The sequence of the \textit{trp} operon of \textit{Bacillus subtilis} 168 (\textit{trpC2}) revisited

The complete genome sequence of \textit{Bacillus subtilis} has been published (4) and is available at the SubtiList site (http://www.pasteur.fr/Bio/SubtiList/).

The more mindful and curious readers were probably surprised by the absence of any detectable defect in the sequence of the \textit{trpC} cistron, despite the well known tryptophan requirement of \textit{B. subtilis} 168, the laboratory strain of choice due to its amenability to genetic analysis (hereafter designated 168 \textit{trpC}). In fact, the deposited sequence of the \textit{trp} operon was derived from the one published by Henner \textit{et al.} (3) performed on strain W168, a prototrophic derivative of 168 \textit{trpC}. In 168, a prototrophic derivative of 168 \textit{trpC}, obtained by transformation with DNA from a different strain, probably W23. A physical map of the \textit{trpC} operon region is shown in Fig. 1.

To fill this gap in our knowledge we sequenced 9413 bp in the \textit{trp} region of strain 168 \textit{trpC}, and compared it to the published sequence. A number of differences were observed between the two sequences, some scattered along the length and most clustered around \textit{trpC} and \textit{trpF}. The scattered mismatches (see updated accession no. Z99115) can easily be attributed to mistakes in sequencing and are thus not relevant to the present discussion. We interpreted the relatively high incidence of differences centred around \textit{trpC}, from nt 2372833 to 2374261 of the entire genome sequence, as due to substitutions of the resident DNA with the incoming sequence upon transformation of 168 \textit{trpC2} to \textit{Trp}+. The overall identity of the two sequences is 91% and extends over 1444 bp. In the 1050 bp of the \textit{trpC} coding sequence, 65 differences were observed, resulting in 15 amino acid changes, 9 of which were conservative substitutions. The most prominent and interesting difference was the absence of three consecutive bp in strain 168 \textit{trpC}, compared to the W168 sequence: a short in-frame deletion of an ATT codon in the sequence ATTATT, corresponding to the junction of the \beta3 strand and \alpha3 helix and not directly involved in the formation of the active site of the enzyme. Nevertheless, they are near two invariant residues (Lys114 and Phe116 in \textit{E. coli}, Lys107 and Phe109 in \textit{B. subtilis}) involved in the active site: the deletion of one of the hydrophobic residues could interfere with the formation of the hydrophobic pocket or with the correct positioning of the phosphate-binding site, thus explaining the reported complete absence of enzyme activity (1).

\textbf{Alessandra M. Albertini*} and \textbf{Alessandro Galizzi}

Dipartimento di Genetica e Microbiologia, Università degli Studi di Pavia, 1 via Ferrata, 1-27100 Pavia, Italy

*For correspondence.

Tel: +39 0382 505549. Fax: +39 0382 528496.

e-mail: albert@pillo.unipv.it

\section*{GUIDELINES}

Communications should be in the form of letters and should be brief and to the point. A single small Table or Figure may be included, as may a limited number of references (cited in the text by numbers, and listed in alphabetical order at the end of the letter). A short title (fewer than 50 characters) should be provided.

Approval for publication rests with the Editor-in-Chief, who reserves the right to edit letters and/or to make a brief reply. Other interested persons may also be invited to reply. The Editors of \textit{Microbiology} do not necessarily agree with the views expressed in \textit{Microbiology Comment}.

Contributions should be addressed to the Editor-in-Chief via the Editorial Office.


