Supplementary Material

Whole genome sequence and *eps* gene clusters comparative analysis of

*Lactiplantibacillus plantarum MC5*

Xuefang Zhao\*, Xuemei Song, Yan Zhang

**\* Correspondence:** Qi Liang: liangqi@gsau.edu.cn

# Supplementary Table

**Supplementary Table 1.** Sugar-specific phosphate transport system in *Lp. plantarum MC5*.

|  |  |  |  |
| --- | --- | --- | --- |
| Locus tag | Sequence length of AA | Description | Pathway definition |
| OOD38\_0177OOD38\_2713  | 651641 | sucrose PTS system EIIBCA or EIIBC component [EC:2.7.1.211] | Starch and sucrose metabolism  |
| OOD38\_0215 |  612 | mannitol PTS system EIICBA or EIICB component [EC:2.7.1.197] | Fructose and mannose metabolism  |
| OOD38\_0217  | 149 | mannitol PTS system EIIA component [EC:2.7.1.197] | Fructose and mannose metabolism  |
| OOD38\_0228 OOD38\_0261OOD38\_0393OOD38\_0396 OOD38\_0985 OOD38\_0994 OOD38\_1214 OOD38\_2514 OOD38\_2615 OOD38\_2996  | 419441453452438435451108452445 | cellobiose PTS system EIIC component | Starch and sucrose metabolism  |
| OOD38\_0244OOD38\_0245OOD38\_0774OOD38\_2644OOD38\_2731OOD38\_3001OOD38\_3005 | 665653483617664624665 | beta-glucoside PTS system EIICBA component [EC:2.7.1.-] | Phosphotransferase system (PTS) |
| OOD38\_0505  | 324 | mannose PTS system EIIAB component [EC:2.7.1.191] | Fructose and mannose metabolism  |
| OOD38\_0506OOD38\_2028  | 268265 | mannose PTS system EIIC component | Fructose and mannose metabolism  |
| OOD38\_0507OOD38\_2027  | 310282 | mannose PTS system EIID component | Fructose and mannose metabolism  |
| OOD38\_0510  | 139 | mannose PTS system EIIA component [EC:2.7.1.191] | Fructose and mannose metabolism  |
| OOD38\_0511 OOD38\_2726  | 172106 | fructose PTS system EIIB component [EC:2.7.1.202] | Fructose and mannose metabolism  |
| OOD38\_0772 OOD38\_2513  | 163148 | sugar PTS system EIIA component [EC:2.7.1.-] | Gluconeogenesis / Starch and sucrose metabolism (PTS) |
| OOD38\_0819OOD38\_1212OOD38\_2322 | 110112115 | cellobiose PTS system EIIA component [EC:2.7.1.196 2.7.1.205] | Starch and sucrose metabolism |
| OOD38\_1060 | 88 | phosphocarrier protein HPr | Phosphotransferase system (PTS) |
| OOD38\_1061  | 576 | phosphoenolpyruvate-protein phosphotransferase (PTS system enzyme I) [EC:2.7.3.9] | Phosphotransferase system (PTS) |
| OOD38\_1213 OOD38\_2323 OOD38\_2514  | 99105108 | cellobiose PTS system EIIB component [EC:2.7.1.196 2.7.1.205] | Starch and sucrose metabolism  |
| OOD38\_1819  | 305 | 1-phosphofructokinase [EC:2.7.1.56] | Fructose and mannose metabolism (PTS) |
| OOD38\_1820 OOD38\_2725  | 655366  | fructose PTS system EIIBC or EIIC component [EC:2.7.1.202] | Fructose and mannose metabolism  |
| OOD38\_1922 OOD38\_3107  | 119125 | glucitol/sorbitol PTS system EIIA component [EC:2.7.1.198] | Fructose and mannose metabolism  |
| OOD38\_2026  | 138 | fructoselysine/glucoselysine PTS system EIIA component [EC:2.7.1.-] | Phosphotransferase system (PTS) |
| OOD38\_2128  | 662 | N-acetylglucosamine PTS system EIICBA or EIICB component [EC:2.7.1.193] | Amino sugar and nucleotide sugar metabolism |
| OOD38\_2211  | 140 | N-acetylgalactosamine PTS system EIIA component [EC:2.7.1.-] | Galactose metabolism  |
| OOD38\_2212  | 271 | galactosamine PTS system EIID component | Galactose metabolism  |
| OOD38\_2213  | 269 | galactosamine PTS system EIIC component | Galactose metabolism  |
| OOD38\_2214  | 160 | galactosamine PTS system EIIB component [EC:2.7.1.-] | Galactose metabolism |
| OOD38\_2450  | 177 | beta-glucoside PTS system EIIA component [EC:2.7.1.-] | Phosphotransferase system (PTS) |
| OOD38\_2482  | 660 | N-acetylglucosamine PTS system EIICBA or EIICB component [EC:2.7.1.193] | Amino sugar and nucleotide sugar metabolism  |
| OOD38\_2727  | 153 | fructose PTS system EIIA component [EC:2.7.1.202] | Fructose and mannose metabolism  |
| OOD38\_3016  | 456 | ascorbate PTS system EIIC component | Ascorbate and aldarate metabolism  |
| OOD38\_3017  | 98 | ascorbate PTS system EIIB component [EC:2.7.1.194] | Ascorbate and aldarate metabolism  |
| OOD38\_3018  | 152 | ascorbate PTS system EIIA or EIIAB component [EC:2.7.1.194] | Ascorbate and aldarate metabolism  |
| OOD38\_3022  | 423 | galactitol PTS system EIIC component | Galactose metabolism /PTS |
| OOD38\_3023  | 98 | galactitol PTS system EIIB component [EC:2.7.1.200] | Galactose metabolism /PTS |
| OOD38\_3024  | 156 | galactitol PTS system EIIA component [EC:2.7.1.200] | Galactose metabolism /PTS |
| OOD38\_3108  | 339 | glucitol/sorbitol PTS system EIIB component [EC:2.7.1.198] | Fructose and mannose metabolism  |
| OOD38\_3109 | 183 | glucitol/sorbitol PTS system EIIC component | Fructose and mannose metabolism |

**Supplementary Table 2.** *Eps* gene clusters information of other 7 strains.

|  |  |  |
| --- | --- | --- |
| Strains | *Eps* gene name | Protein ID |
| *Lp. plantarum* WCFS1 | *epsG* | WP\_011101305.1 |
| *Lp. plantarum* subsp*. plantarum* ST-III | *eps2A**eps2B**eps2C**eps2E**eps3A**eps3B**eps3D**eps3E**eps3F**eps3H**eps3I**eps3J**eps4A**eps4B**eps4C**eps4E**eps4F**eps4G**eps4H**eps4I**eps4J**wzx* | ADN98179.1ADN98180.1ADN98181.1ADN98183.1ADN98203.1ADN98204.1ADN98206.1ADN98207.1ADN98208.1ADN98209.1ADN98210.1ADN98211.1ADN98956.1ADN98955.1ADN98954.1ADN98952.1ADN98184.1ADN98185.1ADN98186.1ADN98187.1ADN98947.1ADN98188.1 |
| *Lp. plantarum* JDM1 | *epsD/epsB* *epsF* | WP\_015640554.1WP\_003643865.1 |
| *Lp. plantarum subsp. plantarum* NC8 | *-* | - |
| *Lp. plantarum subsp. plantarum* ATCC 14917 | *-* | - |
| *Lp. plantarum* 19L3 | *-* | - |
| *Lp. plantarum strain* SMB758 | *epsD/epsB**epsF**epsG* | WDQ20187.1WDQ21455.1 WDQ21011.1 |