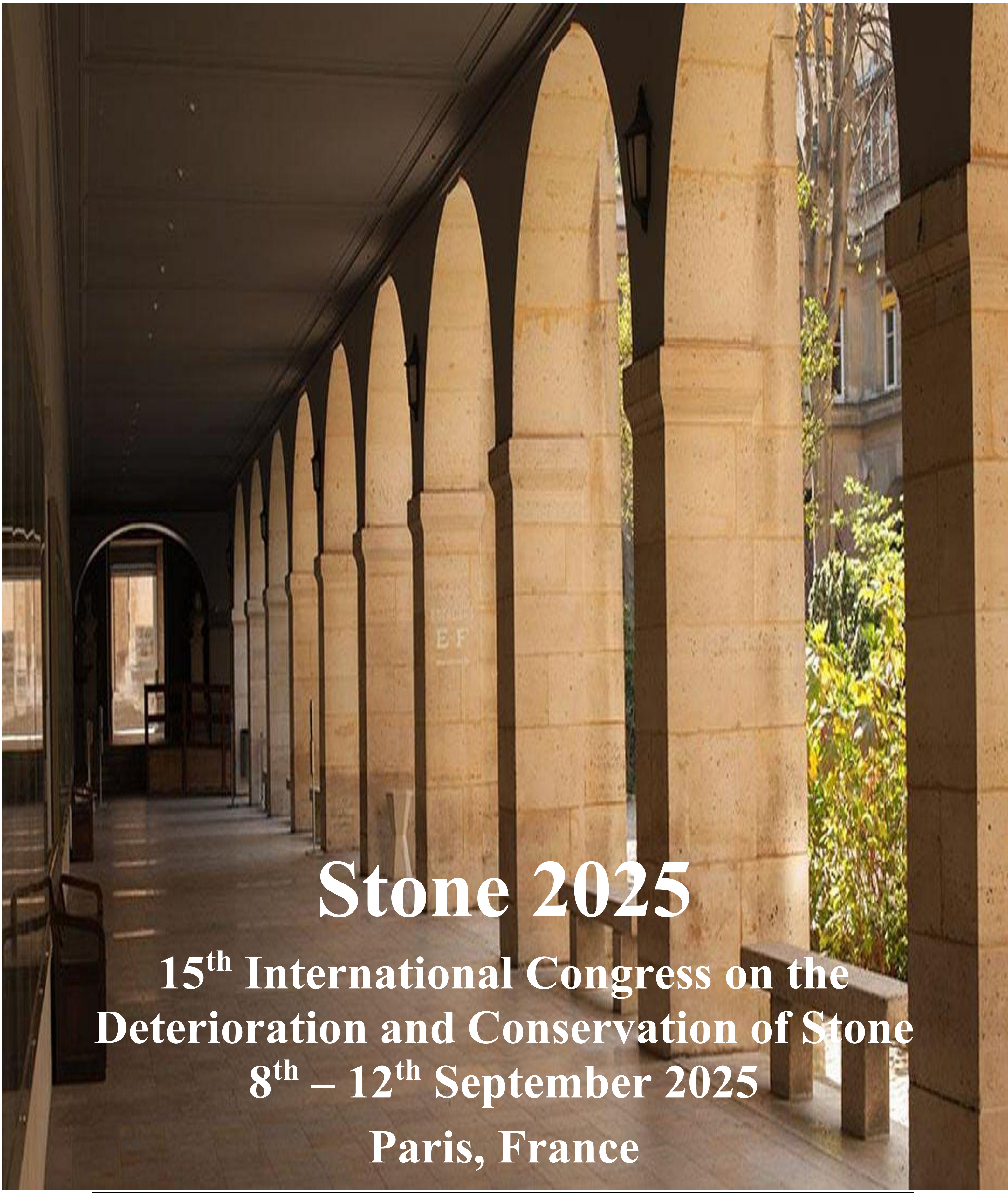

Stone 2025

15th International Congress on the Deterioration and Conservation of Stone

8th – 12th September 2025

Paris, France

STONE 2025
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PREFACE

The 15th International Congress on the Deterioration and Conservation of Stone takes place in Paris in September 2025, at the Campus des Cordeliers. It is jointly organized by the University of Cergy-Pontoise, the Royal Institute of Cultural Heritage (KIK-IRPA), ICOMOS International, the Interdisciplinary Centre for Cultural Heritage Conservation, the French Research Laboratory of Historic Monuments, and Sorbonne University.

Held every four years, the Congress is the leading international forum for researchers and practitioners working on stone deterioration and conservation in cultural heritage. Since the first edition in La Rochelle (France) in 1972, it has established itself as the reference event in the field, offering a unique opportunity to share state-of-the-art knowledge, exchange experiences, and foster collaboration.

This edition brings together 290 professionals, featuring 84 oral presentations and 120 poster presentations. On Thursday, the Annual Seminar of the ICOMOS International Scientific Committee will take place, focusing on the outcomes of its working groups—*Mortar* and *Education*—as well as on the development of future standards for consolidation products.

The scientific program is structured around six thematic areas, encompassing the conservation of all inorganic building materials (stone, mortars, artificial stones, bricks, earth, and more). A central objective of this edition is to bridge scientific advances with practical applications. The six themes are:

1. Characterization and investigation methods
2. Resilient & sustainable conservation
3. Holistic approach of built heritage conservation
4. Digitalization and AI in stone conservation
5. Climate change and risk assessment
6. Alteration mechanisms and conservation treatments

The organizers gratefully acknowledge the support of the EXITE Network, IntoTwin, Remmers, Sint Technology, Triopics France, and IR Laser for their contribution to the conference. Special thanks also go to Cergy Advance Study, the Fondation des Sciences du Patrimoine, DIM Pamir, and RILEM for their support in organizing the Stone Summer School and the Congress.

