



Development of bioconversion system for reutilization
of organic wastes including food waste

()

“ ”

2000. 10. 21.

()

:
:

:
:
:

.

.

가

.

catabolite repression resistant

가

가

.

가

.

, pH

,

가

.

가

. , 1)
 , 2)
 , 3)
 가 가 . , 1)
 , , 2)
 , , 3)
 가 , 4)
 가 , 5)
 . ,
 가
 .
 가가 2
 가 ,
 가가
 가
 가
 .
 .

1.

(50

)

2.

(

6%

80%

)

3.

4.

5. Bt (*Bacillus thuringiensis*)

1×10^9 M \emptyset

6. 60BIU (Bt)

가

Bt

7. Pilot Plant

1

8. Pilot Plant

1

9. Pilot Plant

2

2

10.

(

,

, Lay-out,

)

.

.

1.

- , key enzyme , ,

- 80% 2 가

2.

- protease, cellulase,
amylase

Bacillus thermoglucosidasius (EFB3)

-
Bacillus thermoglucosidasius catabolic repression insensitive
mutant

- *Bacillus thermoglucosidasius* catabolic
repression insensitive

3.

- 가 *Saccharomyces*
cerevisiae, *Lactobacillus* sp., *Acinetobacter* sp.

- 가 *Bacillus thuringiensis*

4.

- 1

5. Bt

- 1 Bt

- Bt

6.

- (1) 5L pilot plant

- , , pH

- 10

.

●

● 가 ,

●

가

● 가 , 가가 , ,

, ,
가 .

●

가 . 가

S U M M A R Y

Despite many efforts to reuse of food wastes, most case has been restricted to use as compost or animal feed. We have developed a novel cost-effective method using two-stage fermentation system to produce valuable products from food waste.

As amylase and cellulase were key enzymes for degrading food wastes, we isolated *Bacillus thermoglucosidasius* (EFB 3) producing the enzymes from food wastes. And this strain was mutated by NTG and UV for resistance against glucose catabolite repression. The phenomenon, catabolite repression, is widespread system in microorganisms, whereby the presence of a rapidly metabolizable carbon source in the growth medium inhibits the synthesis of catabolic enzymes for other carbon source.

The primary fermentation step using the catabolite repression insensitive mutant of thermophilic *Bacillus thermoglucosidasius*, producing amylase, protease and cellulase, was designed for preparation of glucose-rich standardized substrate for bacterial cultivation.

In the secondary fermentation, the useful microorganisms were cultivated in the supernatant from the primary step. The growth rates of *Saccharomyces cerevisiae*, *Lactobacillus* sp., *Acinetobacter* sp. and *B. thuringiensis* were higher than in case of cultivation in the rich media such as Potato dextrose broth, MRS broth and Nutrient broth. The primary fermentation of food waste at 55 °C for 24h resulted in the reduction of initial solid content of 7% to 2.5%, and

increasing of glucose concentration from 5g/l to 8g/l.

For scale-up of the bioconversion system, we also pretreated food wastes by heat shock (80 °C for 5min) instead of autoclave (121 °C for 15min) and condition for primary fermentation was optimized. The optimal temperature, fermentation time and maximum solid content of food wastes were 55 °C, 24 hours and 8% (w/v), respectively. In secondary fermentation for cultivation of Bt, optimal C/N ratio was 40.

In fed batch bioconversion system having biofilter for removal of unpleasure odor, products of 90% from primary fermentation was used standardized substrate for secondary fermentation for Bt, and the rest of products was used as seed culture for consecutive fermentation. And this system was compared with anaerobic digestion system. Digestion ratio of solid content and cell number of BtgMu series in this system were 40% (w/w) and 1.5×10^7 CFU/ml till sixth batch, respectively.

Our results revealed that the products from the primary fermentation of food waste could be used as a medium for the cultivation of useful microorganisms such as Bt, and this novel method could be a powerful tool for bioconversion of organic wastes including food wastes to valuable microbial products.

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1

1

“

“

(standard substrate)

1

(biopesticide),

(nitrogen-fixing bacteria)

가가

2

(bioconversion)

2

:

가

, 1)

, 2)

, 3)

가 가 .
, 1)
, 2) ,
, 3) 가
가 , 4)
, 5) .
,

가 (1).
: 가

Single Cell Protein (, 가
) (Lactic acid) “
” (2).

가가 가

가

:

가가

가

:

3

가

가가 2

가 ,

가가

가

Lactic acid

(3, 4).

:

2%

가 가

1)

가가

, 2)

, 3)

가

, 4)

가

가가

•

:

2

가

2005

가

3

1.

가. 1998

- 가
- single cell protein
- lactic acid , 가가
- Thermo-Tech 가
- (5).
- 1998
- Thermo-Tech
- 가

2.

가. 1998

- IMF
- Thermo-Tech

. 1998

-

가

-

-

가가

-

-

가

4

●

(50

)

●

(

6%

80%

)

●

● 1

● BT(Bacillus thuringiensis)

1 × 10⁹ Mℓ

● 60BIU(BT)

가

BT

● Pilot plant 1

- Pilot plant 1
- Pilot plant 2
- (,
- , Lay-out,)

2

1

1.

가.

- ,
· ,
· 가
· , 가
· ,
·
- 1) : ,
homogenizer 0.1mm
- 2) : dilution
alpha-amylase,
cellulase, proteinase, lipase .
- 3) Key enzyme : 가 key
enzyme 6% 55 , 24

. 24

ice machine

amylase

glucose , protease free

spectrophotometer, chromatography

4) : Alpha-amylase, cellulase, proteinase

5) : 가

(amylase, cellulase, proteinase)

2.

