Microbial terroir of Brazilian Coffea canephora: regional differentiation of yeasts and impacts on beverage quality

Joana Scarparo Novello
Federal Institute of Education, Science and Technology of Espírito Santo, Venda Nova do Imigrante
Tomás Gomes Reis Veloso
Federal University of Viçosa
Gracieli Lorenzoni Marotto
Federal Institute of Education, Science and Technology of Espírito Santo, Venda Nova do Imigrante
Marliane de Cássia Soares da Silva
Federal University of Viçosa
Taís Rizzo Moreira
Instituto Nacional da Mata Atlântica (INMA)
José Maria Rodrigues da Luz
Federal University of Viçosa
Enrique Anastacio Alves
Empresa Brasileira de Pesquisa Agropecuária – EMBRAPA Rondônia
Aldemar Polonini Moreli
Federal Institute of Education, Science and Technology of Espírito Santo, Venda Nova do Imigrante
Willian dos Santos Gomes
Federal Institute of Education, Science and Technology of Espírito Santo, Venda Nova do Imigrante
Lucas Louzada Pereira
lucaslozada@hotmail.com

Federal Institute of Education, Science and Technology of Espírito Santo, Venda Nova do Imigrante

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Abstract

Microbial communities present on *Coffea canephora* fruits play a crucial role in the spontaneous fermentation process, directly influencing the sensory characteristics of the final beverage. This study aimed to characterize the yeast communities associated with *C. canephora* fruits in different coffee-producing regions of Brazil and to evaluate their impact on coffee quality. Samples were collected from seven locations in the states of Espírito Santo, Bahia, and Rondônia, representing important production regions. A total of 35 fruit samples were analyzed through DNA extraction, PCR amplification, and sequencing to identify Amplicon Sequence Variants (ASVs). The results revealed significant regional differences in yeast diversity and taxonomic composition. Espírito Santo and Bahia exhibited greater microbial diversity and taxonomic balance, whereas Rondônia showed a more specialized microbiota due to its more acidic and lower-fertility soils. The main yeast genera identified included *Hannaella*, *Papiliotrema*, *Candida*, *Hanseniaspora*, and *Saccharomyces*, with some species known for their biotechnological potential in controlled fermentations. Beta diversity analysis identified three distinct microbial clusters, influenced by environmental variables such as temperature, precipitation, and soil properties. Sensory evaluation of the coffees showed that regions with greater microbial evenness exhibited superior beverage quality, particularly in the attributes of acidity, balance, and sweetness. These findings highlight the influence of yeasts on the quality of *C. canephora* coffee and the potential of specific microbial strains for use as starter cultures in controlled fermentations. This study contributes to a better understanding of the microbial ecology of *C. canephora* fruits and provides a basis for improving fermentation processes, enhancing coffee quality, and promoting sustainable agricultural practices in Brazilian coffee production.

Introduction

Coffee is one of the most economically and socially relevant agricultural crops worldwide, with Brazil being the largest global producer and exporter of the beverage (ICO, 2024). *Coffea canephora*, a species of great importance in the country, has gained increasing recognition due to its high productivity, resistance to pests and diseases, and its strategic role in blend composition and the production of specialty coffees (PARTELLI; CAMPANHARO, 2020).

Despite the growing prominence of this species, scientific research related to the beverage quality of *C. canephora* remains more limited compared to *Coffea arabica*, particularly regarding the microbiological factors involved in fermentation and the development of sensory compounds.

The microbiota present on coffee fruits performs important functions during spontaneous fermentation, contributing to biochemical transformations that directly influence the aromatic profile and flavor of the beverage (SIMMER et al., 2022). The environment shapes the microbiome, directly impacting the final coffee quality. Microbial diversity and interactions are determined by the environmental conditions under which the crops are cultivated, which are reflected in the sensory characteristics of the beverage (VELOSO et al., 2020).

Microorganisms present on coffee fruits, such as lactic acid bacteria (LAB), play an essential role in the control, reproducibility, and quality of processing. Their metabolism of carbohydrates, citrate, and amino acids aids in fruit demucilagination through pulp acidification, in addition to producing metabolites that enrich coffee flavor, highlighting the relevance of microbiota in defining the beverage's sensory profile (PEREIRA et al., 2020). Yeasts stand out for their ability to metabolize sugars and generate metabolites that impact coffee sensory quality (BRESSANI et al., 2021; SIMMER et al., 2022).

Yeast strains *P. fermentans* YC5.2 and *Saccharomyces* YC9.15 show strong potential as starter cultures in wet coffee processing, helping to control and standardize fermentation while producing coffees with new and desirable flavor profiles (PEREIRA et al., 2014). Sensory analysis revealed that these cultures positively influenced beverage flavor, with the highest scores observed for fruity, buttery, and fermented aroma attributes. This demonstrates the role of yeasts in improving coffee quality through the production of specific volatile compounds.

The isolation and identification of yeasts for the development of starter cultures in coffee fermentation are essential processes that should be continuously investigated (HAILE; KANG, 2019b). Likewise, the use of starter cultures has proven to be a viable strategy for producing high-quality coffees with unique flavors, thereby adding value to the product (MARTINS et al., 2019). This approach, combined with the use of specific yeasts, may further enhance flavor diversity and complexity in coffee, underscoring the importance of continued research in this area.

Studies in *C. arabica* have demonstrated that microbiota significantly influence the final beverage quality (PEREIRA et al., 2022; VELOSO et al., 2020); however, there remains a substantial lack of information regarding yeast diversity and their role in *C. canephora*, especially across different Brazilian terroirs.

Therefore, this study aimed to characterize the yeast community associated with *C. canephora* fruits from different coffee-producing regions of Brazil. By identifying and understanding the fungal microbiota present on the fruits of this species, this work seeks to address the current knowledge gap and provide a foundation for developing new approaches in the processing and valorization of Brazilian *C. canephora* coffee.

The characterization of these yeasts may contribute to the selection of microbial cultures with beneficial potential, enabling the improvement of fermentation processes and the production of coffees with differentiated sensory profiles, thereby adding value to the final product and strengthening its competitiveness in the international market.

