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Roles played by the RNA chaperone Hfq on the *Burkholderia cepacia* resistance to stress and virulence

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The *Burkholderia cepacia* complex (Bcc) is a group of closely related bacteria that emerged as problematic opportunistic pathogens, especially to cystic fibrosis (CF) patients. Although several virulence factors have been identified in Bcc, the knowledge of their relative contribution to Bcc pathogenicity remains scarce. A strategy involving plasposon random mutagenesis and selection of attenuated mutants in the nematode *Caenorhabditis elegans* as an infection model, led to the identification of a *B. cepacia* IST408 mutant containing a disruption in the *hfq* gene, encoding an RNA chaperone, involved in the riboregulation of target mRNAs by small regulatory non-coding RNAs (sRNAs) in other bacteria. In this work we describe the overproduction and purification of the *B. cepacia* Hfq protein, and show results indicating that the protein forms hexamers and binds sRNAs. When provided in trans, the *B. cepacia* IST408 *hfq* gene complemented the *E. coli* *hfq* mutant strain GS081. Results showing that the *B. cepacia* *hfq* mutant is more susceptible to stress conditions mimicking those faced by Bcc bacteria when infecting the CF host will also be presented and discussed. The presence of Hfq orthologues among other Bcc members strongly suggest that Hfq plays a major role on the survival of Bcc bacteria under stress conditions, contributing to their success as CF pathogens.

Keywords: RNA chaperone Hfq, stress resistance, virulence, *Burkholderia cepacia* complex