()

가.

nutrient

agar plate 30 50 24 72

. Plate colony

single colony . colony plate

soluble starch, CMC amylase, cellulase

(6). amylase cellulase

0.1% soluble

starch 1% cellulose 900μl ()

100 μ l 가 55 30 DNS (Dinitro
 salicylic acid) 15 570nm

100 μ l 가
 (Unit) 55 30 가 가
 0.001

55 ° C, 48
 plate

6% solid content(%),
 (CFU/ ml), (gram/ liter)

1
 가

utilization glucose
 UV TG (7).
 nutrient broth (beef extract 0.3%, peptone 0.5%) 5ml 55
 24 NTG 1mM 2
 가 1%

UV 20 erg 40

30mM 2- 100 μ l 55
24 2-

Group translocation

glucose가 0.3%, soluble starch CMC
(carboxymethyl cellulose)가 1% 가
24 1/ 10N iodine 0.1% Congo-red
가 가 amylase, cellulase
catabolite repression resistant

1 가 1 90% 1
amylase
cellulase
가,
가

3. Bt

가. Bt

(1), Bt
, Bt (2). Bt
Bacillus sporulation rate
, agar plate , sporulation rate heat shock
agar plate

bio assay

가

1 가
 (*Saccharomyces* sp.), (*Lactobacillus* sp.) Gram
Acinetobacter sp.

4.

가. 1

1) : 8%
 12% (w/w)

2) :
 121 80 heat shock

3) : 1
 (NaOH) 가 1
 가

1
 1) : 30, 37, 45, 50, 55
 24

2) : 96

3) pH : NaOH potassium
 phosphate buffering

- 4) :
- 5) (NAOH) 가 :
가

- 6) :
1 90% (v/v)
10

- 2
- 1) : Ultra filtration
2 1 2
2
- 2) 가 :
1 가 BT

pilot plant
(5 liter) piolot plant

2

1

가.

2 ,

1

Bt () 가가

2 (1)

가

, 가

84.16%, pH 6.8, , ,

27.3%, 11.5%, 2.83%, 56.8%

1.42%, potassium 0.23%

:

1) : 4%, 6%,

7%, 8.5%, 10%, 12%

alpha-amylase, cellulase, proteinase, lipase

6 7%

가

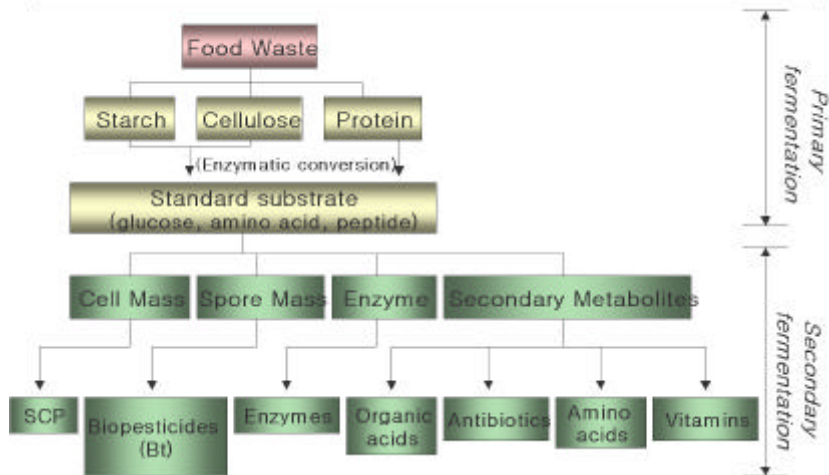
6%

2) Key enzyme : 가

key enzyme 6%

alpha-amylase가 가 key enzyme

Two Stage Fermentation of Food Waste



1. 2

가가

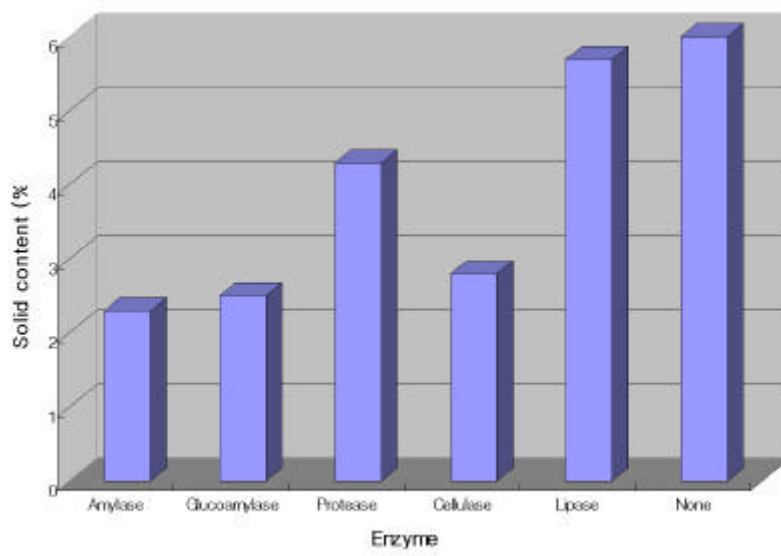
. 55 , 24 alpha-amylase 6%
 2.1% 65%
 glucoamylase (58%), proteinase (30%), cellulase (55%), lipase
 (9%) . Amylase가 6%
 2.1% key enzyme (2).
 3) : Alpha-amylase, cellulase, proteinase
 6%
 1.2% 80% .
 key enzyme
 alpha-amylase cellulase proteinase가 .
 1.2%

4) : 가
 (amylase, cellulase, proteinase)
 80%
 (3).

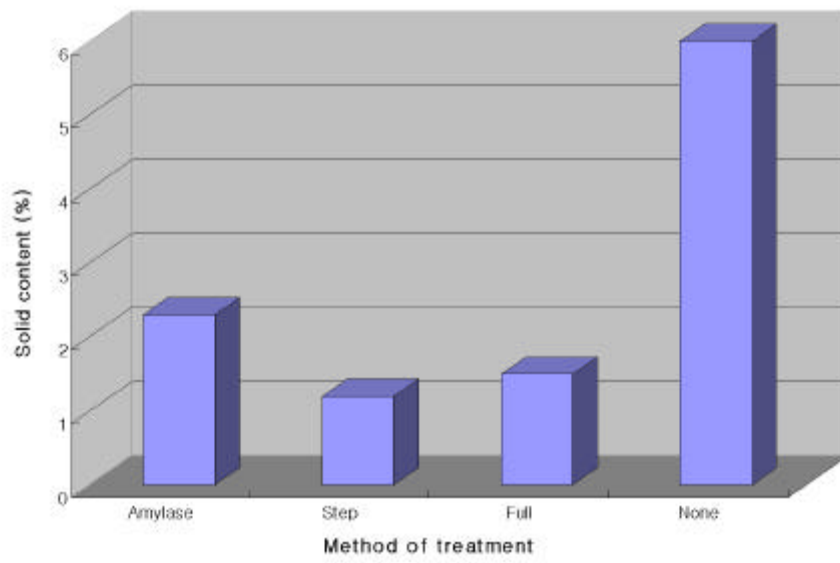
5) :
 가가
 2 , 80%
 amylase, cellulase

2.

