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The Lactococcus lactis CodY regulon - Identification of a conserved cis-regulatory element
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Den Hengst et al. - Supplementary material

Supplementary Fig. 1

L. lactis sequences used for the identification of overrepresented motifs among CodY-regulated genes

>dppP

AGATAAAAATTTTTTCAAAAAGTTTGTGAAAAGTTTCCGCTATTA AAAAATTA AATGTTAATT
TTCAGAAAACATAACCATTATACTCTACAATTCAGGTTGAATTAAGTATAATACCAATATAA
TAAATTTTCTGACAATAATAAAAATTGCGAAGTCAGACACAATTCATGAAAGAGGGAAATT
ACATGAAGACTTGG

>dppA

CATCATGAACTTTCAGAAGTTGTTGAAAAATTATAATGACAAAAAAGTACTCGACAAGAG
TCGGTACTTTTTAGTTTTGTTAAATTGTCAGAAAAATACAATAATATTCTTGACATTAGATTT
TCGAAGAAGTATAATAGGTCCACGTTTAAATTTTCAGAATATTAGAAAATTCGATAGTACTTT
TAGGATTTGGAGAA

>ctrA

GAAAGCACCAGAAGTACTGACAGAAATTGATTTTAATAAAAATAATTTACTGACGAATCTGTC
AGTATTTTTTTGAAAAAATTTTATACTGCATAAAGTTAATTCTTGACAATTGTCTGACAATT
CGGTAAAATACAGTTTATTGAAATTTTAGTTACAAATTCAGAAAAATGAGGATTTATTAT
GGGATTTATGAGA

>oppD

AAAAGCAGTTTTTAGTATGATTACTGCTTTTTATTATTTCTCCAAAACTTTTGCTTTACCTTTA
TTTCGCGTAATGTTTCAGAAAATTCATGAACATACCTAAAATAGTAAATTTTTGCAAATATGC
AGAAAAAGTAGTATACTTTTATTAAGTCTATTTAGAAAAGATTTTATTGAGGTAAATATGGAA
AGTGAAAAATATT

>pepN

GAAGCAACTAAATAATTAATGACAAAAAATTGAGGATATTGATAAGAGTGAATATCCTCTG
TAAAAGCTGTCAGTAGACAGTTTTTTTAATAAGTTAAAGAAAAGATGTAATTTTTCTTTGTAC
TCGAAATTTTCTATTCAATTTGATATAATTATTAATACTGAATATTTAGGAGAAGATATGG
CTGTAAAACGTTT

>pepC

TCAATGATGGCTTGAAAGTTGCGCACCCGTGGCTTTTAGAAGCAAAGAAAGATTTAGAAAAT
CAGCTTTCCTAGCTGATTTTTTTGATAATTTAGATTATAATAGAAGAATGTAAAAAATAATA
GAATATCATTAAATCAAAAATCGATAATGATTATTTTTATCGAACTTTTGTGAGAAGTTTCGAT
TTATTGGGAGGTA

>serC

CCAAAGAAGTTGAATGGAACATGTTATTACTTGATTTGTTAAATTGGTAAGATGCTGTTTAG
ACAGAAGTTCACATCATTGATGTGATTTTTGTGCAACAGTATTTTTTTATATTGAATTATCA
GAAAATTATATTATAATAGTGTTAATAAATAATTTGAGGAAGTGAAATCGATGATTTATAA
TTTTGGTGCAGGA

>ilvD

TTAAGCATAAGTATTTTCAATTATTCCGATGAATTTTTAAAAAGAAAGCAAAGTATTTTATAG
ACTTTATTGAATGTTCTGACAAATTATTGTATTTTCAATTTTTTAATGATAAAATAACTCTAT
AAAAATTTACGGGGAGGTCAAAAAGATAACATATGGAATTCAAATATAACGGAAAAGTTGA
ATCAATAGAGCTCA

>hisC

CTGATGCTAAGATGAACCACACTCATCGCTATCTTACTCACCAAATAATTGTGAGCGTTGGC
TACGGTACTGCTGAGTTTAAACATAAACTCACTGAGTCTACTTTTGTGAAAAAGTAGTAAATT
AAGGTGGAACCACGACATTACCGTCTTTAAGCCAAGTGCTTAAAGGCGCTTTTTTTGTATT
ATATTTATCATTTT