Materials and methods

Study area location and sampling procedure

The study of yeasts associated with *Coffea canephora* fruits was conducted on seven farms located in three states: Espírito Santo, Bahia, and Rondônia. The coding of the locations is presented in Table 1.

Table 1
Sampling locations of *Coffea canephora* fruit samples included in this study.

Code	Location	Brazilian State
AC	Afonso Cláudio	Espírito Santo
CC	Conceição do Castelo	Espírito Santo
SDN	São Domingos do Norte	Espírito Santo
SGP	São Gabriel da Palha	Espírito Santo
JM	Jerônimo Monteiro	Espírito Santo
TF	Teixeira de Freitas	Bahia
CA	Cacoal	Rondônia

Within each field, three random and spatially separated points were selected. At each point, three coffee plants were chosen, from which three composite fruit samples were collected. The fruits were harvested from three different portions of the plant stem: lower (skirt), middle, and upper (near the canopy). Thus, each composite sample consisted of ten fruits obtained from the three selected plants, totaling 30 fruits per point (Fig. 10).

For microbiological analyses, all samples were placed in plastic bags and stored on ice until transported to the laboratory, where they were processed and/or maintained at − 20°C for proper storage.

Sample preparation for sensory analysis

Coffees subjected to the natural treatment underwent drying on a suspended and covered patio (African Bed – elevated drying system). Drying was carried out under sunlight for a period of 15 to 18 days, using a suspended structure covered with plastic. During this period, the average recorded temperature was 19.54°C, with daytime peaks of up to 45.72°C and nighttime minima of 9.07°C. Temperature monitoring was performed using an Arduino Uno R3 system equipped with an HC-06 RS232 Bluetooth module, a DHT22 AM2302 humidity and temperature sensor, and an SD card module.

For sample roasting, a Probatino roaster (Probat©, Illinois, USA) was used, along with an Agtron-SCAA disk set, at a temperature of 170°C. The roast level was determined according to the color standards established by disks #65 and #55 for specialty coffees (SCAA, 2013). Roasting was performed 24 hours prior to sensory analysis, and grinding was carried out after an 8-hour resting period. All samples were roasted within a time range of 9 to 10 minutes.

Sensory analysis

After roasting and cooling, the samples remained sealed, following the sensory analysis methodology established by the Specialty Coffee Association of America (SCAA, 2013). Coffee samples were ground using a Bunn© G3 electric grinder (Illinois, USA) to a medium–coarse particle size.

Each coffee lot was evaluated using five cups, adopting the ideal concentration of 8.25 g of ground coffee per 150 mL of water, according to the midpoint of the ideal balance chart for achieving the “Golden Cup” (SCAA). The water infusion temperature ranged from 92 to 95°C. Q-Graders began the evaluations when the cup temperature reached 55°C, waiting 4 minutes after infusion before tasting.

The sensory quality of the coffee was evaluated using the Uganda Coffee Development Authority (UCDA) Sensory Analysis Protocol, with six Q-Graders. The ideal number of Q-Graders in a sensory panel was proposed by Pereira et al. (2017). Beverage quality, as assessed by the UCDA protocol, is expressed on a 100-point scale. The evaluation form allows for the analysis of ten sensory attributes: fragrance/aroma, uniformity, clean cup, sweetness, flavor, acidity, body, aftertaste, balance, and overall impression. The final score corresponded to the sum of all sensory attribute scores.

The sensory analysis was approved by the institution's ethical review board, under the number of Presentation Certificate for Ethical Review: 31567320.2.0000.5072.

All analyses were performed using the easyanova package (ARNHOLD et al., 2013) available in R software (R Core Team, 2024).

DNA Extraction, PCR, and Sequencing

Yeast species identification was performed based on the Internal Transcribed Spacer 1 (ITS1) region located within the ribosomal RNA gene cluster (18S and 5.8S) of yeasts. For this purpose, approximately five fruits randomly selected from the composite sample described in Fig. 1 were cut into small pieces using a scalpel and macerated in liquid nitrogen until a homogeneous powder was obtained. About 250 mg of this homogenized powder was used to extract genomic DNA from the yeast community present on the fruits using the NucleoSpin Soil® kit (Macherey-Nagel).

To specifically amplify the fungal ITS1 region described above, the primer pair ITS1F (5’-CTTGGTCATTTAGAGGAAGTAA-3’) and ITS2 (5’-GCTGCGTTCTTCATCGATGC-3’) (Gardes and Bruns, 1993) was used. The amplification product of each sample was labeled with specific sequences (barcodes) and subjected to a new amplification using a PCR master mix (Phusion® High-Fidelity PCR Master Mix; New England Biolabs). Since the size of the ITS1 region is variable, PCR products were separated by electrophoresis on a 2% agarose gel stained with SYBR Green, from which bands ranging from 400 to 450 bp were selected for purification using the Qiagen Gel Extraction Kit (Qiagen, Germany) and subsequently pooled in equimolar amounts for sequencing on the Illumina NovaSeq 6000 platform.

Bioinformatics Analyses

Reads from the fungal ITS1 region had adapters and barcodes removed, and the remaining fragments were subjected to quality control by eliminating low-quality sequences, chimeras, and singletons (sequences present only once in the sample). The remaining high-quality sequences were processed using the Divisive Amplicon Denoising Algorithm (DADA2; CALLAHAN et al., 2016) to determine Amplicon Sequence Variants (ASVs), which were annotated using fungal taxonomy databases (UNITE; NILSSON et al., 2018).

Subsequently, the FUNGuild software (NGUYEN et al., 2016) was used to select only fungi exhibiting yeast-like growth habits. The names of each taxon were manually curated using a curated fungal species database (MycoBank). All subsequent analyses (microbial diversity, relative abundance of microorganisms, correlation analyses, etc.) were performed in R software (R Core Team, 2020).