()



2.



3.

가.

agar plate 37 ° C 24 48
plate colony .
colony 3ml nutrient broth

Ba (*Bacillus amyloliquefaciens*), L32 (*Bacillus licheniformis*), EFB
(1-38, *Bacillus thermoglucosidasius*), Hot (1-8,), New (1-5,
) 43 , .

43 soluble starch, casein, CMC
plate 24 plate
clear zone .

, Ba, EFB3 amylase activity가 ,
L32 Hot8 amylase activity가 . Protease activity
EFB3 가 43
. CMC cellulase L32,
EFB3, Hot8 EFB3 cellulase
activity가 3 .

43 55 ° C, 48
Hot1-8, New 1-5, EFB1-38

6% Ba, L32, EFB3, Hot8,
New2-3 30 ° C 144 solid
content(%), (CFU/ ml), (gram/ liter)
EFB3 2.0%, 5.5 X 10⁸, 1.7g/ l , 가

(classical mutation)

50

Bacillus

thermoglucosidasius (Btg)

glucose

glucose 가

Btg classical mutation

glucose utilization pathway block

1) BtgMu : UV/ NTG

glucose

amylase 가 (4).

2) BtgCelMu : UV/ NTG

glucose

cellulase 가 (4).

3) BtgMu BtgCelMu glucose utilization : BtgMu BtgCelMu가

glucose

glucose

(5).

4) BtgMu BtgCelMu : Solid state

BtgMu BtgCelMu

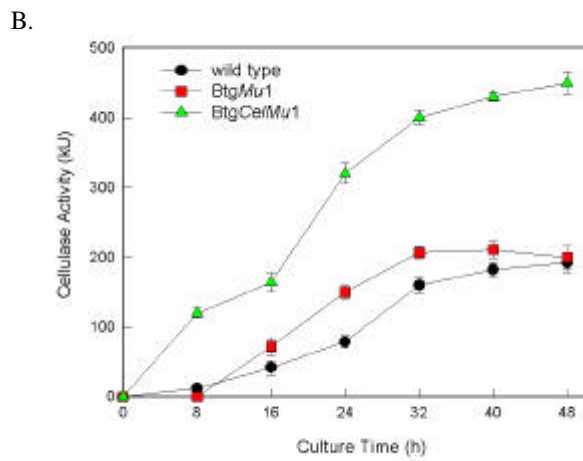
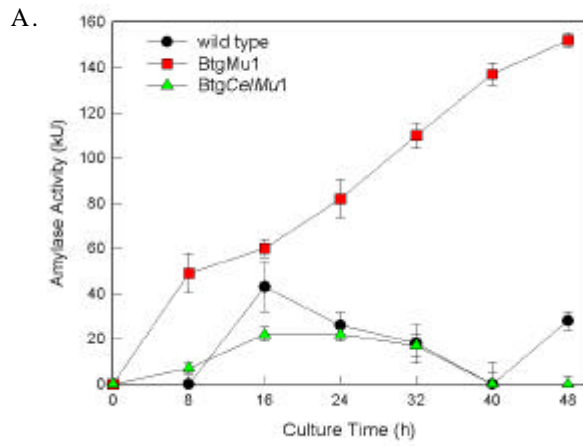
(Reduced Total Weight)

BtgMu BtgCelMu

13

65%

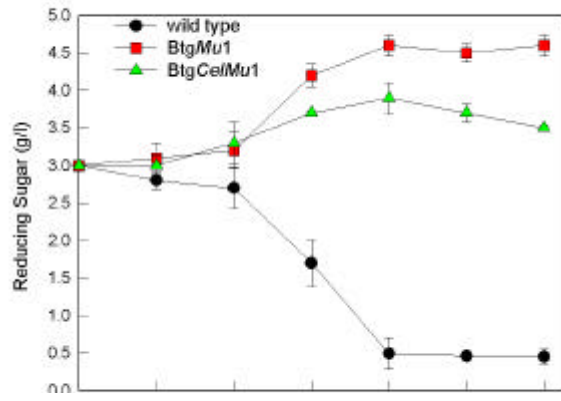
(6).



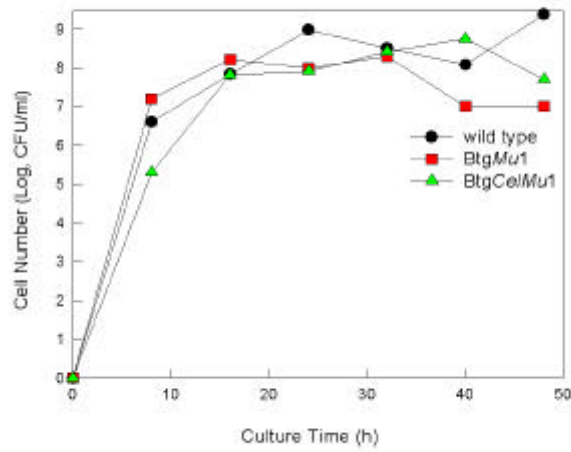
4. Wild type , BtgMu, BtgCelMu amylase cellulase

(A, amylase activity ; B, cellulase activity)

A.



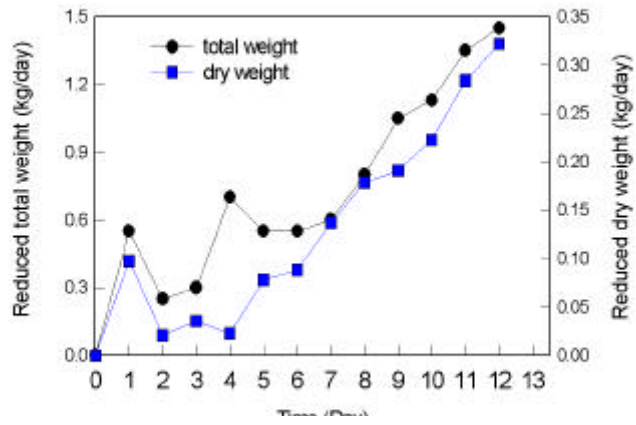
B.



