Structural studies of a cell wall polysaccharide from the probiotic strain \textit{Lactobacillus farcininis} CIP 103136

L. Sadovskaya$^1$, E. Maes$^2$, M. Mercier-Bonin$^3$, V. Theodorou$^1$, T. Grard$^1$ and Y. Guérardel$^1$

1Institut Charles Violette EA 7934, Equipe Biochimie des Produits Aquatiques BPA, USC Anses-Université de Littoral-Côte d’Opale, Boulogne-sur-mer
2Plateforme d’Analyse des Glycosylconjugues PAGès, Université de Lille 1
3Toxalim UMR INRA/INPT/UPS 1331, Toulouse

\textit{Lactobacillus farcininis} is a Gram positive bacteria first isolated from meat products [1] and kimchi, known as health promoting Korean food [2]. It was previously demonstrated that treatment with \textit{L. farcininis} CIP 103136 exerts a beneficial anti-inflammatory effect against colonic inflammation and prevents stress-induced visceral hypersensitivity in rats [3], [4].

Fig. 1. TEM observation of \textit{L. farcininis} CIP 103136 cells indicated the presence of an outside capsular layer (Fig. 1)

In order to understand the rationale of the probiotic activities of this bacterium, we studied its polysaccharide (PS) composition.

![Typical elution profiles of deproteinated extracts on a Sephadex G-50 column (2.6 x 90 cm)](image)

Monosaccharide and methylation analysis of CW PS indicated the presence of GlcNAc and ManNAc; as well as terminal and 4/6 linked Glc and Gal. The PS was subjected to Smith degradation, which led to a complete elimination of Hex residues. The structure of this product was studied by 2D NMR spectroscopy and mass spectrometry, and was shown to be composed of linear trisaccharide repeating units (Fig. 3).

2D NMR studies and methylation analysis of the native CW PS led to the following structure (Fig. 4):

![Proposed structure for \textit{L. farcininis} CIP 103136 CW PS](image)

\textit{In vitro} biological studies of immuno-modulatory properties of the CW PS are in progress.

While the poly-NAc-hexosamine backbone was surprisingly reminiscent of that found in cell wall PS of \textit{Bacillus anthracis} and \textit{Bacillus cereus} [6], [7], the original hexose substitution pattern makes the structure of \textit{L. farcininis} CIP 103136 CW PS novel and unique.

Acknowledgements

The authors gratefully acknowledge the Centre de Microscope Electronique Applicable à la Biologie, Toulouse, for TEM observations.

26th Joint Glycobiology meeting
25 to 27 October 2015
Lille