>prtPM

GCTAAATAATAACGCTAAAAGTTAATTTACAGATAAAAAAATTAATAGAAGATTA AAAATTTT
CGTTGAATTTGTTCTTCAATAGTATATAATATAATAGTATATAATATTATATTATATAATATA

ATCTTAACTACATCAAGCGTAGGCTTTGATTTGGTTATGAACTTTTGGAAAGTGGAGGATA
TTGGATGCAAAGG

>glbD

ATTCATTCTTTTATCTTATGATTTTAGATGTTTTTTGTCTATTGTAAGGGTCTTCATCTATTAG
ATAAAGCTATTAAAAATTACATTTATATATAATTATCAGAATATATTGATATTCATCGAAAT
TTTAGTAGAATGAAAGAACCAAATTGTAAAATAAAAGAGGTTGTGTTATGAATAAAGAAGC
TAAACAAGCCAT

>glbA/citB/icd

GAAGCCATTCAAACACAAGACTTATTGATTGAAATTGACTAACTTTAAATTAACCCTACCAT
TATGGTAGGATTTTTTATTTTCTAAAAAAAAGTAATTTTAATTTTCAGAAAATATATAATTTT
CGGAATAAAAAGTGTATAATAATGAAATAGATGGAGGTATTTATGAATTTAATGAATAAAG
AAGAAAAAATGATT

>asnB

TTAAAATTAATAATGATTGGCGCGACCGTAAAATGGATTTAGCTGACTTTGGCTACAATCGT
GATGATTATATGTAATGAAAATAGCGAATTATCGCTATTTTTTGTATTATTATGAAATTTCCA
GACAATTGTGATATAATATTGAAAATTATAATTATTATTGGGGGAAATTATGTGCGGTTTTTT
ATTTATGGAAAC

Supplementary TABLE 1. Occurrence of CodY-box derivatives in the genome of *L. lactis* MG1363

| Gene | Position ^a | Sequence | Score ^b |
|--------------|-----------------------|------------------|--------------------|
| <i>dppP</i> | 278 | AATTTTCAGAAAATT | 11.8 |
| <i>codY</i> | 86 | AATTGTCAGAAAATT | 11.3 |
| <i>serC</i> | 44 | AATTTTCTGATAATT | 11.3 |
| <i>thrA</i> | 56 | AATTTTCAGATAATT | 11.3 |
| <i>ygiD</i> | 103 | ATTTTTCAGAAAATT | 11.3 |
| <i>yjfF</i> | 195 | AATTTTCGGAAAAAT | 11.3 |
| <i>gltA</i> | 51 | AATTTTCAGAAAATA | 11.2 |
| <i>feoA</i> | 68 | ACTTTTCAGAAAATT | 11.1 |
| <i>yghD</i> | 44 | AATTTTCTGAATATT | 11.1 |
| <i>nrdF</i> | 187 | ATTTTTCAGAAAAAT | 11.1 |
| <i>ctrA</i> | 60 | AATTGTCAGACAATT | 10.9 |
| <i>dppA</i> | 108 | ATTTTCTGACAATT | 10.9 |
| <i>oppD</i> | 95 | AATTTTCTGAACATT | 10.9 |
| <i>metA</i> | 195 | ATTTTCCGAAAAATT | 10.9 |
| <i>ychG</i> | 298 | TATTTTCAAAAAATT | 10.8 |
| <i>dppA</i> | 40 | ATTATTCTGAAAAATT | 10.8 |
| <i>lysS</i> | 41 | TATTTTCAAAAAATT | 10.8 |
| <i>dppP</i> | 46 | AATTTTCTGACAATA | 10.7 |
| <i>yeaG</i> | 403 | ATTTTCTGAAAATA | 10.7 |
| <i>gerCB</i> | 234 | ATTTTTCAGAAAATA | 10.7 |
| <i>yqcE</i> | 87 | GTTTTTCTGAAAATT | 10.7 |
| <i>menD</i> | 654 | AATTTTCAGAAGAAT | 10.7 |
| <i>mfd</i> | 397 | AATTTTCTAAAAAGT | 10.6 |
| <i>dppP</i> | 114 | AATTTTCAGAAAACA | 10.6 |
| <i>yfhC</i> | 68 | TATTTTCAAAAAATT | 10.6 |
| <i>arsC</i> | 642 | CATCTTCAGAAAATT | 10.6 |
| <i>amtB</i> | 46 | AATATTTCAGAAAATA | 10.6 |
| <i>purL</i> | 1238 | AATTTTCAAAAAACT | 10.6 |
| <i>yojB</i> | 187 | AATTTTCAGAAAAGA | 10.6 |
| <i>ilvD</i> | 71 | AATGTTCTGACAAAT | 10.6 |
| <i>ysbD</i> | 34 | AATTTTTTGAAAAAT | 10.6 |
| <i>ysdE</i> | 126 | AATTTTTTGAAAAAT | 10.6 |
| <i>ybaB</i> | 103 | ATTTTACAGAAAATT | 10.5 |