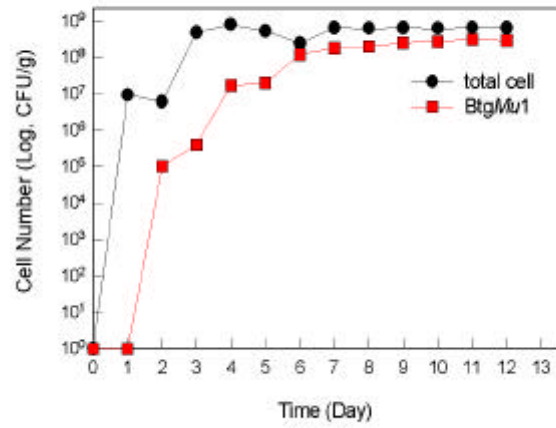
5. Wild type , BtgMu, BtgCelMu glucose utilization

(A, reducing sugar ; B, cell number)

A.



B.



6. BtgMu BtgCelMu

(A)

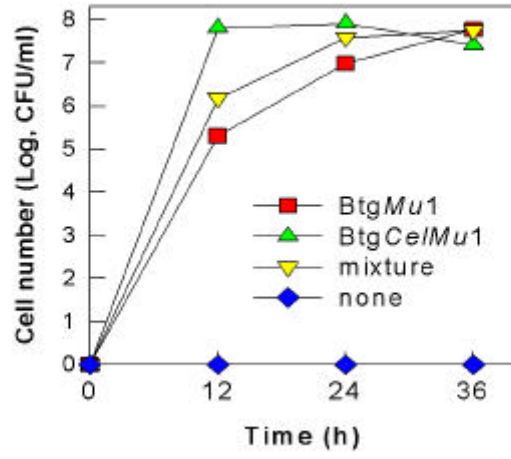
(B)

5) BtgMu BtgCelMu : Liquid state
 BtgMu BtgCelMu
 (Reduced Total
 Weight)가
 .
 6% 2%
 . BtgMu BtgCelMu 가
 (7).

6) BtgMu BtgCelMu :
 Liquid state BtgMu BtgCelMu
 amylase, cellulase
 가
 .
 (8, 9).

7) : Amylase, cellulase
Bacillus thermoglucosidasius glucose
 classical mutation
 BtgMu BtgCelMu glucose
 catabolite repression 가
 , bioconversion
 . Protease
 가 ,
 가 가 .
 . 1 ()
 1 1
 가 amylase
 3 , cellulase 1.5 .

A.



B.

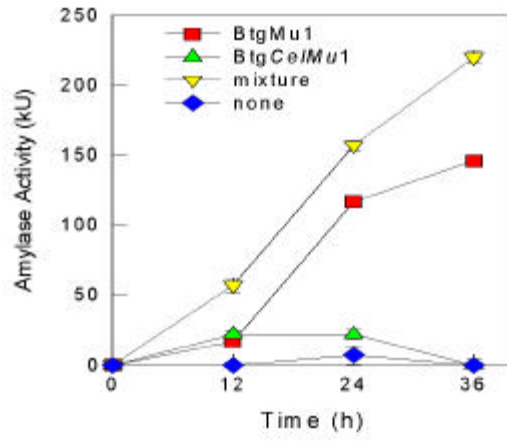


7. BtgMu1 BtgcelMu1

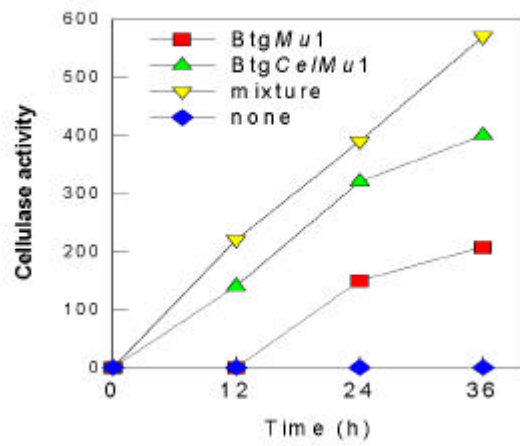
(A) 1 (B)

(BtgMu1, BtgMu1 ; BtgcelMu1, BtgcelMu1 ;
 BtgMu1 BtgcelMu1 ; none,)

A.



B.



8. BtgMu BtgCelMu amylase(A)
cellulase(B) 가

가

(1).

가

5.3 g/ liter

8.4 g/ liter

가

1. 1

	0	1	2	3
Amylase activity (U)	0	119	219	368
Cellulase activity (U)	0	240	310	358
Reducing sugar (g/ L)	5.3	6.6	7.3	8.4

Bacillus thermoglucosidasius

EFB3

가

amylase, cellulase activity

가

EFB3

amylase

cellulase

catabolite repression resistant

. 1

가

3. 2

Bt

가. Bt

: 1

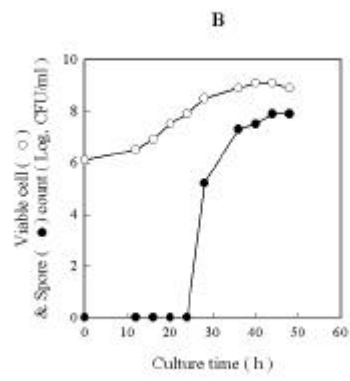
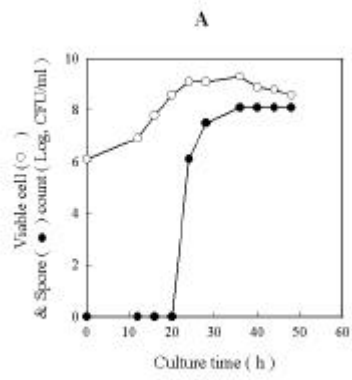
glucose가

가가

Bacillus

thuringiensis (Bt)

(10).



