol 0.10 mg/L, procyanidin B1 0.01 mg/L, procyanidin B2 0.04 mg/L, epigallocatechin gallate 0.04 mg/L, epicatechin 0.06 mg/L, epicatechin gallate 0.06 mg/L, catechin 0.06 mg/L, hesperidin 0.12 mg/L, naringenin 0.16 mg/L, *cis*-resveratrol 0.08 mg/L, *trans*-resveratrol 0.04 mg/L, delphinidin 3-glucoside 0.17 mg/L, cyanidin 3,5-diglucoside 0.07 mg/L, pelargonidin 3,5-diglucoside 0.05 mg/L, malvidin 3,5-diglucoside 0.24 mg/L, citric acid 0.021 g/L, acetic acid 0.001 g/L, succinic acid 0.02 g/L, formic acid 0.026 g/L, lactic acid 0.02 g/L, maltose 0.037 g/L, fructose 0.04 g/L, glucose 0.02 g/L and rhamnose 0.04 g/L.

Torenia flowers cultivated in biocompost had higher ($p < 0.05$) contents of stilbenes *cis* and *trans*-resveratrol (6.77 and 66.71 μg/g, respectively), phenolic acids caftaric, caffeic and chlorogenic acids (14.54, 8.35 and 39.92 μg/g, respectively) and of the flavanone naringenin (3.20 μg/g). In contrast, torenia cultivated in traditional system had higher ($p < 0.05$) contents of the flavanone hesperidin (11.26 μg/g) and of syringic acid (5.07 μg/g).

Torenia flowers cultivated in biocompost had higher ($p < 0.05$) contents of flavanols epigallocatechin gallate and epicatechin gallate (18.57 and 4.30 μg/g, respectively), while flowers cultivated in traditional system had higher ($p < 0.05$) contents of the flavanol epicatechin (5.09 μg/g) (Table 1).

Torenia flowers cultivated in biocompost had higher ($p < 0.05$) contents of maltose (8.11 ± 0.19 *vs* 6.18 ± 0.09 mg/g), while flowers cultivated in traditional system had higher ($p < 0.05$) contents of fructose (87.16 ± 0.10 *vs* 96.71 ± 0.74 mg/g) (Table 1). Rhamnose and glucose were detected only in flowers cultivated in biocompost system (Table 1).

Torenia flowers cultivated in biocompost system showed higher ($p < 0.05$) contents of citric (23.56 ± 0.70 *vs* 15.79 ± 0.18 mg/g) and succinic acids (8.36 ± 0.38 *vs* 38 ± 0.12 mg/g). In contrast, flowers cultivated in traditional system had higher ($p < 0.05$) contents of acetic acid (2.42 ± 0.11 *vs* 4.73 ± 0.20 mg/g). Lactic acid was detected only in flowers cultivated in biocompost system (Table 1).

3.4. Volatile composition in torenia flowers

A total of 18 volatile compounds were identified in torenia flowers. Aldehydes and alcohols were the major volatile classes in torenia flowers, regardless of the cultivation system (Table 2).

Torenia cultivated in biocompost showed higher ($p < 0.05$) concentrations of aldehydes hexanal, *cis*-2-hexenal, *trans*-2-hexenal, benzaldehyde (2.37, 32.94, 29.64, 1.36 μg/100 g, respectively) and of alcohols *trans*-2-hexenol and 3-ethyl-4-methylpentan-1-ol (6.48 and 9.91 μg/100 g, respectively). The aldehyde benzeneacetaldehyde and the alcohol 1-hexanol were detected only in flowers cultivated in biocompost system (0.09 and 29.92 μg/100 g, respectively). Terpenes *cis*-2-pentenol and α-terpineol were detected only in torenia flowers cultivated in traditional system (0.21 and 0.07 μg/100 g, respectively) (Table 2).

Torenia flowers cultivated in biocompost had higher ($p < 0.05$) concentrations of ester hexyl acetate and terpene β-cyclocitral (0.09 and 29.92 μg/100 g, respectively). The esters hexyl isovalerate, *cis*-3-Hexenyl 2-methylbutanoate, and the ketone 3-octanone were detected only in torenia flowers cultivated in biocompost system (0.05, 0.03 and 0.12 μg/100 g, respectively). The ester α-terpinyl acetate was detected only in torenia cultivated in the traditional system (Table 2).

3.5. Microbial diversity analysis in torenia flowers

The quality filter of sequences was performed using Trimmomatic (v 0.39) software. A total of 951,427 sequence reads were obtained from all samples from 16S rRNA gene. After quality filtering, 228,643.5 bacterial sequences (an average) were acquired per sample (Table S2). Regarding 18S rRNA gene, a total of 733,421 sequence reads were obtained from all samples. An average of 10,166.75 sequences were acquired per sample after quality filtering (Table S2).

