Sequence motifs in a flagellin of Pseudomonas putida

Winstanley and others (5) reported the cloning and characterization of two flagellin genes from Pseudomonas putida. The flagellins of P. putida strains PRS2000 and PAW8 have an apparent molecular mass of 50 kDa and 81 kDa, respectively. We analysed the predicted amino acid sequences of these two P. putida flagellins using the GCG software package (1). Alignments were done using the tool BESTFIT with default parameters (gap weight 3.0, gap length weight 0.1). In order to obtain statistical values for the alignment quality 100 randomizations were carried out.

The central part of the PAW8 flagellin contains a substantial region of excess amino acids not comparable to the PRS2000 flagellin (5). Within this excess region we detect significant sequence homology to flagellins from Campylobacter coli and Campylobacter jejuni (Fig. 1a). The PAW8 flagellin aligns with 60% identity and 83.3% similarity to the flagellins of C. coli strain VC167 and C. jejuni strain 81116 (4). The quality of the alignment is 30, with a mean quality of 16.9 ± 1.1 based on 100 randomizations. The homology extends also to a flagellin of C. jejuni strain TGH9011 (3) showing 48.3% identity and 75.9% similarity to the PAW8 flagellin, and 76.7% identity and 86.7% similarity to the above Campylobacter strains. Interestingly, no similarity can be detected in a flagellin of C. jejuni strain IN1 (2). It has been shown before that flagellins within the same Campylobacter species can be more diverse than flagellins from related Campylobacter species (3).

Furthermore, we report the identification of two distinct repeated sequence motifs, SM1 and SM2, in the central part of the PAW8 flagellin (Fig. 1b, c). We selected amino acids 220–320, 320–420, 350–450 and 450–550 for sequence analysis. Sequence motif SM1 was finally restricted to 33 amino acids (amino acids 246–278) which resulted in a similarity of 53.4% identity and 75.9% similarity to the above Campylobacter strains. The repeats of sequence motif SM2 (Fig. 1c) show a similarity of 53.4% identity and 75.9% similarity and the quality reaches 23.4 (the mean quality is 10.4 ± 1.3).

The central part of bacterial flagellin proteins defines the diameter of the flagellar filament and has been suggested to be variable in sequence, contributing to antigenic diversity (4, 5). Sequence homologies across genus borders have not been reported before in the central part of bacterial flagellins. The conservation of sequence motifs presented here points at possible functions of the central part of the PAW8 flagellin.

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