10. (A)
Bt

(B)

Bt : 2
(spore)

103 107 CFU/ ml
5 가
104 CFU/ ml Bt spore가 가
14
106 CFU/ ml Bt spore가 가 2
2 가
가

2.

(hrs)	(CFU/ml)					-	-
	107	106	105	104	103		
0.0	5	5	5	5	5	5	5
0.5	4	4	5	5	5	5	5
1.0	1	2	5	5	5	5	5
2.0	0	0	5	5	5	5	5
4.0	0	0	2	4	5	5	5
7.0	0	0	1	3	5	5	5
14.0	0	0	0	0	5	5	5
19.0	0	0	0	0	5	5	5
36.0	0	0	0	0	3	5	5
80.0	0	0	0	0	3	5	5
104.0	0	0	0	0	0	5	4
128.0	0	0	0	0	0	0	1
152.0	0	0	0	0	0	0	1

가
Saccharomyces cerevisiae, *Lactobacillus* sp., *Acinetobacter* sp. 1

24 4.2×10^9 , 1.4×10^9 , 1.4×10^{10} CFU/ ml

3.7×10^8 , 4.5×10^8 , 3.5×10^9 CFU/ ml

1 Bt

Bt sporulation rate 가
(10) *Saccharomyces cerevisiae*, *Lactobacillus* sp.,
Acinetobacter sp.

1
가가 2
scale-up
(bioconversion)
가 .

4.

가. 1

1) : 8.5%
agitation aeration 가 .
8.0%

2)

가) Autoclave

autoclave

108CFU
 80 0 5 40
 37 2
 1ml 1 ×
 5 가
 가 1 × 10⁴ CFU/ ml
 (3).

3.

	0day	1day	2day	
pH	6.67	5.28	5.09	5.19
(CFU/ ml)	5.2 × 10 ⁷	1.0 × 10 ⁸	2.6 × 10 ⁸	10 ⁴
(CFU/ ml)	10 ⁵	10 ⁵	10 ⁵	10 ⁴

)

1N NaOH
 pH가 12가 12

가

. 1

1) 1 : 6% *Bacillus*

thermoglucosidasius catabolite repression resistant mutant

30, 37, 45, 50, 55 1 pH,

37, 55 가 가 30

55 가

(11). 55

2) 1 : 37 2

(8

0 , 5) autoclave (121 , 15min) 1

autoclave 65% 가

58%

(12).

3) 1 : 48

55 1

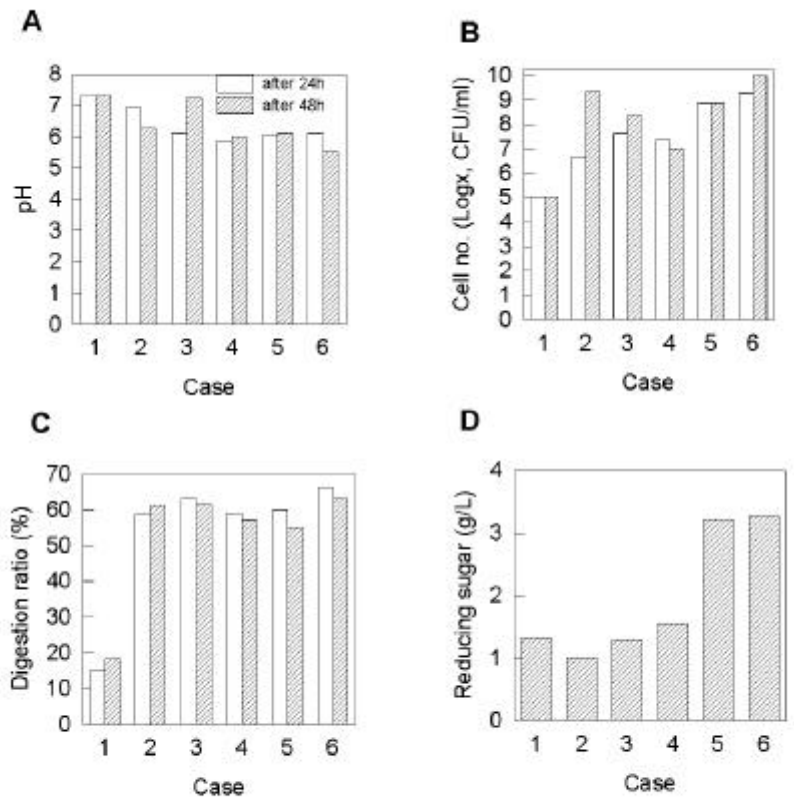
80 5

12 가

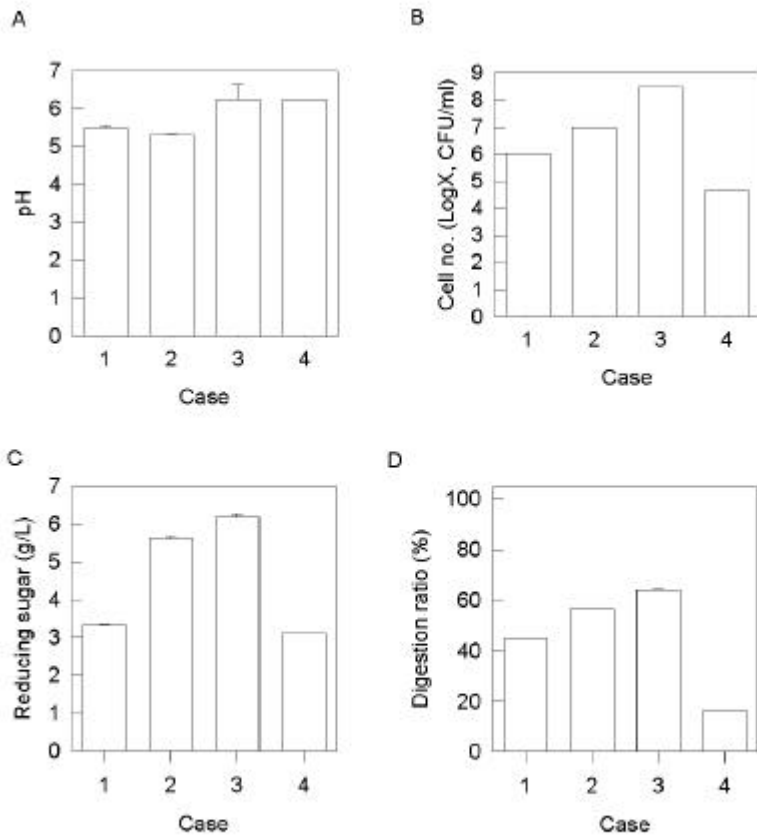
가 가

24 가 24

(13).