Taxonomic assignment obtained by 16S rRNA genes sequencing analysis showed that the OTUs belonged to three major bacterial phyla in the flowers cultivated in biocompost or traditional system, namely *Proteobacteria* (76.0 and 82.7 % respectively), *Cyanobacteria* (21.0 and 14.3 % respectively) and *Bacteroidetes* (1.10 and 0.30 %, respectively) (Table S3). However, torenia flowers cultivated in biocompost showed higher ($p < 0.05$) abundance of *Cyanobacteria* (21.0 *vs* 14.3 %), and lower abundance of *Proteobacteria* (76.0 *vs* 82.7 %) than flowers cultivated in traditional system (Table S3). On the other hand, the taxonomic

Table 2
Volatile composition in *Torenia fournieri* F. Lind. (torenia) cultivated in different systems.

Class	Compound (μg/100 g)	LRI*	Biocompost	Traditional
Aldehydes	Benzeneacetaldehyde	1042	0.09 ± 0.02 [a]	ND
	Benzaldehyde	958	1.36 ± 0.34[a]	0.68 ± 0.06[b]
	trans-2-Hexenal	851	29.64 ± 0.80[a]	11.75 ± 0.17[b]
	cis-2-Hexenal	847	32.94 ± 0.13[a]	13.75 ± 0.78[b]
	Hexanal	<800	2.37 ± 0.30[a]	1.62 ± 0.05[b]
Alcohols	3-Ethyl-4-methylpentan-1-ol	1057	9.91 ± 0.27[a]	5.08 ± 0.52[b]
	1-Hexanol	865	29.92 ± 0.70[a]	ND
	trans-2-Hexenol	861	6.48 ± 0.19[a]	2.59 ± 0.54[b]
	cis-2-Pentenol	<800	ND	0.21 ± 0.04[a]
Esters	3-Hydroxy-2,2,4-trimethylpentyl 2-methylpropanoate	1385	0.02 ± 0.01[a]	0.01 ± 0.00[a]
	α-Terpinyl acetate	1357	ND	0.11 ± 0.07[a]
	cis-3-Hexenyl 2-methylbutanoate	1317	0.03 ± 0.01[a]	ND
	Hexyl isovalerate	1250.66	0.05 ± 0.02[a]	ND
	Hexyl acetate	1014	0.07 ± 0.00[a]	0.02 ± 0.00[b]
Terpenes	β-Cyclocitral	1226	0.06 ± 0.01[a]	0.02 ± 0.00[b]
	α-Terpineol	1193	ND	0.07 ± 0.04[a]
	β-Linalool	1100	0.09 ± 0.02[a]	0.10 ± 0.04[a]
Ketone	3-Octanone	986	0.12 ± 0.02[a]	ND

* Linear Retention Index. Values are expressed as the mean ± standard deviation. ND: Not Detected. Different superscript capital letters in the same row denote difference ($p < 0.05$) among the same compound in torenias of distinct cultivations, based Student's *t*-test.

assignment by 18S rRNA gene sequencing showed that the three major fungal phyla in flowers cultivated in biocompost or traditional system were *Basidiomycota* (71.44 and 79.69 %, respectively), *Ascomycota* (25.54 and 19.37 % respectively) and *Mucoromycota* (0.05 and 0.004 %, respectively). Only *Mucoromycota* phylum differed ($p < 0.05$) by the cultivation system (Table S3).

In torenia flowers cultivated in biocompost or traditional systems, the majority of OTUs corresponding to bacterial classes were *Gammaproteobacteria* (64.5 and 71.8 %, respectively), *Oxyphotobacteria* (21.0 and 14.4 %, respectively), and *Alphaproteobacteria* (11.4 and 10.9 %, respectively) (Table S4). However, the flowers cultivated in biocompost showed higher abundance ($p < 0.05$) of *Oxyphotobacteria* than flowers from traditional system. Regarding fungal classes, the majority was assigned to torenia from biocompost and traditional systems were *Tremellomycetes* (70.6 and 78.7 %, respectively) and *Dothideomycetes* (20.2 and 14.0 %, respectively). However, *Dothideomycetes* and *Sordariomycetes* showed higher ($p < 0.05$) abundance in flowers cultivated in biocompost (20.2 and 3.1 %, respectively) (Table S4).

At the bacterial order level, in flowers from both biocompost and traditional systems, the majority of OTUs were attributed to *Enterobacteriales* (61.5 and 66.3 %, respectively) (Fig. 1A; Table S5). However, torenia flowers cultivated in biocompost showed higher abundance ($p < 0.05$) of *Acetobacterales* (1.3 *vs* 0.4 %, respectively) and lower abundance ($p < 0.05$) of *Betaproteobacteriales* (0.8 *vs* 1.3 %, respectively) than flowers cultivated in traditional system (Fig. 1A; Table S5). The majority of the fungal order level was assigned to *Tremellales* in torenia cultivated in biocompost or traditional systems (70.5 and 78.7 %, respectively). *Cladosporiales*, *Hypocreales*, *Trichosphaeriales* showed higher abundance ($p < 0.05$) in torenia cultivated in biocompost (14.1, 1.7 and 1.1 % respectively) than in traditional system (9.4, 0.6 and 0.3 % respectively) (Fig. 1B; Table S5).

