Testing Nano Effect onto Model Bacteria: Impact of Speciation and Genotypes Testing Nano effect onto model bacteria: impact of speciation and genotypes

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Given the intensive production and incorporation of engineered nanomaterials in virtually all industrial fields, important concerns exist regarding their potential impact to ecosystems. However, toxicity mechanisms associated to nanomaterials are not fully understood, partly because of an incomplete physico-chemical characterization of these objects during toxicity tests, but also because of an unsuficient genotype description of the strains used.

In this study, the gram-negative bacteria *Escherichia coli* were used as a prokaryotic model for testing the toxicity of ZnO nanoparticles (nano-ZnO), which toxicity is often refered to Zn^{2+} released from nanoparticles in the culture medium. Two model *E. coli* strains MG1655 and W3110, showing slight differences in their genome, were submitted to nano-ZnO or Zn^{2+} in order 1) to refine the nano-ZnO toxicity mechanisms to *E. coli* as a function of their genotypes, and 2) to investigate whether toxicity resulted from a real "nanoparticle" effect or from the release of Zn^{2+} in solution.

To do so, both strains were submitted to various concentrations (0.1 to 1 mM) of nano-ZnO or Zn^{2+} in Luria Bertani (LB) medium. These toxicity studies take into account the nano-ZnO solubility in the culture medium by specifically monitoring the Zn^{2+} released in our experimental systems. A real "nano" effect is here clearly demonstrated by comparing the overall toxicity to the toxicity resulting only from Zn^{2+} released during nano-ZnO dissolution. Also, in our experimental conditions, differences in tolerance to nano-ZnO or Zn^{2+} between both strains was clearly evidenced. W3110 is generally more tolerant to metal than MG1655, the latter showing no real difference in its sensitivity to the two zinc added forms unlike W3110. The differences in behavior between both strains could be attributed to differences in the two genomes as a mutation named "amber" in W3110.