11. 1
 (1, culture at 4 ; 2, at 30 ; 3, at 37 ; 4, 45 ; 5, 50 ; 6, 55)
 (A, pH ; B, cell number ; C, digestion ratio ; D, reducing sugar)

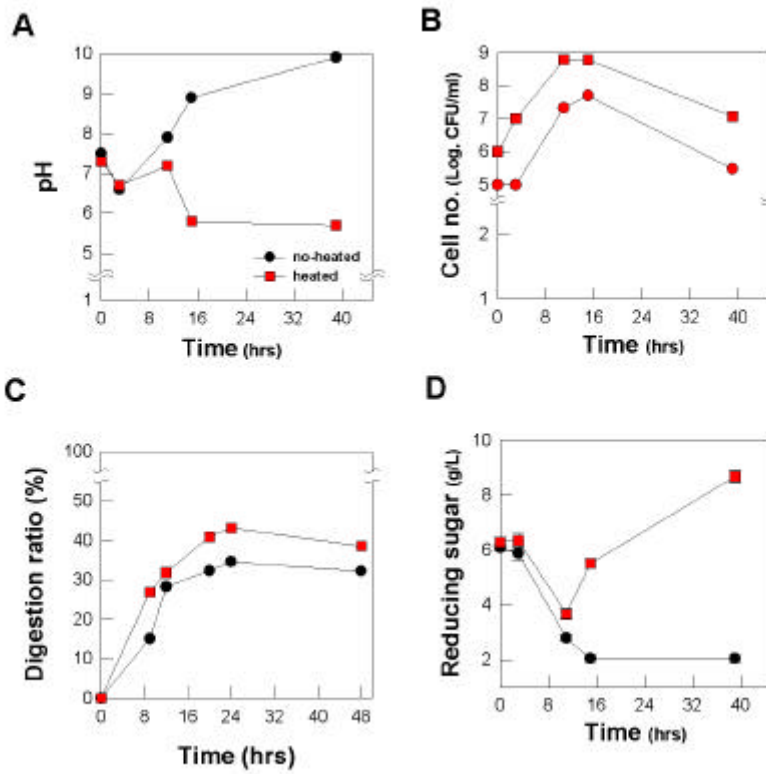


12.

1

(1, Btg ; 2, Btg ; 3, autoclave Btg ;
4, Btg)

(A, pH ; B, cell number ; C, reducing sugar ; D, digestion ratio)



13.

1

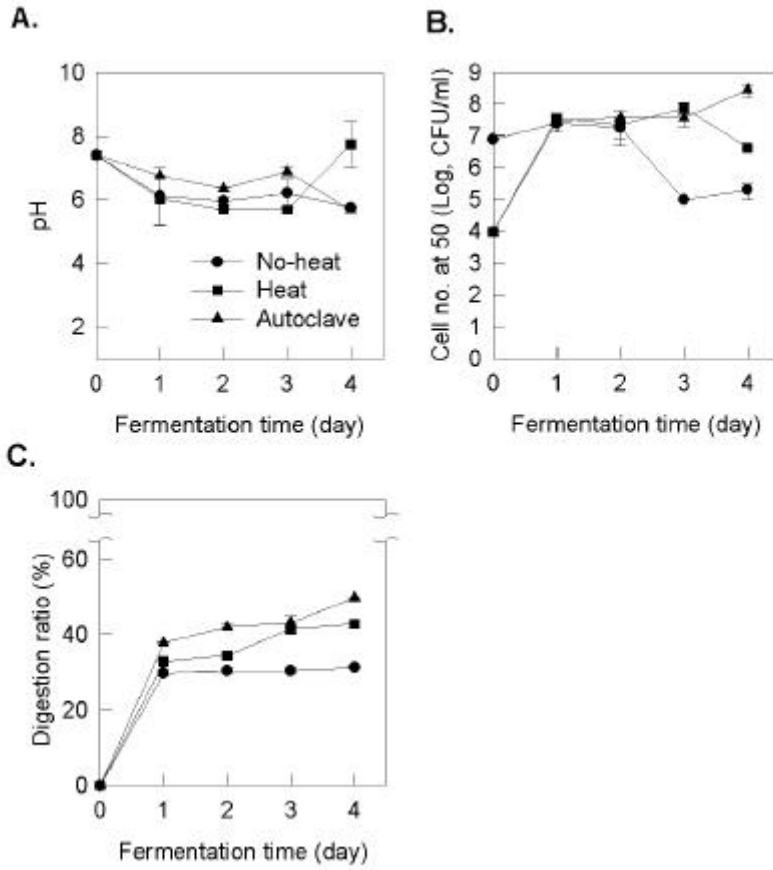
(A, pH ; B, cell number ; C, digestion ratio ; D, reducing sugar)

4) :