Results

Sensory quality assessment of coffees

The sensory analysis of coffees collected from the seven farms evaluated in this study revealed significant results. Coffees from Cacoal (CA), Jerônimo Monteiro (JM), São Gabriel da Palha (SGP), and Afonso Cláudio (AC) stood out, achieving the highest final scores, all above 80 points, which classifies them as high-quality coffees within the “Specialty Coffee” category (Fig. 2).

Assessment of the diversity of yeasts present in C. canephora

A total of 268 yeast species were identified (Supplementary Table 1). Figure 3 illustrates the variation in yeast community composition among the different locations. Beta diversity analysis revealed that yeast community profiles differed among the farms, with Cacoal (CA) showing the most distinct community compared to the others.

In addition to beta diversity, alpha diversity analysis showed that AC and CA exhibited the highest evenness and diversity values, indicating that coffee plants in these locations harbor a more balanced distribution of species. Thus, each species likely has greater representation in terms of relative population abundance. This difference is statistically significant, as indicated by the letters associated in Fig. 3B. In contrast, SGP showed the lowest diversity, indicating dominance by a few abundant species.

These results suggest that different locations harbor distinct fungal community profiles, reflecting the environmental conditions and specific characteristics of each region.

Taxonomic Composition of Yeasts

Of the 268 yeast species identified, 173 (65%) belonged to the Basidiomycota group, while the remaining 35% were Ascomycota. This greater richness of basidiomycetes was reflected in the highlighting of the 15 most abundant species in Fig. 4.

These 15 species include 12 basidiomycete species represented by the genera *Hannaella*, *Papiliotrema*, *Kockovaella*, and *Malassezia*, in addition to three ascomycete species belonging to the genera *Candida*, *Aureobasidium*, and *Hanseniaspora*. The most representative species associated with *Coffea canephora* fruits was *Hannaella luteola*, followed by *Papiliotrema tapputi*.

Figure 5 presents the abundance of different yeasts in coffee fruit samples. The ten most abundant yeasts in *Coffea canephora* fruits were: *Hannaella luteola*, *Candida vaughaniae*, *Papiliotrema tapputi*, *Kockovaella* sp. (unknown ASV 2), *Hannaella sinensis*, *Papiliotrema perniciosa*, *Papiliotrema flavescens*, *Hannaella oryzae*, *Malassezia* sp. (unknown ASV 2), and *Hannaella phyllophila*. It is noteworthy that among the ten most abundant species, only one is an ascomycete (*Candida vaughaniae*).

The CA locality stood out for its unique composition, with the presence of seven exclusive species in the fruits: *Hanseniaspora pseudoguilliermondii*, *Hanseniaspora meyeri*, *Slooffia cresolica*, *Hanseniaspora uvarum*, *Hanseniaspora guilliermondii*, *Phialophora oxyspora*, and *Saccharomyces cerevisiae*. In contrast to the previously observed pattern, most of these species are ascomycetes (six out of seven species).

Influence of yeast diversity on the sensory attributes of coffee

The analysis of relationships between yeast community metrics (richness, evenness, and diversity) and coffee sensory attributes (Fig. 6) indicated that yeast richness was not correlated with sensory characteristics, with most correlation coefficients equal to or lower than 0.30.

In contrast, yeast evenness showed moderate and statistically significant correlations with acidity, balance, flavor, and sweetness, suggesting that a more homogeneous distribution of species may be associated with improvements in these attributes. Yeast diversity exhibited the strongest correlations, particularly for acidity ($r^2 = 0.50$), flavor ($r^2 = 0.54$), and sweetness ($r^2 = 0.52$).

These results suggest that the number of species may not be the primary factor determining higher sensory quality, but rather an appropriate balance among them, as reflected by diversity values.

Discussion

Microbial Diversity

Beta diversity analysis revealed that the microbial communities present on *C. canephora* fruits differ according to farm location, with the most distinct community observed in CA. These differences may be attributed to specific environmental factors in each region, such as altitude, temperature, and agricultural practices, which influence the microbiota present on coffee fruits (VELOSO et al., 2020). Previous studies have shown that distinct environmental conditions can shape microbial composition in coffee fruits, directly affecting the final beverage quality (VALE, 2009).

In the analysis of yeast community metrics (richness, evenness, and diversity), the AC and CA locations exhibited greater diversity of yeast-like fungi (Fig. 3B), whereas the lowest diversity was observed in SG. Species richness is an important indicator of the health and stability of a microbial community (ZHOU et al., 2014), suggesting that management practices and climatic conditions may be negatively influencing the health of the fruit microbiota.

The CA and AC locations showed the highest evenness values, indicating a more balanced distribution among species. Evenness reflects how uniformly species are distributed within a community, while diversity accounts for both richness and evenness (MAGURRAN, 2004). High values of both indices suggest more stable and resilient microbial ecosystems capable of performing essential ecological functions. Studies indicate that microbial diversity is associated with ecosystem stability and resilience (GIBBONS; GILBERT, 2015). Greater evenness within microbial communities enhances coexistence and stability (MAGURRAN, 2004).

Taxonomic composition and abundance of yeasts in the fruits of C. canephora.

Recent studies evaluating fungal composition in *C. canephora* samples have reported a greater abundance of ascomycetes compared to basidiomycetes (GOMES et al., 2024; VELOSO et al., 2023). However, in the present study, which assessed only fungi with yeast-like growth habits, the opposite pattern was observed, with basidiomycetes predominating, while a higher presence of ascomycetes was recorded only in the CA locality. Among the ten most frequently detected species in *C. canephora*, the genera *Hannaella* spp. and *Papiliotrema* spp. exhibited the highest number of species associated with the fruits. Since yeast-like fungi are generally the primary contributors to the coffee fermentation process, this work suggests that studies should place greater emphasis on this group rather than on ascomycetes, which are more commonly explored due to the commercial relevance of many species within that group.

In addition, species of *Hannaella* spp. have demonstrated the ability to ferment various sugars, including grape must, producing ethanol and glycerol at desirable levels (MANČIĆ et al., 2021). This characteristic makes them promising as fermentative agents, as glycerol positively influences the sensory perception of coffee. Its viscosity contributes to a fuller body sensation, making the beverage more rounded and pleasant on the palate (BLOK et al., 2020). Furthermore, glycerol acts as a precursor in Maillard reactions, promoting the formation of complex aromatic compounds that enrich coffee flavor (SMARRITO-MENOZZI et al., 2013).