In both torenia flowers cultivated in biocompost and traditional systems, the dominant bacterial family was *Enterobacteriaceae* (61.5 and 66.3 %, respectively). Torenia cultivated in biocompost showed higher abundance ($p < 0.05$) of *Oxyphotobacteriaceae* and *Acetobacteraceae* (20.7 and 1.3 %, respectively) compared to torenia from traditional system (14.1 and 0.4 %, respectively), while torenia cultivated in traditional system showed higher abundance ($p < 0.05$) of *Burkholderiaceae* (1.3 %) (Fig. 2A; Table S6). The dominant fungal family in torenia cultivated in biocompost or traditional system was *Trimorphomycetaceae* (68.4 and 76.8 %, respectively). Higher abundance ($p < 0.05$) of *Cladosporiaceae*, *Nectriaceae* and *Trichosphaeriaceae* was observed in torenia flowers cultivated in biocompost (14.1 %, 1.7 % and 1.1 %, respectively) than in those from traditional system (9.4 %, 0.6 % and 0.3 %, respectively) (Fig. 2B; Table S6).

In torenia from both cultivation systems, the majority of OTUs corresponded to the bacterial genus *Pantoea* (54.45 *vs* 61.4 %) ($p \geq 0.05$). Torenia cultivated in biocompost showed higher abundance ($p < 0.05$) of *Raoultella* and *Granulibacter* (5.1 and 1.15 %) compared to flowers cultivated in traditional system (2.6 and 0.2 %) (Table 3). *Saitozyma* was the major fungal genus ($p < 0.05$) in both torenia cultivated in biocompost and traditional systems (68.4 % and 76.8 %, respectively) (Table 3). Torenia cultivated in biocompost showed higher abundance ($p < 0.05$) of *Cladosporium*, *Fusarium* and *Nigrospora* (14.1 %, 1.7 % and 1.1 %, respectively) compared to flowers cultivated in traditional system (9.4 %, 0.6 % and 0.3, respectively), while torenia cultivated in traditional system showed high abundance ($p < 0.05$) of *Cryptococcus* (0.2 %) ($p < 0.05$).

The Venn diagrams (Fig. 3) show the distribution of assigned bacterial and fungal genera in torenia flowers cultivated in different systems. A total of 98 bacterial genera were shared between torenia cultivated either in biocompost or traditional system (Fig. 3; Tables S7 and S8). On the other hand, 58 genera were detected only in torenia cultivated in biocompost and 34 genera were detected only in torenia cultivated in traditional system (Fig. 3A; Table S7). Regarding fungal genera, a total of 92 genera were shared by torenia cultivated in both biocompost and traditional system. From the assigned genera, 40 were detected only in torenia cultivated in biocompost and 22 were detected only in torenia cultivated in traditional system (Fig. 3B; Table S8).

4. Discussion

Fertilizers impact the nutrients available and their release in the soil, influencing the nutrients uptake by flowers during cultivation (Bistgani et al., 2018). The composition of biocompost (residues from fruits and vegetables) contributes significantly to increasing the pH value and the K and Ca levels in the soil. Changes in pH influence the nutrient mineralization and availability of the soil, primarily of N and P (Kizito et al., 2019). Ca plays a crucial role in controlling the nutrients adsorption complex, which is important for maintaining soil fertility, while high concentrations of K can decrease Mg levels due to competition for root uptake, explaining the lower values of this mineral in soil with biocompost (Xu et al., 2020). On the other hand, increased K soil levels can stimulate metabolic reactions and increase specific sugars and phenolic compounds (Karimi, 2017; Shen et al., 2018).

Sugars, organic acids and mainly phenolic contents could vary in flowers with the cultivation system. The synthesis of secondary metabolites in edible flowers is modulated by numerous environmental factors (temperature, light intensity, irrigation), cultivation system and plant/microorganism interactions (Pina, Oliveira, Matias & Silva, 2018). Since the flowers received the same irrigation, temperature and light

