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A new test method to assess the bacterial deterioration of cementitious materials

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ABSTRACT

The biodegradation of cement-based matrices by agro-industrial effluents is a very complex phenomenon. In this work, a test was developed – the *Build-Mat Bio-test* (*BMB test*) – to examine the degradation mechanisms caused by microbial activity on any type of building material. The main objective of this device was to analyze and distinguish between the effects caused by the bacteria and those caused by their metabolites in the deterioration. In this study, the BMB test was used to evaluate the impact on cementitious matrices of the bacterium *Escherichia coli*, found in liquid manure. The mechanisms and kinetics of deterioration resulting from exposure to the bacterial culture or to the metabolites were compared with those obtained with synthetic organic acids alone. It was notably observed that the bacterial suspension caused more intense deterioration and higher alteration kinetics as compared to the medium without microorganisms and to the synthetic acid solution.

1. Introduction

Agro-industrial and agricultural structures made of concrete (animal houses, treatment plants, dairy plants, storage silos, etc.) are severely damaged by agrofood and breeding waste waters, such as whey, silage effluents and liquid manure [1]. These effluents, the compositions of which are complex and very variable, contain compounds in solution or in suspension: organic substances, mineral compounds, and, in most cases, microorganisms. Organic matter is degraded by these microorganisms (Aerobacters sp., faecal *Streptococci, Lactobacillus*, etc.) and may then be transformed into biomass (microbial proliferation) and into various compounds, notably organic acids (volatile fatty acids, lactic, citric acids, etc.) [2–4]. Acidic and biological components in the effluents are aggressive agents for concrete since it is a strongly basic, mineral material.

The chemical degradation caused in cementitious matrices by organic acids found in effluents has been investigated extensively by considering organic acids alone [5–13]. However, the influence of microbial activity in the effluents on the degradation of concrete has not been well identified. The most detailed studies addressing the mechanisms of interaction between microorganisms and cementitious matrices concern sewage systems [14–18]. In this case, the organisms responsible for the deterioration belong to the sulphate reducing and sulphur oxidizing bacteria [17–19]. These bacteria interact with concrete through the H_2S cycle, which differs considerably from the situation occurring in agro-industrial environments (possible carbonation, consumption of some elements of the cement paste) [20–22], except, perhaps, for those occurring under certain conditions in manure (collecting systems, for example).

Moreover, progress in the understanding of the interactions between materials and media bearing microorganisms is mainly hindered by the difficulty of designing and implementing a test method allowing examination of each component of the system individually. Up to now, most experimental studies performed to analyze the interactions between microorganisms and concrete have used laboratory test benches based on quite a simple design: the immersion of specimens in a microbial culture medium [23–28] or sometimes a more elaborate one [29]. These studies have enabled interesting preliminary results to be obtained on the bio-receptivity of mortars and cement pastes [25,26] and some interesting mechanisms for degradation of the cementitious matrix to be highlighted [27]. However, in all cases, the specific effect of the action of the microorganisms could not be distinguished from the degradation induced by the metabolites produced by the microorganisms (dissolved CO_2, H_2S, organic acids, nitric acid, etc.) in the growth medium. Moreover, it is impossible to directly isolate the growing bacterial cells in order to analyze their specific effect on the matrix. During growth, bacteria cannot be separated from their metabolites since they are continuously produced by the microorganisms. A suitable approach for identifying the specific alterations of matrix caused by the microbial cells would be to subtract the effects caused by the metabolites alone from those caused by the growing bacterial cells plus their metabolites.

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