Some studies on *Papiliotrema* spp. indicate that species within this genus may be used as plant growth promoters (LIU et al., 2024), highlighting the need for further research on the application of this yeast in coffee cultivation. However, it is known that, as oleaginous yeasts, species of this genus are capable of accumulating significant amounts of lipids, which may directly influence the final quality of the coffee beverage. This is because lipids play an important role in aroma formation during the roasting process, as well as in their composition and oxidative reactions, which contribute to the development of characteristic flavors (VIEIRA et al., 2020; SPEER & KÖLLING-SPEER, 2019).

Agnoletti et al. (2023), in a study on *C. canephora* from Espírito Santo and Rondônia, highlighted how complex interactions between agricultural and environmental factors result in coffees with chemical and sensory characteristics unique to each terroir. This may indicate that such interactions also contribute to the distinct microbiota found in fruit samples from Rondônia (CA), suggesting the need for more in-depth studies on these factors.

The genus found in greatest abundance in the CA locality was *Hanseniaspora* spp., encompassing the species *Hanseniaspora pseudoguilliermondii*, *Hanseniaspora meyeri*, *Hanseniaspora uvarum*, and *Hanseniaspora guilliermondii*.

Studies on yeasts of the genus *Hanseniaspora* spp. demonstrate that, although they are not the primary ethanol producers, they contribute to the formation of aromatic compounds such as esters, aldehydes, and alcohols, which enrich the aroma and flavor of fermented beverages (JOLLY et al., 2014). In wine fermentation, for example, species such as *Hanseniaspora uvarum*, *Hanseniaspora meyeri*, and *Hanseniaspora opuntiae* play important roles in the early stages of fermentation, where they produce aromatic compounds that enhance the flavor profile and are associated with the production of compounds that increase the aromatic complexity of the final product (WYK et al., 2023; MARTÍN et al., 2018; JOLLY et al., 2014).

Among these species, *Hanseniaspora pseudoguilliermondii* is a non-conventional yeast that stands out in fermentation, particularly for improving food flavor. In cider co-fermentations, it demonstrated high production of volatile compounds, enhancing aroma and reducing alcohol content due to greater sugar consumption (SOLA et al., 2024). Although there are no specific studies on its use in coffee fermentation, it is plausible that its application could result in a beverage with more complex and pleasant aromatic notes. Furthermore, research on coffee fermentation indicates that the introduction of non-conventional yeasts can modulate the chemical and sensory profile of the beverage, suggesting potential application of *H. pseudoguilliermondii* in this context (SILVA et al., 2020).

Another species found exclusively in CA fruits was *Saccharomyces cerevisiae*. Numerous studies have explored the metabolic and fermentative potential of this yeast, considering it an important microorganism in coffee processing. Gomes et al. (2024) highlighted the ability of *S. cerevisiae* to metabolize sugars present in the mucilage of the bean, contributing to the formation of volatile compounds that enhance coffee aroma and flavor. Among these compounds are acetaldehyde, which imparts a “fruity” note; decanal, associated with “peel, citrus, floral” sensations; furfural, responsible for “almond, sweet” notes; and benzaldehyde, perceived as “fruity, cherry” (PEREIRA et al., 2014; PEREIRA et al., 2020; RIBEIRO et al., 2017; SILVA et al., 2013; YANG et al., 2016; LEE et al., 2017; GROOT; DE BONT, 1998; OTT et al., 2000).

Moreover, the use of this yeast in controlled fermentations can ensure greater standardization of coffee quality, reducing undesirable variations and preventing contamination by unwanted microorganisms (PEREIRA et al., 2020; EVANGELISTA et al., 2015). Thus, the presence of *S. cerevisiae* in indigenous fruit

microbiota may indicate improved final product quality and can be exploited in induced or spontaneous fermentations.

Using *S. cerevisiae*, *Candida parapsilosis*, and *Torulaspora delbrueckii* as starter cultures in the fermentation of Catuai Amarelo coffee, all coffee lots achieved scores above 80 according to the SCAA protocol, indicating excellent quality (MARTINEZ et al., 2017). *S. cerevisiae* also demonstrated the ability to modify flavor, enhancing quality and increasing the final score of Catuai Vermelho coffee (MARTINEZ et al., 2020).

Beyond the effects provided by individual strains, the strategic combination of different bacterial and yeast strains may result in synergistic effects, amplifying strain-specific modulation characteristics and improving the final coffee flavor (WANG et al., 2020). The use of yeasts as starter cultures emerges as a promising alternative for obtaining high-quality coffees with distinctive flavors (EVANGELISTA et al., 2014), in addition to enhancing coffee functionality, such as increasing its antioxidant activity (KWAK; JEONG; KIM, 2018).

Influence of yeast diversity on the sensory attributes of coffee

The results showed that environments with greater microbial evenness achieved higher sensory scores, suggesting that better beverage quality is more strongly associated with fruits harboring balanced and diverse communities than with fruits exhibiting high species richness alone. Some studies have demonstrated that the diversity of microbiota present on coffee fruits affects the composition of organic acids and volatile compounds during fermentation, directly influencing beverage quality (ZHANG et al., 2019; PEREIRA et al., 2021). In addition, communities with greater balance and diversity promote the coexistence of multiple taxa without a single species dominating the community (COOK et al., 2021).

In the context of spontaneous fermentation, these ecological principles are also evident. In this process, which occurs in an open environment, the in situ microbiota—comprising yeasts, bacteria, and fungi naturally present on the fruits and in the surrounding environment—plays a fundamental role in fermentation dynamics. In this scenario, the unique microbial terroir of each region contributes to the formation of distinct and region-specific sensory profiles, as local microorganisms directly influence flavor development (BATISTA et al., 2015; DE BRUYN et al., 2017).