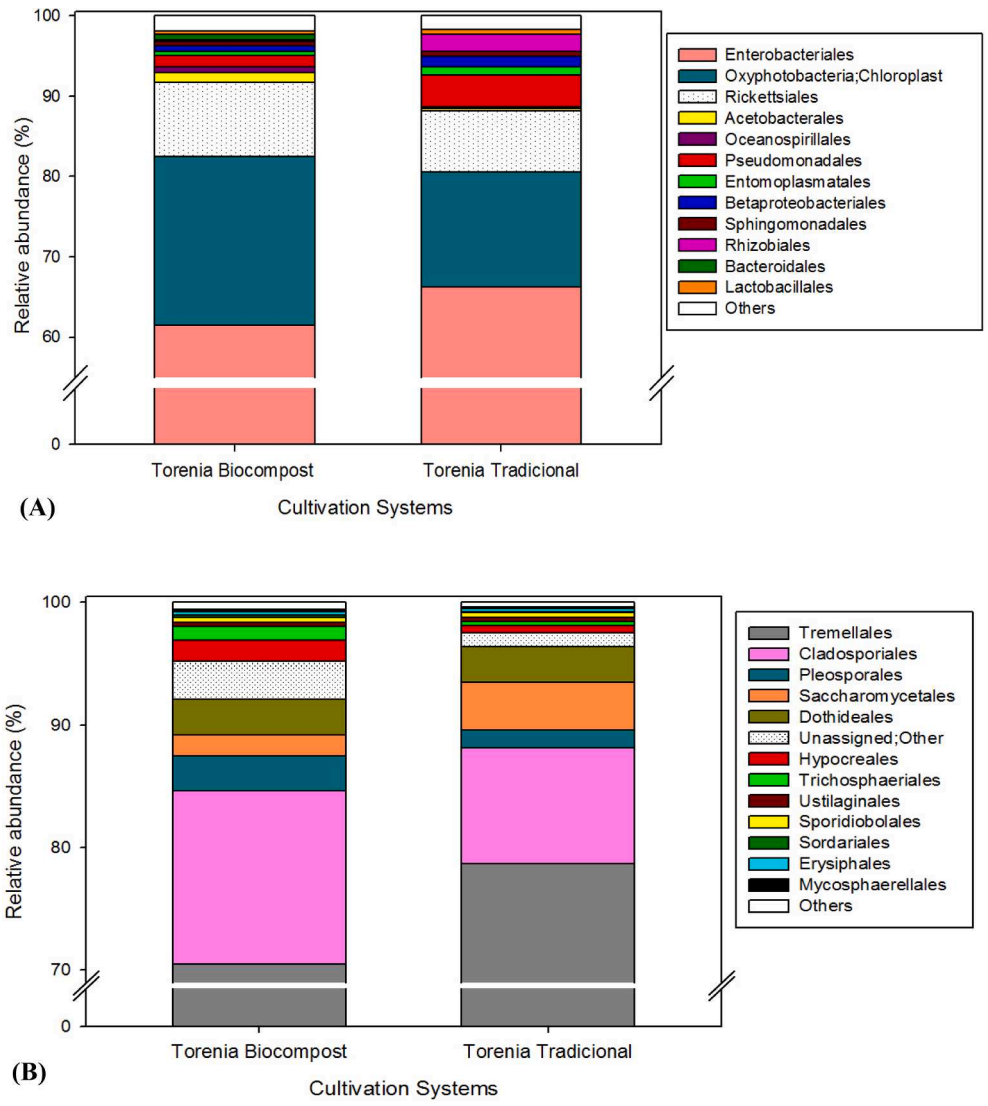

Fig. 1. Relative abundance of microbiota in torenia cultivated in biocompost and traditional system, to the order level, obtained by 16S rRNA (A) and 18 rRNA (B) genes sequencing using OTUs with abundance values above 0.1 %.

conditions in biocompost and traditional systems, the factors influencing the concentrations of phenolic compounds were the source of nutrients and the plant/microorganism interaction (Muscolo et al., 2020). When there is a decrease in N availability for plants (as observed in soils with increased pH), surplus photosynthates are converted into sugars, or metabolism is shifted to the production of secondary metabolites, such as phenolics (Prescott et al., 2020). These phenomena can explain the presence of rhamnose and glucose only in flowers cultivated in biocompost. In addition, potassium is required for the synthesis and translocation of sugars (Karimi, 2017) and the greater availability of potassium in biocompost system may explain in part the higher contents of sugars found in torenia cultivated in biocompost.

Different sugars (and their concentrations) have been identified in edible flowers, including those identified in torenia cultivated in biocompost or traditional system. Fernandes, Ramalhosa, Pereira, Saraiva, & Casal (2020) reported higher sucrose contents in the blue flower *Borago officinalis* L. compared to the pink flower *Camellia japonica* L., which in turns had higher concentrations of glucose and fructose. Both were cultivated in traditional system. Pires, Dias, Barros, & Ferreira (2017) identified sucrose, glucose and fructose as the major sugars in *Centaurea cyanus* L. (blue flower), however the cultivation system was not mentioned in the study.

On the other hand, organic acids are required in the mobilization of inorganic P. Furthermore, the accumulation of organic acids may indicate metabolism, explaining the higher contents of citric and succinic acids (intermediate compounds in several biochemical routes) in torenia cultivated in biocompost (Canarini, Kaiser, Merchant, Richter, & Wanek, 2019). No prior studies have compared the organic acids in flowers cultivated in different organic systems. Citric and succinic acids were reported as the main organic acids found in *Centaurea cyanus* L. (Fernandes et al., 2020), while quinic and malic acids were identified as abundant in petals of purple flowers (*Rosa damascena* 'Alexandria', *R. gallica* 'Francesa' and *R. canina*) (Pires, Dias, Barros, & Ferreira (2017).

