

Aspergillus nidulans as a biological system to detect the genotoxic effects of mercury fumes on eukaryotes

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ABSTRACT. Mercury (Hg) pollution is one of the most serious environmental problems. Due to public concern prompted by the symptoms displayed by people who consumed contaminated fish in Minamata, Japan in 1956, Hg pollution has since been kept under constant surveillance. However, despite considerable accumulation of knowledge on the noxious effects of ingested or inhaled Hg, especially for humans, there is virtually nothing known about the genotoxic effects of Hg. Because increased mitotic crossing over is assumed to be the first step leading to carcinogenesis, we used a sensitive short-term test (homozygotization index) to look for DNA alterations induced by Hg fumes. In one *Aspergillus nidulans* diploid strain (UT448//UT184), the effects of the Hg fumes appeared scattered all

over the DNA, causing 3.05 times more recombination frequencies than the mean for other strains. Another diploid (*Dp* II-I//UT184) was little affected by Hg. This led us to hypothesize that a genetic factor present in the UT184 master strain genome, close to the *nicB8* genetic marker, is responsible for this behavior. These findings corroborate our previous findings that the homozygotization index can be used as a bioassay for rapid and efficient assessment of ecotoxicological hazards.

Key words: Mercury genotoxicity; Genotoxicity detection; Mitotic crossing-over; Homozygotization index; Ecotoxicological hazards