Thus, the identification of yeasts capable of beneficially fermenting coffee fruits may contribute to improving sensory quality. The results indicated that the highest sensory scores were achieved in locations where microorganisms known for their positive effects were present, suggesting a potential favorable influence on the final product. However, further studies are necessary to deepen this relationship. This identification represents only a first step toward advances in the post-harvest processing of *Coffea canephora*. The microorganisms identified should now be isolated and tested in

fermentation processes, both individually and in consortium, to evaluate the sensory profile they are capable of promoting.

Conclusion

This study contributed to the understanding of yeast diversity associated with *Coffea canephora* fruits in different coffee-producing regions of Brazil and its relationship with coffee sensory attributes. The results indicated that fungal microbiota composition varies according to location, being influenced by environmental factors and cultivation practices.

The analysis demonstrated that evenness had a greater impact on beverage sensory quality than other community metrics, confirming that environments with greater microbial balance are associated with coffees exhibiting higher scores for acidity, sweetness, and flavor.

The yeasts identified on the fruits show strong potential for application in controlled fermentations, suggesting new possibilities for optimizing coffee fermentation processes and improving beverage quality.

Thus, this work paves the way for future research on the use of yeasts in coffee fermentation, enabling the development of biotechnological processes that further enhance the value of Brazilian *C. canephora* coffees in the specialty coffee market.

Declarations

Conflict of 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.

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Author Contribution

J.S.N. and L.L.P. conceived and designed the study. J.S.N. performed the sampling and laboratory analyses. T.G.R.V., G.L.M., and M.C.S.S. contributed to the chemical and molecular analyses. J.M.R.L. assisted with data processing, statistical analyses, and manuscript revision. E.A.A. contributed to sampling logistics and regional coordination. A.P.M. assisted in data interpretation. W.S.G. contributed to data analysis, interpretation of results, and manuscript writing. L.L.P. supervised the study and revised the manuscript critically for important intellectual content.All authors reviewed and approved the final version of the manuscript.

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Figures

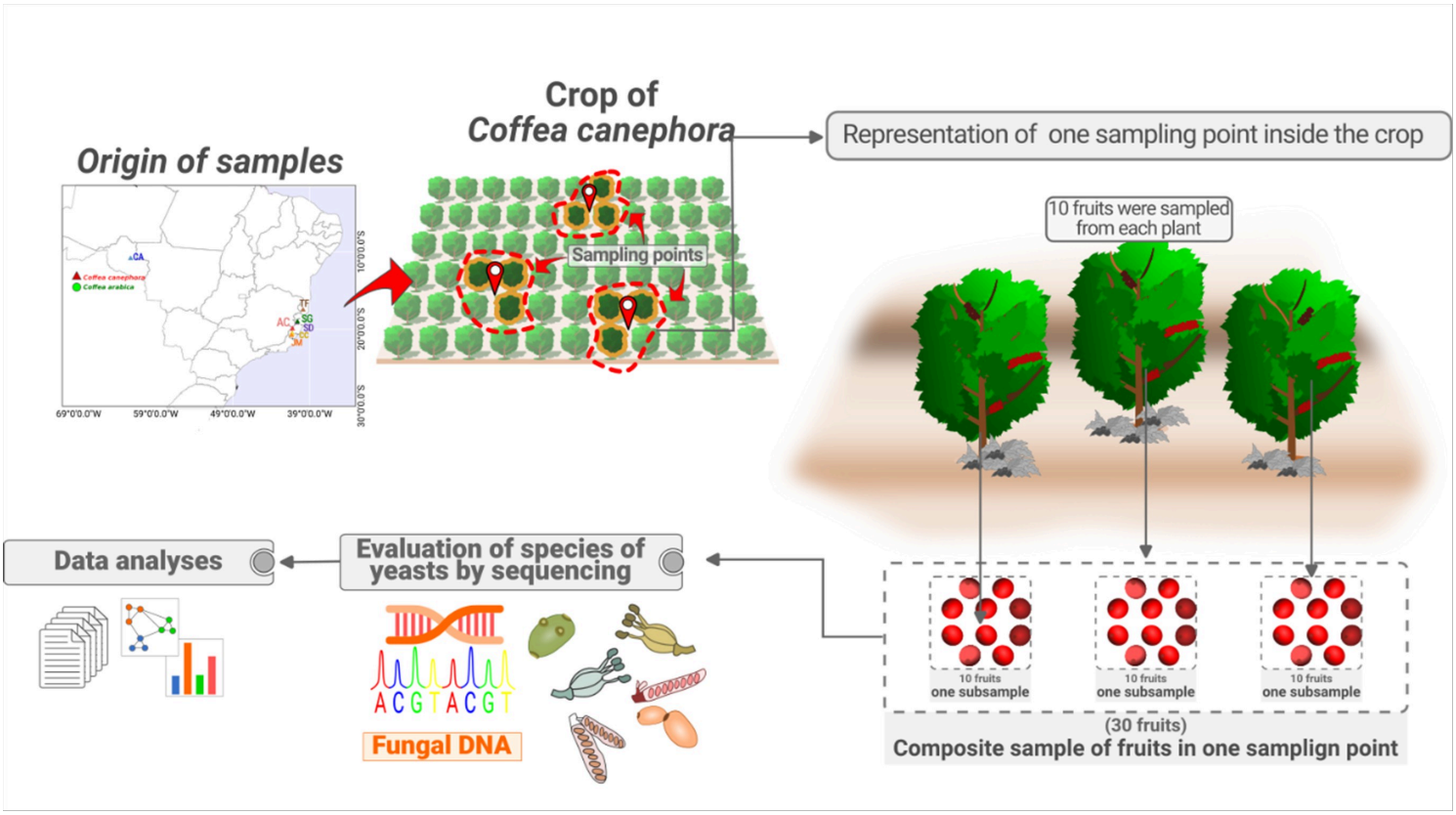

Figure 1

Overview of the sampling design and analytical workflow for *C. canephora* fruit samples

