A new open access paper in Frontiers in Microbiology looked at the microbial communities found on buildings of the Auschwitz concentration camp in Poland. I’m currently travelling, so I only have time to post the abstract here. One Hundred Years by The Cure, a song about war and destruction, seemed a good choice for this post.

The paper is:

Metabolomic and high-throughput sequencing analysis — modern approach for the assessment of biodeterioration of materials from historic buildings

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Preservation of cultural heritage is of paramount importance worldwide. Microbial colonization of construction materials, such as wood, brick, mortar and stone in historic buildings can lead to severe deterioration. The aim of the present study was to give modern insight into the phylogenetic diversity and activated metabolic pathways of microbial communities colonized historic objects located in the former Auschwitz II-Birkenau concentration and extermination camp in Oświęcim, Poland. For this purpose we combined molecular, microscopic and chemical methods.

Selected specimens were examined using Field Emission Scanning Electron Microscopy (FESEM), metabolomic analysis and high-throughput Illumina sequencing. FESEM imaging revealed the presence of complex microbial communities comprising diatoms, fungi and bacteria, mainly cyanobacteria and actinobacteria, on sample surfaces. Microbial diversity of brick specimens appeared higher than that of the wood and was dominated by algae and cyanobacteria, while wood was mainly colonized by fungi. DNA sequences documented the presence of 15 bacterial phyla representing 99 genera including Halomonas, Halorhodospira, Salinisphaera, Salinibacterium, Rubrobacter, Streptomyces, Arthrobacter and 9 fungal classes represented by 113 genera including Cladosporium, Acremonium, Alternaria, Enghyodontium, Penicillium, Rhizopus and Aureobasidium. Most of the identified sequences were characteristic of organisms implicated in deterioration of wood and brick. Metabolomic data indicated the activation of numerous metabolic pathways, including those regulating the production of primary and secondary metabolites, for example, metabolites associated with the production of antibiotics, organic acids and deterioration of organic compounds.

The study demonstrated that a combination of electron microscopy imaging with metabolomic and genomic techniques allows to link the phylogenetic information and metabolic profiles of microbial
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communities and to shed new light on biodeterioration processes.