Finally, we warmly thank all participants for joining us in Paris and for making this event possible.

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DIVERSITY OF MICROBIAL COMMUNITIES ON NATURAL STONES APPLIED IN THE ARCHITECTURAL HERITAGE OF TIANCIZHUANG CAMPUS, SUZHOU, CHINA

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Extended abstract

Keywords: Natural stones, biodeterioration, microenvironment, architectural heritage, conservation.

1. Introduction

Natural stones provide a favourable environment for microbial growth (Louati *et al.,* 2020). The biodeterioration process is often influenced by lithological properties, including mineral composition and porosity, as well as environmental factors such as climate, temperature, humidity, pollutants, and microenvironmental conditions (Liu *et al.,* 2020; Zhang *et al.,* 2020; Warscheid and Braams, 2000; Meng *et al.,* 2023). As the first Christian university established in China, Tiancizhuang Campus of Soochow University is recognized as a nationally designated architectural heritage site, with significant historical and architectural value. However, detailed information regarding the materials used and their decay patterns—particularly natural stones—remains limited. This study identified the microbial communities on the surfaces of different stone architectural heritages at Tiancizhuang Campus, offering valuable insights for developing conservation approaches that balance efficiency with location's characteristics and material specificity.

2. Materials and methods

Microorganisms were sampled from five natural stone surfaces exhibiting visible yellow, orange, grey, and black biofilms or discolouration. Through both micro-destructive and non-destructive sampling methods, stone fragments and microbiological samples were collected. Three samples (AN3, AN4 and AN10) were taken from granite surfaces at Anderson Hall, while two samples (AL1 and AL2) were obtained from the southern balustrade of Allen Hall—one from a granite surface and the other from a grey rhyolite surface. Sampling sites were selected based on a set of criteria including material diversity, variations in discolouration, biological colonization, and spatial distribution. To observe the micro-morphology of microorganisms, a digital microscope (Hirox-01, Japan) and a variable pressure scanning electron microscopy coupled with energy dispersive spectroscopy (SEM-EDS) (Hitachi 3700N, Japan) were utilized to observe the microorganisms. DNA was extracted, amplified, and sequenced from the collected biological samples. The sequencing data were analysed using Shannon diversity index, alpha and beta diversity, and principal component analysis to assess the richness and diversity of microbial communities across the samples.

3. Results and discussion

The sequencing results revealed a significant diversity of microbial communities on the natural stone surfaces. *Proteobacteria* is the most abundant bacterial phylum on all stones (55.51%). This group is widely involved in the biodeterioration of stone heritage worldwide (Meng *et al*., 2023; Ding *et al*., 2021). Additional bacterial phyla detected included *Actinobacteria*, *Firmicutes*, and *Cyanobacteria*. Common bacterial genera across the samples included *Massilia* (13.87%), *Methylobacterium* (16.08%), and *Sphingomonas* (7.02%). In contrast, fungal groups are relatively less diverse. Most fungal sequences belonged to the phylum *Ascomycota* (92.53%). Statistical analysis indicated that AL2 exhibited the highest bacterial and fungal diversity. This suggests that rhyolitic rocks are more susceptible to microbial colonization than granitic rocks, potentially due to their higher porosity (Warscheid and Braams 2000). Furthermore, on granite

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surfaces, *Massilia* displays a significantly higher relative abundance (40.42% in AL1), which is known for presenting white, yellow, or orange colour, explaining the pronounced orange and yellow biofilms observed on the stone surfaces (Li *et al*., 2021). However, even when similar orange staining was observed on rhyolite, Massilia did not exhibit significant dominance in the AL2 sample from Allen Hall's balustrade. Even among granite samples collected from different parts of the same building façade, distinct microorganism species were detected. The microbial communities in AN3 and AN4 were the most similar and they showed minor differences from AL1, but exhibited more pronounced dissimilarity from AN10. This may be attributed to the unique microenvironment surrounding AN10, which is located at the base of the building plinth surrounding a humid garden.

4. Conclusion

This study investigated the microbial communities present on natural stone surfaces in architectural heritage. DNA sequencing analyses revealed significant diversity in microbial communities, indicating varying degrees of microbial contamination dependent on the specific properties of the stones and microenvironmental conditions. The results showed that: a) *Proteobacteria* and *Ascomycota* fungi are predominantly found in areas where patina formation on the stone surfaces was detected; b) Despite the physical proximity of the samples, variations in appearance and microbial communities were observed, highlighting the influence of stone properties on the colonization process by microorganisms; c) Distinct microbial communities were detected in granite samples from different parts of the same facade, indicating that microenvironmental factors, influenced by environmental conditions and human activities, play a crucial role in the levels of microbial contamination. The distinct differences observed across lithologies and microenvironments suggest that both material properties and site-specific conditions significantly governed the microbial colonization of stones. However, it is also plausible that the microbial community may reflect, rather than determine, surface alterations induced by physical weathering processes—such as freeze-thaw cycles, salt crystallization, or wetting–drying. In this view, the observed microbial variations might be a consequence of prior material degradation, rather than its direct cause. These findings contribute to a more nuanced understanding of microorganism-related stone decay, highlighting the complex interplay between microbial colonization, material properties, and site-specific environmental conditions. By acknowledging the potential bidirectionality of these interactions. This study underlines the need for a deep understanding of the interactions among microbial communities, stone characteristics, and microenvironmental factors to support the effective maintenance of architectural heritage.

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