^a) Distance of the 3'-end of the CodY-box relative to the position of the initiating codon of the downstream ORF.

^b) Arbitrary score of similarity of the element with the CodY-box consensus.

Supplementary TABLE 2. Occurrence of CodY-box derivates in the genome of *L. lactis* IL1403

| Gene | Position ^a | Sequence | Score ^b |
|--------------|-----------------------|-----------------|--------------------|
| <i>yghD</i> | 99 | AATTTTCTGAAAATT | 11,8 |
| <i>optS</i> | 227 | AATTTTCAGAAAATT | 11,8 |
| <i>feoA</i> | 85 | AATTTTCTGAAAAAT | 11,6 |
| <i>codY</i> | 86 | AATTTTCTGACAATT | 11,4 |
| <i>birA2</i> | 156 | ATTTTCTGAAAATT | 11,3 |
| <i>yrbI</i> | 524 | TATTTTCTGAAAAAT | 11,3 |
| <i>dinG</i> | 710 | TATTTTCTGAAAAAT | 11,3 |
| <i>thrA</i> | 55 | AATTTTCAGATAATT | 11,3 |
| <i>ygiD</i> | 99 | ATTTTTCAGAAAATT | 11,3 |
| <i>serC</i> | 44 | AATTATCAGAAAATT | 11,3 |
| <i>metA</i> | 209 | AATTTTCCGAAAAAT | 11,2 |
| <i>gltA</i> | 51 | AATTTTCAGAAAATA | 11,2 |
| <i>amtB</i> | 47 | TATTTTCTGACAATT | 11,1 |
| <i>yeiD</i> | 243 | AATTGTCTGAAAAAT | 11,1 |
| <i>pi249</i> | 186 | TATCTTCTGAAAATT | 10,9 |
| <i>ygcC</i> | 397 | AATTTTCAGAAAAAA | 10,9 |
| <i>yeaG</i> | 403 | TATTTTCTGAAAAGT | 10,9 |
| <i>ctrA</i> | 60 | AATTGTCAGACAATT | 10,9 |
| <i>mfd</i> | 396 | AATTTTCTAAAAAAT | 10,9 |
| <i>ywdD</i> | 940 | AATGGTCAGAAAATT | 10,8 |
| <i>noxD</i> | 681 | AATGGTCAGAAAATT | 10,8 |
| <i>pi303</i> | 242 | ATTTTTCAGATAATT | 10,8 |
| <i>ynaD</i> | 110 | AATTATCGGAAAAAT | 10,8 |
| <i>yjiF</i> | 199 | AATTTTATGAAAATT | 10,8 |
| <i>lysS</i> | 40 | TATTTTCAAAAAATT | 10,8 |
| <i>optA</i> | 114 | TGTTTTCTGAAAATT | 10,8 |
| <i>optS</i> | 40 | AATTTTCAGAATAAT | 10,8 |
| <i>optA</i> | 108 | ATTTTCTGATAATT | 10,8 |
| <i>yceD</i> | 309 | TTTTTCTGAAAAAT | 10,8 |
| <i>yrbA</i> | 112 | TATTTACTGAAAATT | 10,7 |
| <i>arcB</i> | 635 | AATTTGCTGAAAAAT | 10,7 |
| <i>ileS</i> | 170 | ATTTTCTAAAAAATT | 10,7 |
| <i>ysbD</i> | 354 | ATTTTCAAAAAATT | 10,7 |
| <i>pepF</i> | 133 | AATTTTCAGCAAAAT | 10,7 |
| <i>pepXP</i> | 45 | TATTTACTGAAAATT | 10,7 |

^a) Distance of the 3'-end of the CodY-box relative to the position of the initiating codon of the downstream ORF.

^b) Arbitrary score of similarity of the element with the CodY-box consensus.