Overall, sugars are the most abundant primary metabolites in edible flowers and, together with organic acids, impact the nutritional properties and are reliable indicators of acceptability by consumers since they promote pleasant sensory properties (Fernandes et al., 2020; Marchioni et al., 2020a; Schulz et al., 2021). In this way, flowers cultivated in biocompost are more interesting for food use than those cultivated in the traditional system.

Torenia flowers cultivated in biocompost had higher contents of specific phenolic compounds. Mainly, the anthocyanins delphinidin 3-glucoside and cyanidin 3,5-diglucoside, which are natural pigments

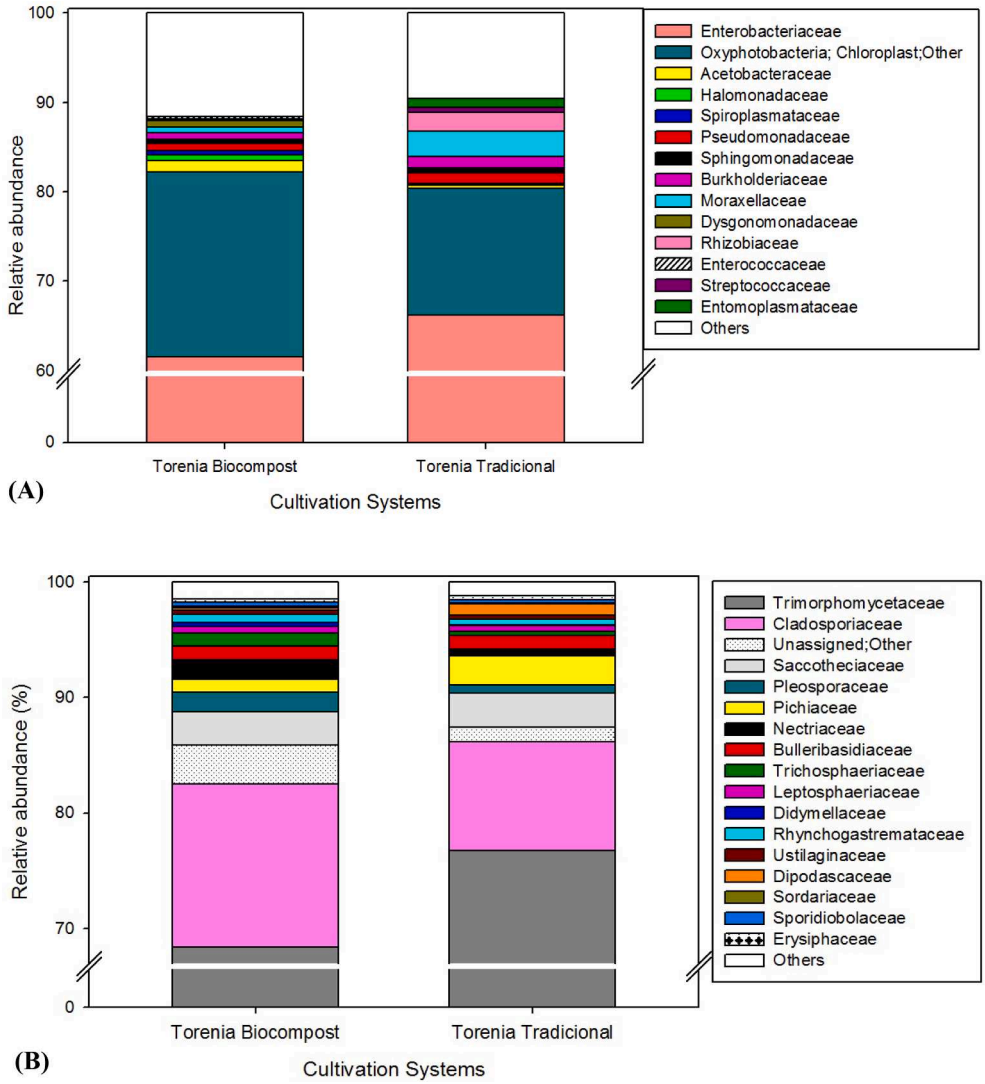

Fig. 2. Relative abundance of microbiota in torenia cultivated in biocompost and traditional system, to the family level, obtained by 16S rRNA (A) and 18 rRNA (B) genes sequencing using OTUs with abundance values above 0.1 %.

that together with other anthocyanins give the petals a bluish-purple hue (Mekapogu et al., 2020; Morais et al., 2020). The anthocyanins found in higher contents in flowers cultivated in biocompost are bioactive compounds related to the antioxidant activity in torenia (Morais et al., 2020). Furthermore, due to the chemical structure, delphinidin 3-glucoside and cyanidin 3,5-diglucoside have stronger antioxidant activity than pelargonidin 3,5-diglucoside and malvidin 3,5-diglucoside, found in higher contents in torenia cultivated in traditional system (Kuskoski, Asuero, García-Parilla, Troncoso, & Fett, 2004). Considering that food sources of antioxidants must be part of the human diet (Pinto et al., 2021), cultivating torenia in biocompost seems an interesting approach to obtaining flowers with high added value. Furthermore, color is one of the most important factors in selecting and using torenia flowers in foods. Torenia cultivated in biocompost had a more intense and darker purple color than the torenia cultivated in the traditional system, which is interesting to catch the consumer's attention. In addition, torenia cultivated in biocompost had higher chroma values, making them usually more attractive to the human eye (Espejel et al., 2019). The influence of specific anthocyanins on the color of petals was previously reported by Park et al. (2015) for *Dendranthema grandiflorum* Ramat cultivated in soil with sand on the surface. The researchers observed increased amounts of anthocyanins in the petals of purple flowers compared to lighter colors.

