

ISSR-PCR Based Genetic Diversity Analysis on Copper Tolerant versus Wild Type Strains of Unicellular alga *Chlorella Vulgaris*

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Abstract : The unicellular alga *Chlorella vulgaris* was isolated from Al-Asfar Lake, which is located in the Al-Ahsa province of Saudi Arabia. Two different isolates were sub-cultured under laboratory conditions. The wild type was grown under a regular concentration of copper, whereas the other isolate was grown under a progressively increasing copper concentration. An Inter Simple Sequence Repeats (ISSR) analysis was performed using DNA isolated from the wild type and tolerant strains. The sum of the scored bands of the wild type was 155, with 100 (64.5%) considered to be polymorphic bands, whereas the resistant strain displayed 147 bands, with 92 (62.6%) considered to be polymorphic bands. The sum of the scored bands of a mixed sample was 117 bands, of which only 4 (3.4%) were considered to be polymorphic. The average Nei's genetic diversity (h) and Shannon-Weiner diversity indices (I) were 0.3891 and 0.5394, respectively. These results clearly indicate that the adaptation to a high level of copper in *Chlorella vulgaris* is not merely physiological but rather driven by modifications at the genomic level.

Keywords : *chlorella vulgaris*, copper tolerance, genetic diversity, green algae

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