Supplementary TABLE 3. Occurrence of CodY-box derivatives in the genome of *S. pneumoniae* R6

| Gene | Position ^a | Sequence | Score ^b |
|----------------|-----------------------|------------------|--------------------|
| <i>ilvD</i> | 69 | AATTTTCAGAAAATT | 11,8 |
| <i>ilvE</i> | 73 | AATTTTCTGAAAATT | 11,8 |
| <i>rgg</i> | 39 | AATTTTCTGAAAAAT | 11,6 |
| <i>thrC</i> | 42 | AATTTTCTGAAAAAT | 11,6 |
| <i>IS1381</i> | 31 | AATTTTCTGAAAAAT | 11,6 |
| <i>leuA</i> | 34 | TATTTTCTGAAAATT | 11,5 |
| <i>gapN</i> | 55 | TATTTTCTGAAAATT | 11,5 |
| <i>amiA</i> | 72 | AATATTCTGAAAATT | 11,3 |
| <i>codY</i> | 55 | AATTATCTGAAAATT | 11,3 |
| <i>livJ</i> | 46 | AATTTTCTGATAATT | 11,3 |
| <i>spr0332</i> | 59 | AATTTTCGGAAAAAT | 11,3 |
| <i>asD</i> | 16 | AATTTTCTAAAAATT | 11,2 |
| <i>zwF</i> | 79 | AATTTTCCGAAAAAT | 11,2 |
| <i>gdhA</i> | 79 | AATTTTCTAAAAATT | 11,2 |
| <i>ppmA</i> | 53 | GATTTTCAGAAAAAT | 10,9 |
| <i>hom</i> | 8 | AATTTTGTGAAAATT | 10,8 |
| <i>pnp</i> | 128 | ATTCTTCAGAAAATT | 10,8 |
| <i>mtlD</i> | 154 | ATTATTCTGAAAATT | 10,8 |
| <i>spr0157</i> | 18 | AATTTTCAGAATAAT | 10,8 |
| <i>spr0806</i> | 40 | CATTATCAGAAAATT | 10,7 |
| <i>pepA</i> | 221 | TATTTTCTGTAAATT | 10,6 |
| <i>spr1436</i> | 40 | TATTATCTGACAATT | 10,6 |
| <i>spr1115</i> | 209 | AAATTTTCAGAAAAAT | 10,6 |
| <i>gldA</i> | 49 | AATCGTCAGAAAAAT | 10,6 |
| <i>aqpZ</i> | 74 | GATTTTCAAAAAATT | 10,5 |
| <i>thrS</i> | 128 | TATTTTCTGAAAGTT | 10,5 |
| <i>spr0685</i> | 23 | ATTTTTCAGAAAATC | 10,5 |

^a) Distance of the 3'-end of the CodY-box relative to the position of the initiating codon of the downstream ORF.

^b) Arbitrary score of similarity of the element with the CodY-box consensus.

Supplementary TABLE 4. Occurrence of CodY-box derivates in the genome of *B. subtilis* 168

| Gene | Position ^a | Sequence | Score ^b |
|---------------|-----------------------|------------------|--------------------|
| <i>yvbF</i> | 221 | AATTTTCTGAAAAGT | 11,2 |
| <i>glnQ</i> | 45 | AATTTTCAGAAAAGT | 11,2 |
| <i>ytkC</i> | 66 | ATTTTCTGAAAAAT | 11,1 |
| <i>ynA</i> | 15 | AATATTCAGAAAAAT | 11,1 |
| <i>phoA</i> | 141 | ATTTTCTGAAAAAT | 11,1 |
| <i>yerL</i> | 157 | AATATTCAGAAAAAT | 11,1 |
| <i>yufN</i> | 114 | TATTATCAGAAAATT | 11,0 |
| <i>yuiA</i> | 21 | TATTATCAGAAAATT | 11,0 |
| <i>spoIIQ</i> | 27 | TATTTTCAGAAAAGT | 10,9 |
| <i>opuBA</i> | 49 | ATTTTTCAGACAATT | 10,9 |
| <i>lipB</i> | 69 | AATTTTCAGAAAAAA | 10,9 |
| <i>yocS</i> | 77 | AATTTTCTGAATAAT | 10,8 |
| <i>ykrQ</i> | 75 | AATTTTCTGAAAATTT | 10,8 |
| <i>ydjJ</i> | 242 | AATTTTCAGAAAATTT | 10,8 |
| <i>ykwB</i> | 36 | TATTTACTGAAAATT | 10,7 |
| <i>yfmB</i> | 79 | ATTTTCTGAAAATA | 10,7 |
| <i>braB</i> | 44 | TATTATCTGACAATT | 10,6 |
| <i>citB</i> | 57 | AATTTTCTCACAATT | 10,6 |
| <i>ynzD</i> | 120 | TATTTTCAGAAAAAA | 10,6 |
| <i>ileS</i> | 17 | TATTTTCTGAAAAAA | 10,6 |
| <i>nasD</i> | 106 | AATTTTATGAAAAAT | 10,6 |
| <i>yxiE</i> | 84 | AGTTTTCAAAAAATT | 10,5 |
| <i>yurP</i> | 85 | TATTTTCTGAAAATTT | 10,5 |
| <i>yurF</i> | 104 | CATTTTCTGACAAAT | 10,5 |
| <i>ykuW</i> | 119 | CATTTTCAGAAAATA | 10,5 |
| <i>ybgA</i> | 100 | TAATTTCTGAAAATT | 10,5 |