Similar to phenolics synthesis, the volatiles production in edible flowers is influenced by the release rate of nutrients linked to the biosynthesis of secondary metabolites (Ghanbari, Khajoei-Nejad, Erasmus, & van-Ruth, 2019). Torenia cultivated in biocompost showed a higher concentration of some aldehydes and alcohols (hexenal, *cis*-2-hexenal, *trans*-2-hexenal, benzaldehyde, 2-hexenol and 3-ethyl-4-methylpentan-1-ol), which directly influences the perception of aroma in flowers. The alcohol 1-hexanol has a fruity/green/sweet aroma (Ferrão et al., 2020; Lu et al., 2020), while the *cis*-2- hexenal, *trans*-2-hexenal and hexenal aldehydes present a fresh green/leafy/fruity aroma (Cheng, Peng, & Yuan, 2020). In addition, compounds such as benzaldehyde (almond aroma) can exert a synergistic effect increasing aroma/flavor perception (Mohsen, Younis, & Farag, 2020; Yu et al., 2020). The cultivation of torenia in biocompost allowed an accumulation of volatiles, which confer a more intense fresh fruity aroma and probably distinguish flavor characteristics. It is important to note that aldehydes and alcohols are produced as a defense response to insect visitation and are mainly emitted after mechanical damage (Vincenti et al., 2019). Considering that insecticides were not used in cultivation systems of torenia, the increased concentrations of these volatile compounds in flowers cultivated in biocompost suggest that insects more visited them.

Terpene β-cyclocitral and esters *cis*-3-hexenyl 2-methylbutanoate, hexyl isovalerate and hexyl acetate detected in higher concentrations

Table 3
Relative abundance of genera inferred from 16S rRNA and 18S rRNA gene amplicon sequencing in *Torenia fournieri* F. Lind. (torenia) cultivated in different systems.

Amplicon sequencing	Genera	Biocompost	Traditional
16 S rRNA	*Pantoea*	54.45 ± 4.8 [a]	61.4 ± 1.5 [a]
	Raoultella	5.1 ± 0.7 [a]	2.6 ± 0.2[b]
	Acinetobacter	0.6 ± 0.5 [a]	2.75 ± 1.9 [a]
	Pseudomonas	0.8 ± 0.0 [a]	1.2 ± 0.8 [a]
	Granulibacter	1.15 ± 0.1 [a]	0.2 ± 0.1[b]
	Ochrobactrum	0.0 ± 0.0 [a]	1.4 ± 1.6 [a]
	Rosenbergiella	0.05 ± 0.1 [a]	1.4 ± 1.3 [a]
	Sphingomonas	0.4 ± 0.0 [a]	0.6 ± 0.3 [a]
	Entomoplasma	0.0 ± 0.0 [a]	1.0 ± 1.2 [a]
	Dysgonomonas	0.75 ± 0.8 [a]	0.0 ± 0.0 [a]
	Candidatus Portiera	0.60 ± 0.7 [a]	0.15 ± 0.1 [a]
	Massilia	0.25 ± 0.1 [a]	0.4 ± 0.1 [a]
	Escherichia-Shigella	0.35 +± 0.3 [a]	0.15 ± 0.1 [a]
	Enterobacteriaceae; Other	0.35 ± 0.1 [a]	0.30 ± 0.0 [a]
	Cercis gigantea	0.2 ± 0.0 [a]	0.15 ± 0.1 [a]
	Vagococcus	0.25 ± 0.3 [a]	0.05 ± 0.1 [a]
	Verticia	0.15 ± 0.1 [a]	0.20 ± 0.1 [a]
	Spiroplasma	0.45 ± 0.5 [a]	0.05 ± 0.1 [a]
18S rRNA	*Saitozyma*	68.4 ± 6.5 [a]	76.8 ± 0.6 [a]
	Cladosporium	14.1 ± 2.0 [a]	9.4 ± 2.1[b]
	Aureobasidium	2.9 ± 0.1 [a]	2.9 ± 0.4 [a]
	Hannaella	1.2 ± 0.6 [a]	1.2 ± 0.1 [a]
	Rhodosporidiobolus	0.3 ± 0.1 [a]	0.3 ± 0.1 [a]
	Fusarium	1.7 ± 0.3 [a]	0.6 ± 0.1[b]
	Papiliotrema	0.7 ± 0.3 [a]	0.5 ± 0.1 [a]
	Pichia	1.1 ± 1.2 [a]	2.5 ± 2.7 [a]
	Curvularia	1.2 ± 0.6 [a]	0.4 ± 0.1 [a]
	Nigrospora	1.1 ± 0.3 [a]	0.3 ± 0.0[b]
	Ampelomyces	0.6 ± 0.1 [a]	0.5 ± 0.4 [a]
	Cryptococcus	0.1 ± 0.0[b]	0.2 ± 0.0 [a]
	Galactomyces	0.1 ± 0.1 [a]	0.7 ± 0.8 [a]
	Podosphaera	0.3 ± 0.0 [a]	0.3 ± 0.0 [a]

Data are expressed as means ± SEM. Values in lines followed by different letters indicate significant differences between treatments according to Tukey test ($p < 0.05$).