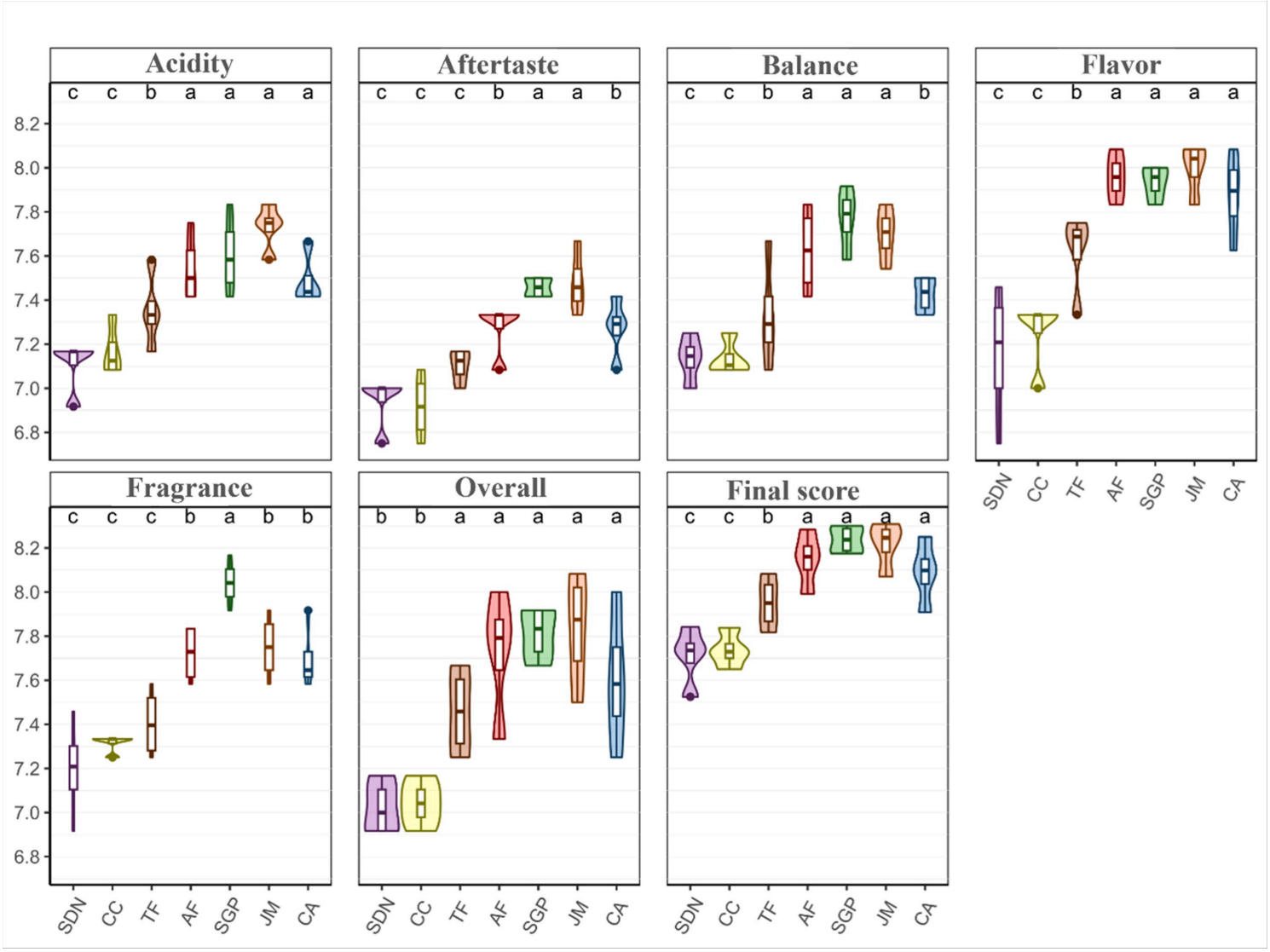

Figure 2

Sensory analysis of Coffea canephora samples cultivated in different regions of Brazil. Means followed by the same letter do not differ statistically according to Tukey's test at the 5% significance level.