^a) Distance of the 3'-end of the CodY-box relative to the position of the initiating codon of the downstream ORF.

^b) Arbitrary score of similarity of the element with the CodY-box consensus.

Supplementary TABLE 5. Occurrence of CodY-box derivatives in the upstream regions of genes identified by Molle *et al.* (2003) as being direct targets of CodY of *B. subtilis* 168

| Gene | Position ^a | Sequence | Score ^b |
|-------------|-----------------------|-------------------|--------------------|
| <i>yufN</i> | 114 | TATTATCAGAAAATT | 11.0 |
| <i>citB</i> | 57 | AATTTTCTCACAATT | 10.6 |
| <i>yurP</i> | 85 | AAATTTTCAGAAAATA | 10.2 |
| <i>yhdG</i> | 166 | ATTTTTCTAACAATT | 10.2 |
| <i>gggA</i> | 184 | TTTTTGCTGAAAATT | 10.1 |
| <i>yxbC</i> | 70 | AATCCTCTGATAATT | 10.1 |
| <i>yhjC</i> | 144 | TAATTTTCAGACAATT | 10.1 |
| <i>ybgE</i> | 103 | AAATTTTCAGAATATT | 10.1 |
| <i>ilvD</i> | 48 | AATAAACTGAAAATT | 9.9 |
| <i>ispA</i> | 132 | AATCTTCAAATATT | 9.8 |
| <i>appD</i> | 83 | AATTTTTTCGATAATT | 9.8 |
| <i>yoaD</i> | 8 | TTTTTTATGAAAAAT | 9.8 |
| <i>ykaA</i> | 161 | ATTTATCAAAAAAGT | 9.6 |
| <i>comK</i> | 15 | ATTTTGCAGAAAAAG | 9.4 |
| <i>citB</i> | 135 | ACTTATGAGAAAAAT | 9.4 |
| <i>yhdG</i> | 43 | TGAATTCAGAAAATT | 9.3 |
| <i>guaB</i> | 13 | TCTTTTTCGGCAAAAT | 9.3 |
| <i>acsA</i> | 63 | TATATTTTAAAAAATT | 9.3 |
| <i>ybgE</i> | 22 | AATATTTTAAACAATT | 9.2 |
| <i>yoaD</i> | 187 | TTCATTCTGAAAATT | 9.1 |
| <i>hutP</i> | 11 | AAAATTCTGATAACT | 9.1 |
| <i>guaB</i> | 10 | CTTCTTTTGAAAATT | 9.1 |
| <i>ureA</i> | 47 | AATTTGCGGAACAGT | 9.1 |
| <i>dppA</i> | 28 | ATTTGTTAGAATATT | 9.1 |
| <i>yusC</i> | 19 | ACTATTCTAAGAAAT | 9.0 |
| <i>ycgM</i> | 91 | AATAATCAGAATCTT | 9.0 |
| <i>ilvD</i> | 117 | AATTGTCAAATAAAA | 9.0 |
| <i>rocA</i> | 73 | TTTTTTTCAGCAAAAAG | 9.0 |

^a) Distance of the 3'-end of the CodY-box relative to the position of the initiating codon of the downstream ORF.

^b) Arbitrary score of similarity of the element with the CodY-box consensus.