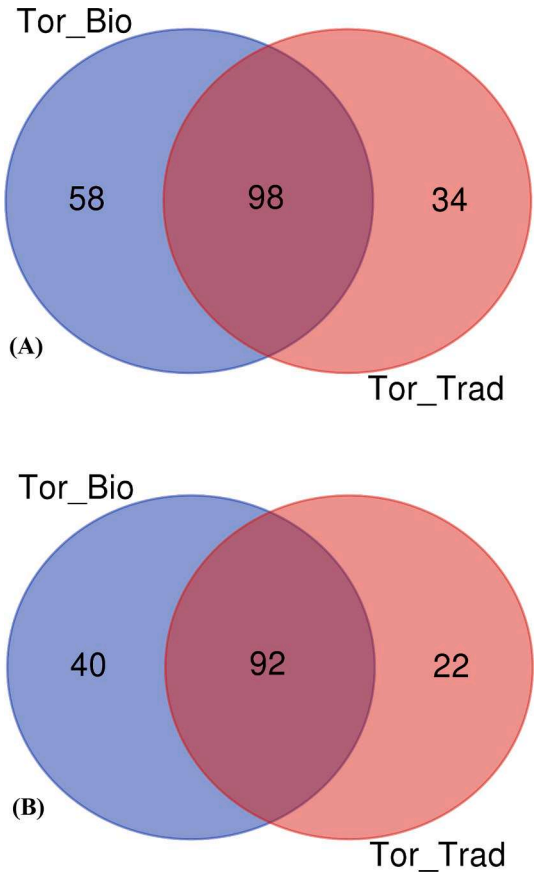

Fig. 3. Venn diagram obtained by 16S rRNA (A) and 18S rRNA (B) genes sequencing using OTUs with abundance values above 0.1 % to the genus level.

in torenia cultivated in biocompost have low threshold perception, exerting important role in the odor of flowers (Villatoro et al., 2008; Sosa-Moguel, Pino, Sauri-Duch, & Cuevas-Glory, 2018; Guo et al., 2021;). These findings suggest that flowers cultivated in biocompost have greater odoriferous potential compared to flowers cultivated in traditional system.

Researchers have reported the major volatile classes in edible flowers, however without consider possible differences associated to the cultivation system. Terpenes were the major compounds in flowers of the *Lamiaceae* family (Ocimeae and Mentheae tribes), cultivated in hochmoor-terflor substrate using nitrophoska fertilizer (Marchioni et al. 2020), but also in *Calendula arvensis* L., *Cosmos bipinnatus* Cav., *Viola tricolor* L. and *Viola* × *wittrockiana* cultivated in traditional organic system (Fernandes et al. 2019). On the other hand, the major class in *Borage officinalis* L. from traditional system comprised esters (Fernandes et al. 2019).

Flowers are substrates suitable for the survival of microorganisms that originate from the soil, water and air, or carried by pollinators and non-pollinators (Wilczyńska, Kukułowicz, & Lewandowska, 2021). Torenia cultivated in traditional system showed a higher abundance of *Proteobacteria*. This phylum has a positive relationship with the increased availability of N and C in the soil (Dai et al., 2018; Zhou, Qiu, Zhang, & Tao, 2019). The animal manure used as fertilizer in the traditional system increases the N and C availability in soil (Aiysha, & Latif, 2019), favoring the *Proteobacteria* development in the soil and, consequently, its abundance in flowers cultivated on it. In previous studies, *Proteobacteria* showed higher abundance in edible flowers of *Tropaeolum majus* L. (Dal'Rio, Mateus, & Seldin, 2022) *Ranunculus acris* L. and *Trifolium pratense* L. (Gaube, Junker, & Keller 2021) from traditional systems.

On the other hand, *Cyanobacteria* phylum, which is associated with N fixation (Bharti et al., 2021), and *Mucoromycota* phylum, which is linked to resistance to biotic/abiotic stresses in plants (Begum et al., 2019), were found in higher abundance in torenia cultivated in biocompost. The gradual release of N, promoted by the high pH in the soil with biocompost and greater susceptibility to insect visits in this system, probably defined the microbial abundance observed at the phyla level.