6% (w/w) 8% (w/w) pH,
55 4
65% (w/w)
24 (14).
39%

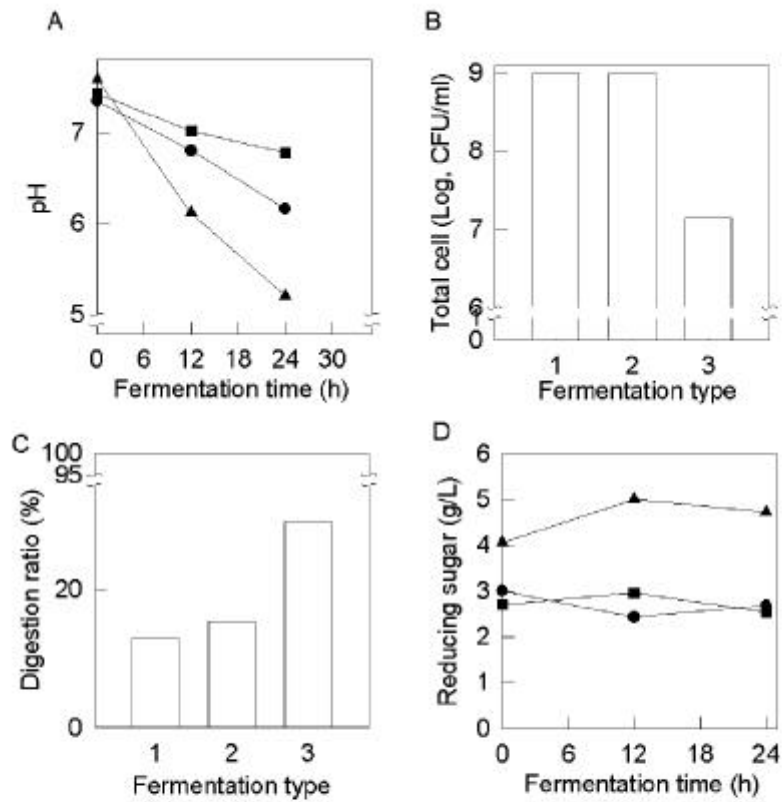
5) NaOH :

1
3가
(NaOH)
pH 12
가
37
80 5 55
가 pH
가 7
5.6
2.4 × 10⁶ CFU/ ml
109 CFU/ ml
2.4 × 10⁷ CFU/ ml
5.0g/ L 가
가 (15).



14. 8% (w/w) 1

(A, pH ; B, cell number ; C, digestion ratio)



Fermentation type

- 1, anaerobic fermentation of itself after NaOH treatment ;
- 2, aerobic fermentation of Btg after NaOH treatment ;
- 3, aerobic fermentation of Btg after heat treatment

- anaerobic fer.
- Btg fer. after NaOH
- ▲ Btg fer. after heat

15. NaOH

(A, pH ; B, total cell number ; C, digestion ratio ; D, reducing sugar)

6) Buffering effect : pH
 potassium phosphate buffering .
 buffer 1
 potassium phosphate 0, 5, 10, 50, 100, 200mM
 , pH .
 . buffer 가
 10mM

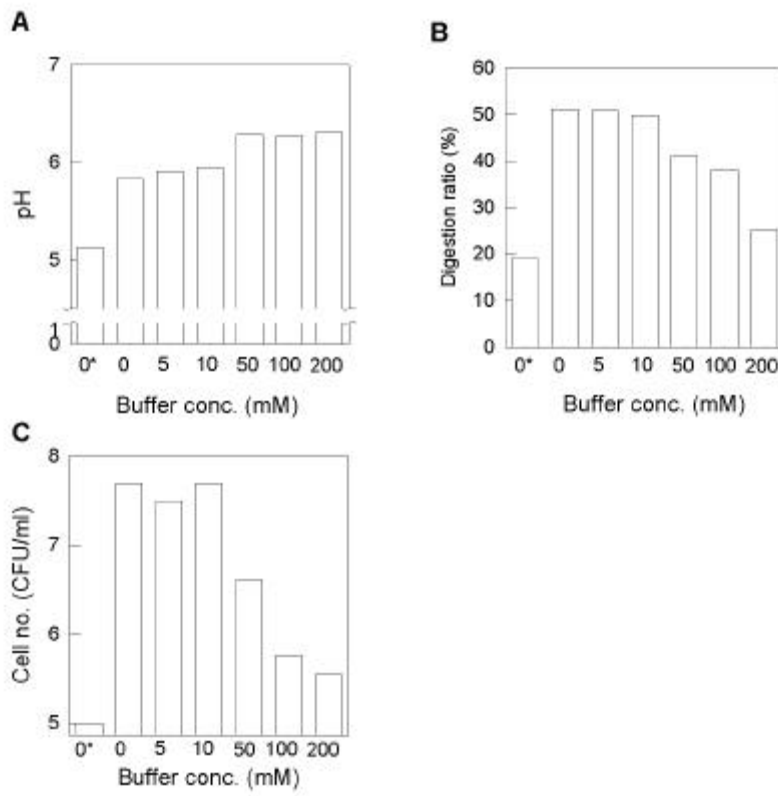
(16).

7) : 5 liter catabolite
 106 CFU/ ml (1% v/ v) 8%
 1 . 24
 10% 8% (w/ w)
 volume 90% .
 pH .
 pH buffering 5N NaOH
 , 가 .
 4 34% 가 106
 CFU/ ml .
 buffering NaOH
 (17).

. 2 2

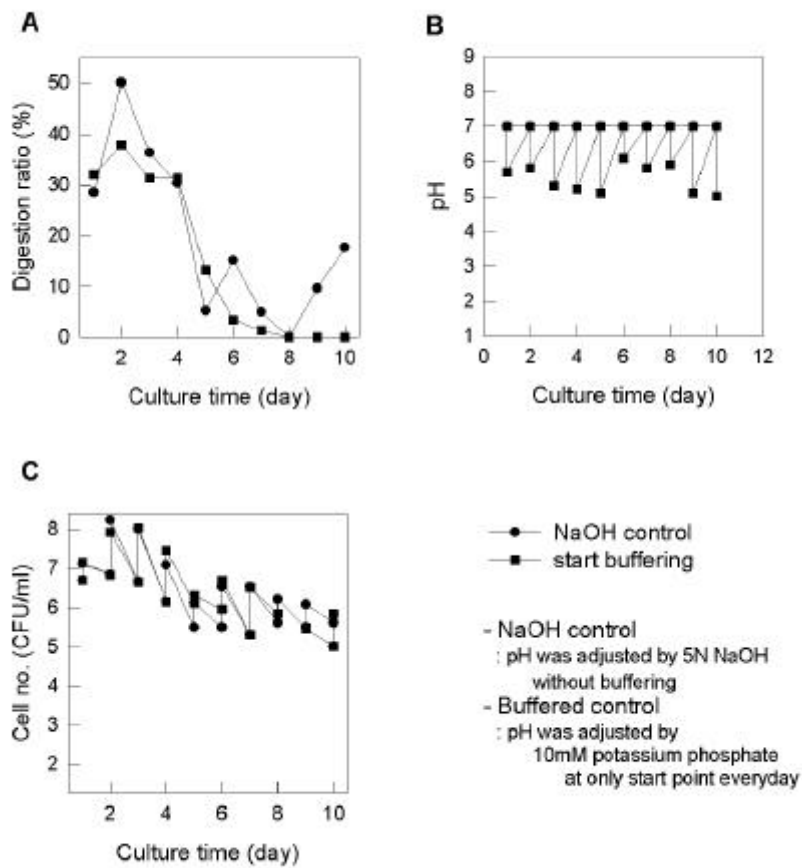
1)

1 8,000rpm 15 1
 Bt
 3.0×10^8 2.9×10^8 CFU/ ml . 1
 Bt
 .