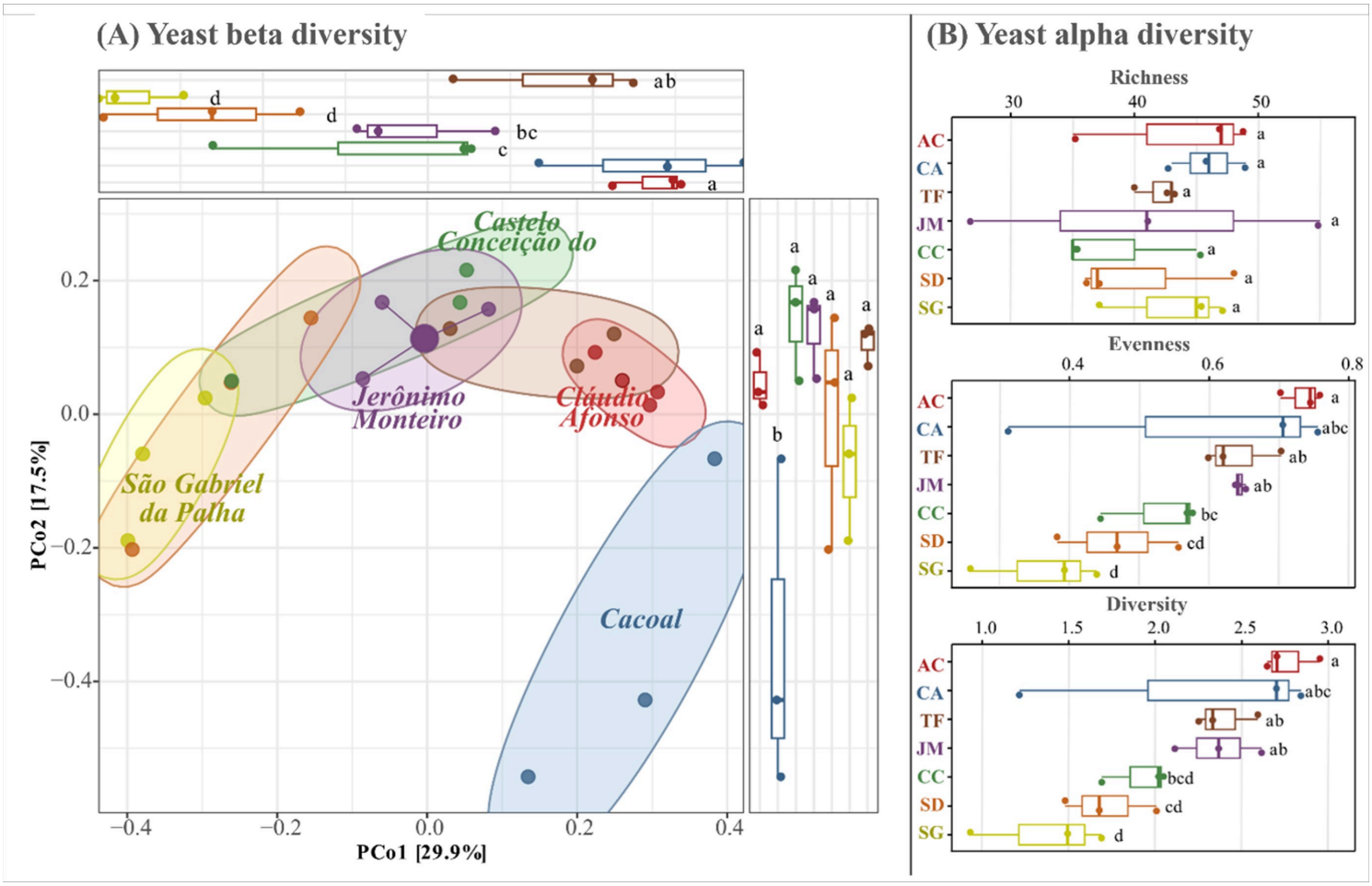

Figure 3

Alpha and beta diversity of the yeast communities associated with *C. canephora* fruits cultivated in different regions. Regions: AC (Afonso Cláudio), CA (Cacoal), TF (Teixeira de Freitas), JM (Jerônimo Monteiro), CC (Conceição do Castelo), SD (São Domingos do Norte), and SG (São Gabriel da Palha).

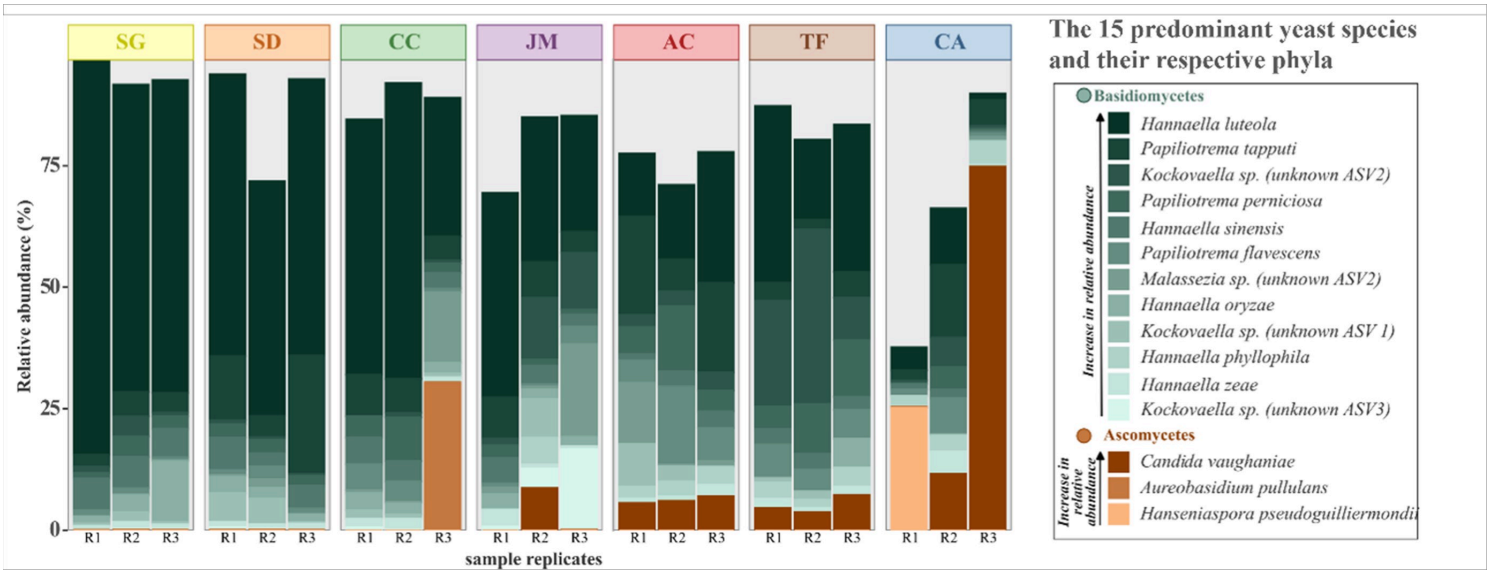

Figure 4

Relative abundance (%) of the 15 predominant yeast species across sampling sites (SG, SD, CC, JM, AC, TF, and CA)

