



Electrophoresis and spectrometric analyses of adaptation-related proteins in thermally stressed *Chromobacterium violaceum*

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ABSTRACT. *Chromobacterium violaceum* is a Gram-negative proteobacteria found in water and soil; it is widely distributed in tropical and subtropical regions, such as the Amazon rainforest. We examined protein expression changes that occur in *C. violaceum* at different growth temperatures using electrophoresis and mass spectrometry. The total number of spots detected was 1985; the number ranged from 99 to 380 in each assay. The proteins that were identified spectrometrically were categorized as chaperones, proteins expressed exclusively under heat stress, enzymes involved in the respiratory and fermentation cycles, ribosomal proteins, and proteins related to transport and secretion. Controlling inverted repeat of chaperone expression and inverted repeat DNA binding sequences, as well as regions recognized by sigma factor 32, elements involved in the genetic regulation of the bacterial stress response, were identified in the promoter regions of several of the genes coding proteins, involved in the *C. violaceum* stress response. We found that 30°C is the optimal growth temperature for *C. violaceum*, whereas 25, 35, and 40°C are stressful temperatures that trigger the expression of chaperones, superoxide dismutase, a probable small heat shock protein, a probable phasing, ferrichrome-iron receptor protein, elongation factor P, and an ornithine carbamoyltransferase catabolite. This information improves our comprehension of the mechanisms involved in stress adaptation by *C. violaceum*.

Key words: CIRCE; Chaperones; Heat shock response; HSP; Differential gene expression