

# Effect of UV-C radiation on genomic variation on *Chlamydomonas reinhardtii*

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Microalgae are unicellular organisms characterized by a genome with all the information necessary to cope with normal physiological functions as well as very strong selective pressures such as light and pH variation or nutrient starvation. Therefore, it is possible to hypothesize that they possess molecular tools (e.g., methylation, acetylation, mutagenesis or recombination) that allow them to reorganize the genomic and transcriptomic apparatus to support selective pressures of different natures. Furthermore, generally, mutagenesis represents a force capable of inducing a modification in the genomic structure, which can be lethal if not well managed. The present work implemented a mutagenesis protocol through UV-C radiation on the microalgal *Chlamydomonas reinhardtii*. Usually, UV-C is used to sterilise and kills microorganism, so we tried to manage time exposure to induce genomic variation and evaluate the survival capacity of *C. reinhardtii*. In this way, we obtained different mutated genotypes efficiently and selected the ones with the best biomolecular character, specifically surviving ability and growth rate. These studies highlight a genetic distance between the wild type and the probable mutants exposed at three different times on UV-C (96 minutes, 48 minutes and 12 minutes). Furthermore, the irradiation directly affects the chlorophyll concentration, mirroring the genetic differentiation obtained during the mutagenesis.

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