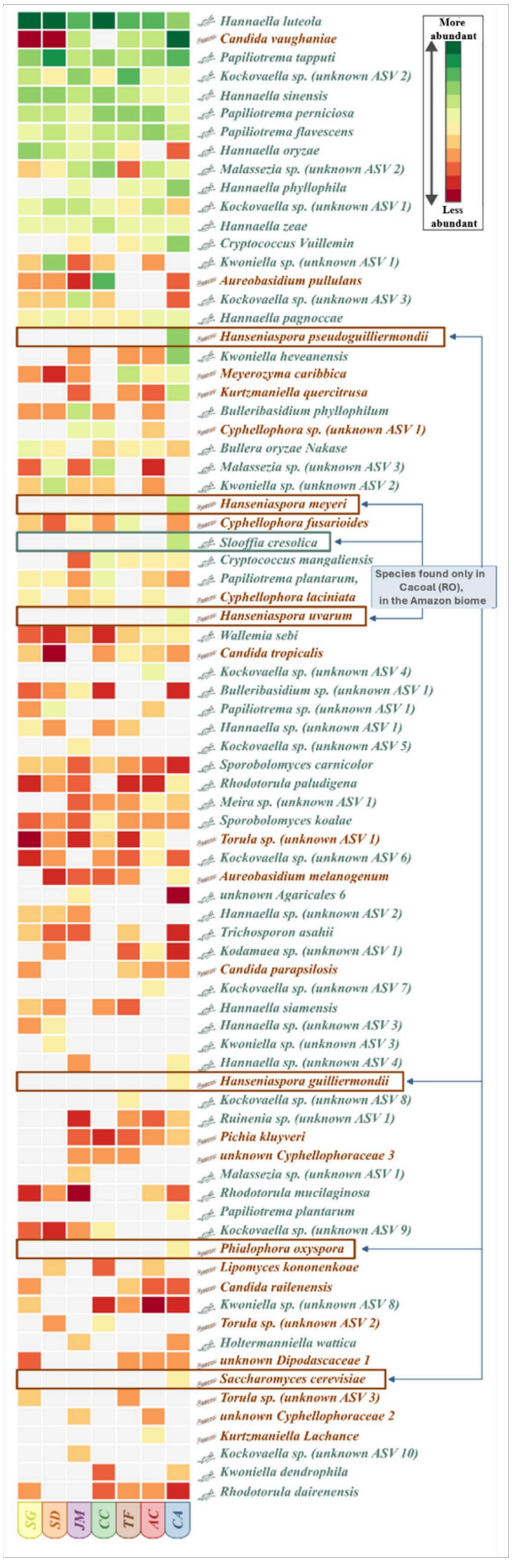

Figure 5

Relative abundance of yeast species identified in Coffea canephora fruits across different sampling sites (SG, SD, JM, CC, AC, TF, and CA).

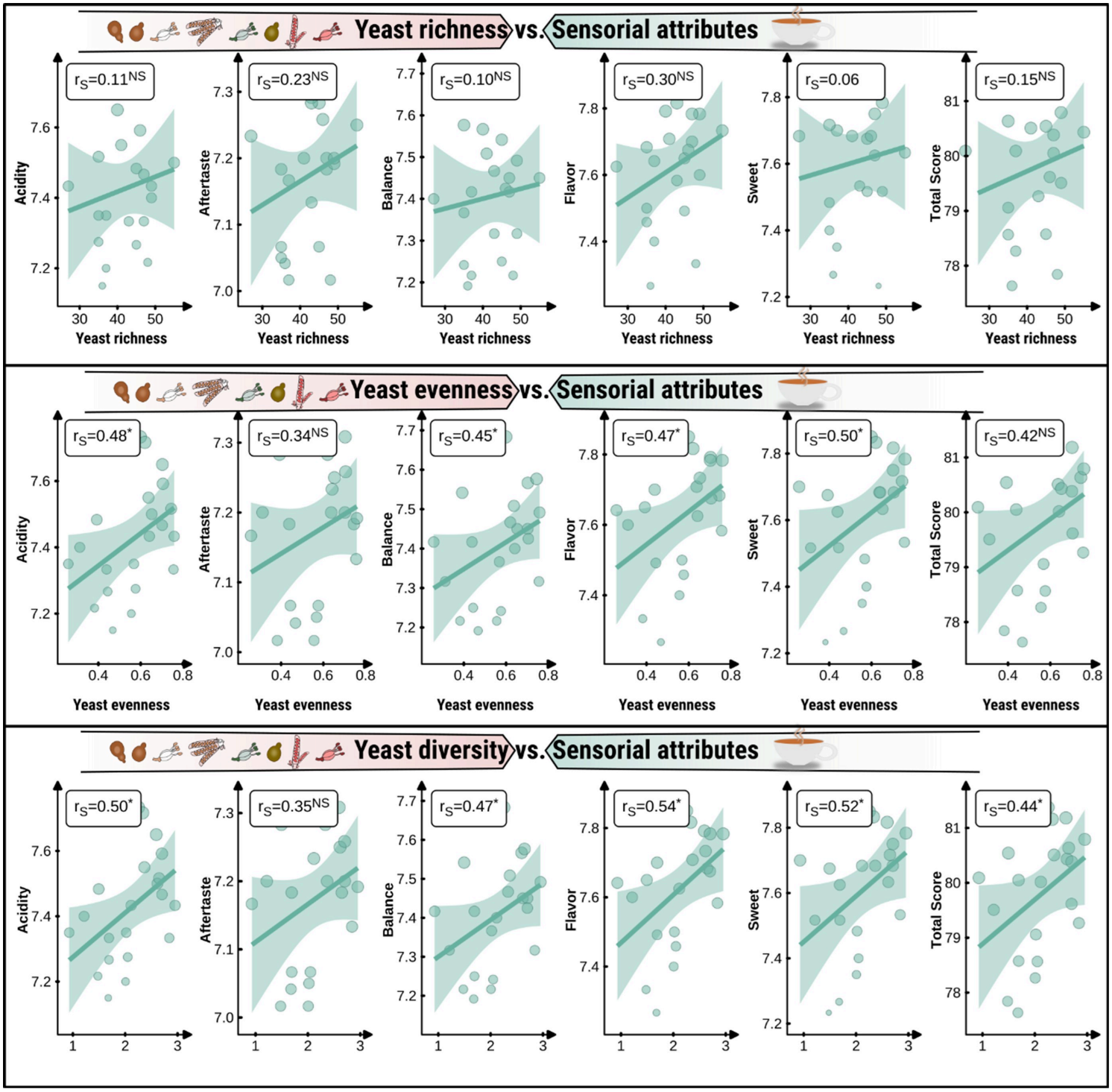

Figure 6

Correlation between sensory attributes and yeast community diversity metrics. Values followed by an asterisk indicate a significant Pearson correlation between the pair of variables at the 0.05 significance level.

Supplementary Files

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- gel.jpeg
- gel2.jpeg