Torenia flowers cultivated in biocompost showed higher abundance of the bacterial class *Oxyphotobacteria*, and fungal classes *Dothideomycetes* and *Sordariomycetes*. These classes are directly linked to improved soil properties, cycling/fixation of nutrients, and positively impact plant growth (Cano-Díaz et al., 2020; Zhang et al., 2021). Furthermore, at level order flowers cultivated in biocompost showed a higher abundance of *Acetobacterales*, which include bacteria associated with biological fixation of atmospheric nitrogen and synthesis of compounds to inhibit phytopathogenic microorganisms (Curi, Jiménez, & Ibarra, 2019). Despite the scarce reports of the composition at classes level in edible flowers, it is known that *Alphaproteobacteria* and *Betaproteobacteria* have higher abundance in *Tropaeolum majus* L. (Dal'Rio, Mateus, & Seldin, 2022). At level order, *Enterobacteriales*, *Rhodospirillales* and *Lactobacillales* orders were found in higher abundances in flowers of *Ranunculus acris* L. and *Trifolium pratense* L. (Gaube, Junker, & Keller, 2021). However, the cultivation system was not considered as an influencing factor of the microbial composition in the cited studies.

Cladosporiales, *Hypocreales* and *Trichosphaeriales* orders were also found in higher abundance in flowers cultivated in biocompost. They comprise endophytic fungi acting in symbiosis with flowers, increasing their resistance to diseases such as black rot (Venkateswarulu et al., 2018). On the other hand, *Betaproteobacteriales*, which are related to the

production of vitamins and phytohormones in plants (Wang, & Sugiyama, 2020) were more abundant in flowers cultivated in traditional system.

Torenia cultivated in biocompost showed a greater relative abundance of *Oxyphotobacteriaceae* and *Acetobacteraceae*. These bacterial families are associated with nutrient fixation and inhibition of phytopathogenic microorganisms in flowers (Cano-Díaz et al., 2020; Curi, Jiménez, & Ibarra, 2019; Zhang et al., 2021). In addition, the fungal families *Cladosporiaceae*, *Nectriaceae* and *Trichosphaeriaceae*, which are endophytes known by the production of phytohormones against pathogens and environmental stress (Bhavana, Prakash, & Nalini, 2020; Dellagi, Quillere, & Hirel, 2020) were also more abundant in torenia cultivated in biocompost. On the other hand, *Burkholderiaceae*, a bacterial family associated with increased availability of phosphorus (P) and biological control of plant diseases was abundant in torenias cultivated in traditional systems (Madhaiyan et al., 2020; Okrasińska et al., 2021).

Pantoea was the major genus, regardless the cultivation system. This genus was previously reported as the most abundant in flowers of *Ranunculus acris* L. and *Trifolium pratense* L. (Gaube, Junker, & Keller, 2021) and it has been associated to growth- promoting potential. *Raoultella* and *Granulibacter* were in greater abundance in torenia cultivated in biocompost. These genera are related to calcium phosphate solubilization and biological nitrogen fixation (Silva et al., 2021), possibly indicating lower nitrogen bioavailability in the system with biocompost. Furthermore, according Ven diagrams *Providencia* and *Achromobacter,* and *Comamonas*, were present only in torenia cultivated in biocompost. *Providencia* and *Achromobacter* are associated with promoting plant growth through phosphorus absorption (Nascimento, Glick, & Rossi, 2021; Shilev, 2020), and *Comamonas* is related to biological control against plant disease (Berg, Kusstatscher, Abdelfattah, Cernava, & Smalla, 2021). On the other hand, *Paenochrobactrum*, *Aureimonas* and *Mesoplasma* (Zhong et al., 2020) were present only in torenia cultivated in traditional system. These genera are associated with the animal manure composting process. Together, these results suggest that flowers cultivated in biocompost had a microbiota related to environmental defense and enhanced use of soil nutrients.

It is important to mention the lack of identification of foodborne bacteria genera since torenia flowers are primarily consumed fresh due to their fragility.

5. Conclusions

The cultivation system influences the chemical composition and the microbiota in torenia flowers. Torenia cultivated in biocompost produced with fruits and vegetable residues showed higher concentrations of sugars, organic acids and phenolics, particularly anthocyanins delphinidin 3-glucoside and cyanidin 3,5-diglucoside, resulting in purpler flowers. Furthermore, torenia cultivated in biocompost showed higher concentrations of aldehydes and alcohols (hexanal, *cis*-2-hexenal, *trans*-2-hexenal, benzaldehyde, 2-hexenol and 3-ethyl-4-methylpentan-1-ol) with fresh and fruity aroma, associated with stress response. Torenia cultivated in biocompost also showed greater abundance of genera related to enhanced uptake of soil nutrients and environmental defense (*Raoultella, Granulibacter, Providencia* and *Achromobacter*). Foodborne pathogens were not identified among the bacterial and fungal communities evaluated. Our findings indicate that cultivating torenia in biocompost contributes to improving the concentration of some bioactive compounds and volatiles in torenia flowers, making them more attractive for consumers.

Declaration of Competing Interest

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

Data availability

Data will be made available on request.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.foodres.2022.111973.

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