Supplemental Material for:

The metabolic regulation of sporulation and parasporal crystal formation in *Bacillus thuringiensis* revealed by transcriptomics and proteomics

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Figure legends

Supplemental Fig. S1 The correlation between changes in mRNA and protein abundance

The quantified proteins in each temporal comparison are clustered into seven groups based on the pattern of changes in mRNA and protein levels: Group I, the mRNA and protein levels have the same change trends; Group II, mRNA is up-regulated but protein is down-regulated; Group III, mRNA is up-regulated but protein is not significantly changed; Group IV, mRNA remains almost unchanged while protein is up-regulated; Group V, mRNA remains almost unchanged but protein is down-regulated; Group VI, mRNA is down-regulated but protein is not significantly changed; and Group VII, mRNA is down-regulated but protein is up-regulated. Group I contains three subgroups: both mRNA and protein are up-regulated synchronously (red color); both mRNA and protein are down-regulated synchronously (green color); and both mRNA and protein remain unchanged

Supplemental Fig. S2   The cannibalism phenomenon in CT-43

Sporulating and nonsporulating cells were obviously discriminated under a phase contrast microscope. Scale bars represent 10 micrometers.

Supplemental Fig. S3 The carbohydrate metabolism network and metabolic regulation of CT-43

The metabolic pathways and related genes are obtained mainly according to the annotated information of the *B. thurigiensis* strain BMB171 in the KEGG database (http://www.kegg.jp/kegg-bin/search_pathway_text?map=btb&keyword=&mode=1&viewImage=true). The colors of the marked genes are: red, up-regulated at 13 h compared to 7 h; purple, specifically induced at 13 h; blue, remaining almost unchanged at each phase; green, down-regulated at 13 h compared to 7 h at the transcriptional level.