16. buffer (potassium phosphate) 1

(A, pH ; B, digestion ratio ; C, cell number)



17. Fed batch 1

(A, digestion ratio ; B, pH ; C, cell number)

2) 2

1 8,000rpm 2

Bacillus thuringiensis

1%

pH NaOH HCl 7.0

glucose

ammonium sulfate 10, 20, 30, 40, 50, 60, 70%

C/ N 가 40

가

(18).

(, , ,)

,)

가 biofilter

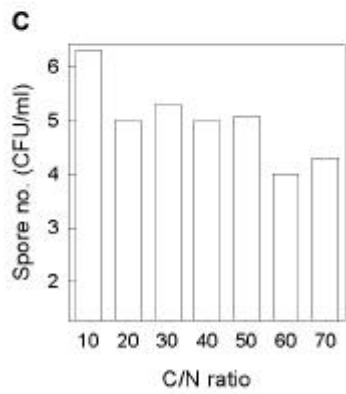
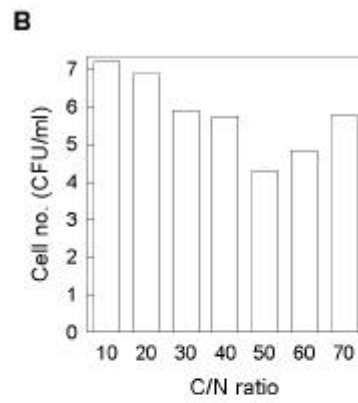
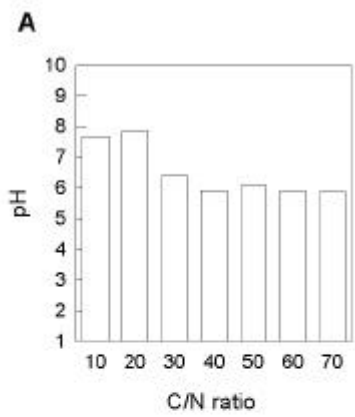
90% 4

4. Biofilter 1

	(ppm)	(ppm)	(ppm)	(ppm)	(ppm)
Biofilter	0	2	2	100	80
Biofilter	0	0	0	10	6

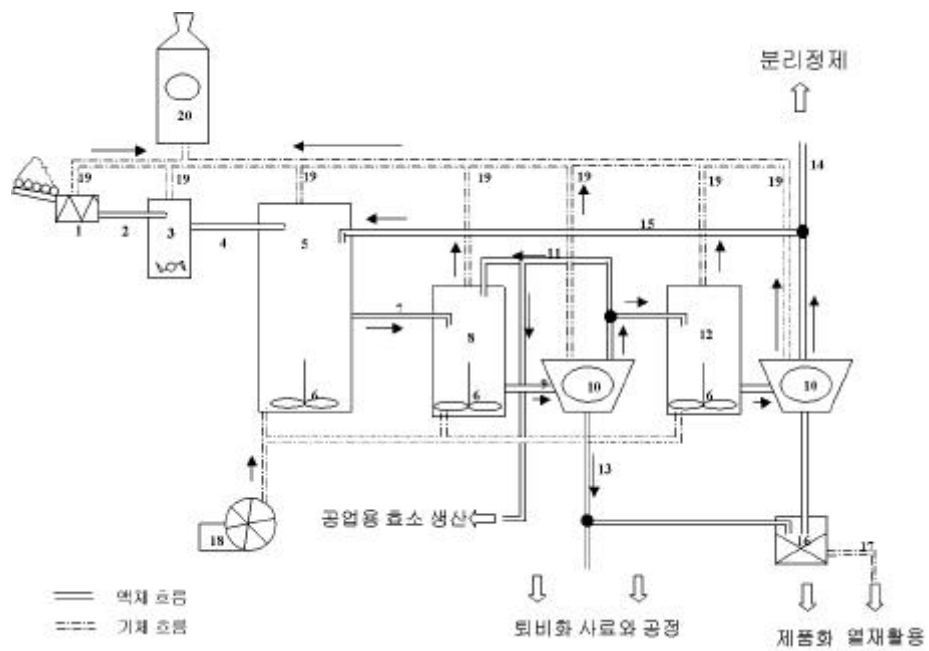
5.

19



18. Bt

(A, pH ; B, spore number ; C, cell number)



19.

(19)

(biofilter, 20)

10

3

6%

(glucose)

glucose

glucose

repression

1

가가

80%

2

Bt

Saccharomyces cerevisiae, *Lactobacillus* sp.,

Acinetobacter sp.

1

가가

2

scale-up

가

가 . Bt

Bt가

가 . 1

1

가

가

-

autoclave

80

가 가

-

NaOH

- 1

1

(55 , 24 ,

8%

)

1

- 1

pH

1

-

-

1

- 2

2

Bt

optimization

- Biofilter

1

●

가 ,
가
가 .

●

.

●

가가

●

가 가
가 Kg 200
가 Kg 100 .
10 (Kg
가 Kg 100 가)
.

●

, 가 가
가 가

●

가

가

가

●

2

1.

●

가 가

●

가

가

●

Thermo-Tech

가

2.

●

● 가 ,

●

● 가 가 ,

, , ,
가 .

●

가 . 가

1. .
(1999)
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1.

2.

3. 가