

(*sHSP*). We searched Heat Shock Response motifs in the *sHSP* promoters and in the 5' DNA sequences - that are equivalent to promoters - of both retrotransposons. Heat Shock Elements (HSEs), Stress Response Elements (STREs) and/or CCAAT boxes were identified in the sequences of *sHSP* promoters and in the 5' DNA sequence of *Surcouf*, but not in that of *Blackbeard*. This result suggests that *sHSP* and *Surcouf* might be partly co-regulated and explains the overexpression of *Surcouf* at high temperature.

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A NEW GREEN ALGAL LINEAGE ISOLATED FROM A VOLCANIC CANYON IN THE CANARY ISLANDS

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Algae are one of the most diverse and highly adapted forms of life on Earth. Here, we report the discovery of a terrestrial green alga isolated from a peculiar habitat in La Palma (Canary Islands, Spain) – a steep volcanic canyon that is constantly exposed to changing weather condi-

tions (floods versus droughts). To understand how the alga adapted to survive and reproduce in this environment, we used axenic cultures, simulated the above-listed stresses and studied their effect on the alga's life history. We found that despite its relatively simple morphology (i.e. a uniseriate filament with intercalary cell divisions), the alga adapted to the fluctuating environment of the canyon through specific life-history traits. (1) Aplanospores enable survival during long drought periods, spreading during floods, and subsequent rapid (re)colonization due to abnormal first cell divisions in germlings leading to the formation of two or even several filaments from one aplanospore. (2) Fragmentation through 'filament splitting' (a unique mechanism, not reported before in green algae and initiated by formation of oblique cross walls) that takes place when the canyon begins to dry out (branch formation) and floods/heavy rain showers occur (fragmentation). (3) Besides that, the alga reproduces asexually during an aquatic life stage by zoospores (numbers of flagella per zoospore differ from 4-24) and may spread and thus maximize colonization during post-flood periods when submerged. Since the observed life history traits could not be assigned to a described taxon, we examined the phylogenetic position of this organism. Interestingly, we found that the alga represents a novel lineage at the genus and family level in the Chaetophorales (Chlorophyceae). In conclusion, our findings clearly indicate that the study of 'non-typical' habitats can help to discover novel microalgal diversity and provide new insights into evolutionary processes that have shaped adaptations of such algae to their specific *habitat*.