Figure S1

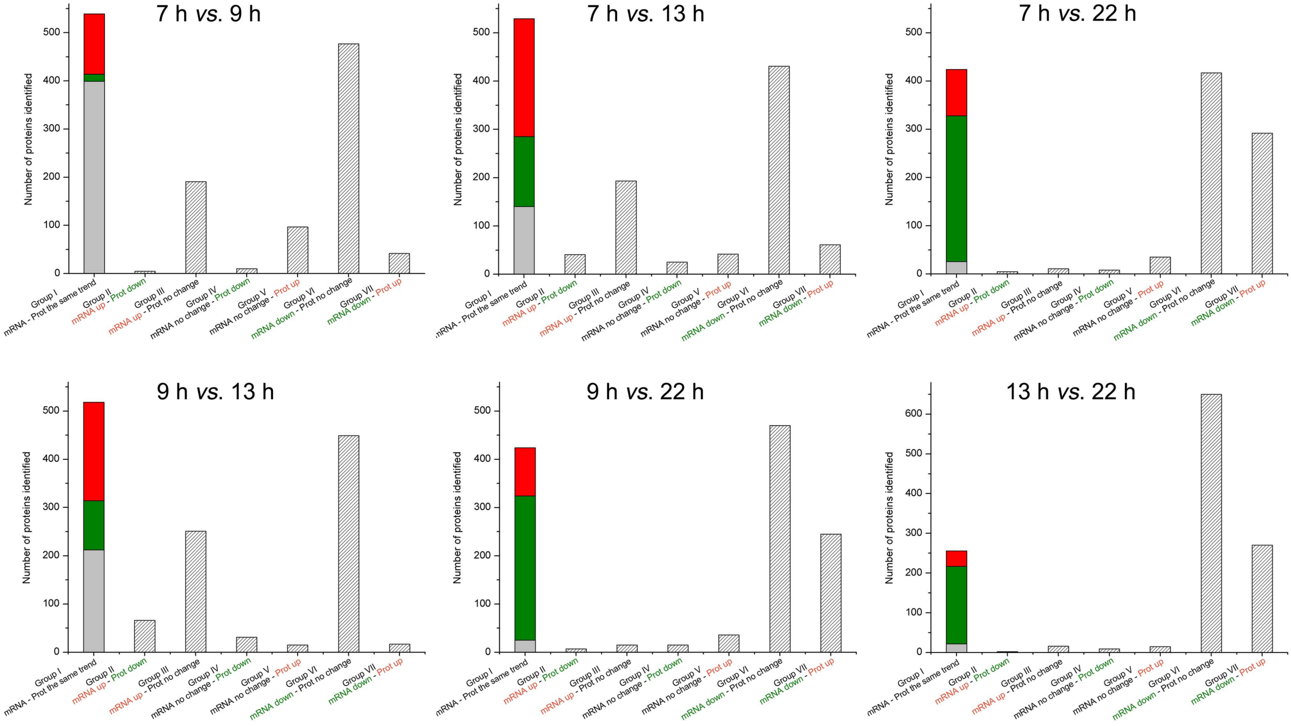

7 h vs. 9 h
7 h vs. 13 h
7 h vs. 22 h
9 h vs. 13 h
9 h vs. 22 h
13 h vs. 22 h
Number of proteins identified
0
100
200
300
400
500
600
Group I
mRNA - Prot the same trend
Group II
mRNA up - Prot down
Group III
mRNA up - Prot no change
Group IV
mRNA no change - Prot down
Group V
mRNA no change - Prot up
Group VI
mRNA down - Prot no change
Group VII
mRNA down - Prot up

Figure S2

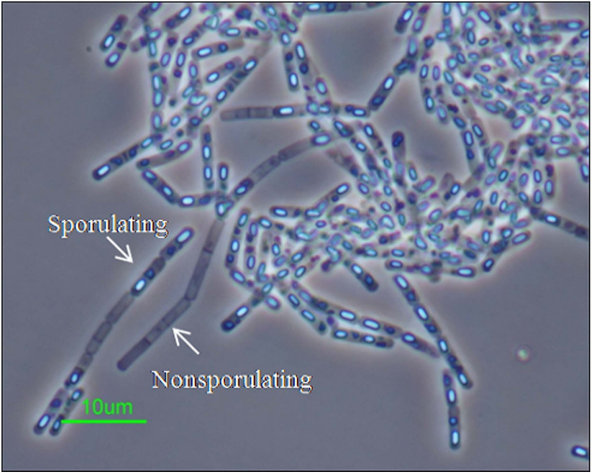
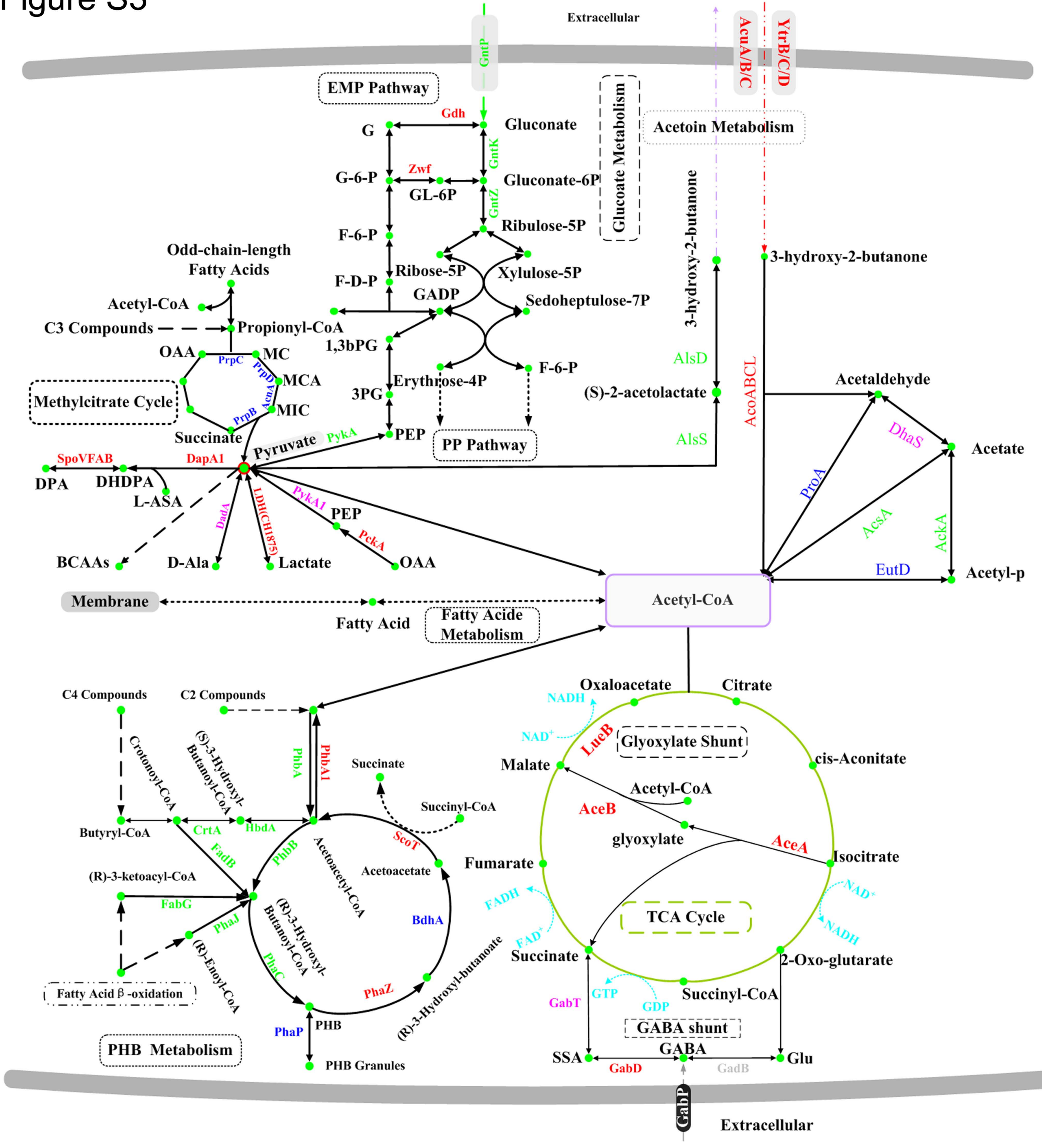


