**Adhesion properties of *Lacticaseibacillus rhamnosus* GG to microalgal proteins**

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The adhesion of probiotic bacterial cells to the surrounding matrix is an important aspect for the development of food supplements. Apart from food matrix *per se*, bacterial adhesion strains or species dependent whilst the cellular surface architecture is also of paramount importance. *Lacticaseibacillus rhamnosus* GG (LGG), one of the most common species used in probiotic supplements, is well-known for its strong adhesion properties to dairy proteins. The surface of LGG cells is composed of exopolysaccharides and pili, which consist of three subunits: one major subunit, SpaA, and two minor subunits, SpaB and SpaC1. SpaC, located at the tip and along the pilus shaft, is a well-established key protein mediating specific adhesive interactions with whey proteins2. Two major mechanisms have been proposed for SpaC-mediated adhesion: a) a zipper-like adhesion mechanism involving multiple SpaC molecules, and b) nanospring properties that enable pili to withstand high forces3.

However, due to increasing consumer awareness about sustainable food proteins, the trend of replacing dairy proteins is steadily growing. A promising alternative to milk-derived proteins is microalgal proteins, such as those obtained from Arthrospira platensis (spirulina) and Chlorella vulgaris. These proteins are attractive due to their high protein content (60-70%) and the presence of phytochemicals (e.g., carotenoids, polyphenols, chlorophylls), along with their high biological value, sustainability, and eco-friendly nature4.

In a recent study, we demonstrated that proteins obtained from spirulina could protect LGG during processing, storage, and gastrointestinal digestion as effectively as whey proteins5. However, the mechanisms underlying the interactions between the food matrix and LGG remain unclear. Therefore, the present work reports on the interactions between LGG and proteins derived from spirulina and chlorella, employing atomic force microscopy (AFM) using the worm-like chain model. For comparison, whey and pea protein isolates were also studied.

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