Figure S3


Extracellular
GntP
AcuA/B/C
YtrB/C/D
EMP Pathway
Glucoate Metabolism
Acetoin Metabolism
Gdh
G
Gluconate
GntK
Zwf
G-6-P
GL-6P
Gluconate-6P
GntZ
Ribulose-5P
F-6-P
Odd-chain-length
Fatty Acids
Ribose-5P
Xylulose-5P
F-D-P
GADP
Sedoheptulose-7P
3-hydroxy-2-butanone
3-hydroxy-2-butanone
Acetyl-CoA
C3 Compounds
Propionyl-CoA
1,3bPG
OAA
PrpC
MC
PrpD
MCA
F-6-P
AlsD
AcoABCL
Methylcitrate Cycle
AcnA
Erythrose-4P
3PG
(S)-2-acetolactate
Acetaldehyde
PrpB
MIC
Succinate
PEP
PP Pathway
DhaS
Acetate
Pyruvate
PykA
AlsS
SpoVFAB
DapA1
DPA
DHDPA
L-ASA
PykA1
PEP
ProA
DadA
LDH(CH1875)
PckA
AcsA
AckA
BCAAs
D-Ala
Lactate
OAA
EutD
Acetyl-p
Membrane
Acetyl-CoA
Fatty Acid
Fatty Acide
Metabolism
C4 Compounds
C2 Compounds
Oxaloacetate
Citrate
NADH
Crotonoyl-CoA
(S)-3-Hydroxyl-
Butanoyl-CoA
PhbA
PhbA1
NAD+
LueB
Glyoxylate Shunt
Succinate
Malate
cis-Aconitate
Acetyl-CoA
Succinyl-CoA
AceB
Butyryl-CoA
CrtA
HbdA
glyoxylate
AceA
ScoT
Isocitrate
FadB
PhbB
Acetoacetyl-CoA
Acetoacetate
Fumarate
(R)-3-ketoacyl-CoA
NAD+
FADH
FabG
BdhA
TCA Cycle
PhaJ
(R)-3-Hydroxyl-
Butanoyl-CoA
FAD+
NADH
(R)-Enoyl-CoA
PhaC
(R)-3-Hydroxyl-butanoate
Succinate
2-Oxo-glutarate
Fatty Acid β -oxidation
PhaZ
GabT
GTP
GDP
Succinyl-CoA
PhaP
PHB
GABA shunt
PHB Metabolism
PHB Granules
SSA
GABA
Glu
GabD
GadB
GabP
Extracellular