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# APPENDIX I

# **DETERMINATION OF NUTRITIVE VALUE**

# 1. Proximate analysis

- 1.1. Determination of moisture by hot-air oven method (Osborne and Voogt, 1972; AOAC, 1990; James, 1995)
- 1.1.1. Dry a coded, clean crucible in the oven for about 30 min, cool in a desiccator and weigh.
- 1.1.2. Mix the prepared sample thoroughly and transfer about 2 g to the crucible. Weigh the crucible and contents, as rapidly as possible
- 1.1.3. Dry in an oven at 101-105°C to constant weight, allowing for 6 h.
- 1.1.4. Remove the crucible from the oven, cool in a desiccator, and reweigh when cold.
- 1.1.5. Dry for a further hour period until successive weighings differ by less than 1.0% of the original mass of food sample.
  - 1.1.6. The percentage of moisture is calculated as follows;

% Moisture = 
$$(w_2 - w_3) / (w_2 - w_1) \times 100$$

where:

 $w_1$  = initial weight of empty crucible

w<sub>2</sub> = weight of crucible + sample before drying

 $w_3$  = final weight of crucible + sample after drying

1.2. Determination of crude protein by Macro Kjeldahl method (Osborne and Voogt,1972; AOAC,1990; James, 1995)

- 1.2.1. Accurately weigh 0.8 1.2 g of sample on the ashless filter paper and transfer to Kjeldahl digestion tube.
- 1.2.2. Add two Kjeltabs (Tecator, Sweden) to the tube, followed by 25 ml of concentrated sulfuric acid nitrogen-free, A.R. grade (E. Merk, Darmstadt, Germany) from an automatic dispenser.
- 1.2.3. Place the tube in the digestor (Buchi 430 Digestor) under the fume hood.
  - 1.2.4. Heat at a mean temperature of 130°C for 30 min.
- 1.2.5. increase the temperature over a 30 min period until the digest is boiling (about 350°C).
- 1.2.6. When the digest is a clear solution, continue boiling for a further 30 min.
- 1.2.7. Remove the tube from the digester and cool to room temperature.
- 1.2.8. Place the tube in the distillation unit (Buchi 322 distillation unit).
- 1.2.9. Place a conical flask containing 25 ml of 4% boric acid A.R. grade, E.Merk (containing modified methyl red indicator, 0.125 g methyl red and 0.0825 g methylene blue in 90% ethanol 100 ml) under the condenser outlet.
- 1.2.10. Dispense 100 ml of nitrogen-free distilled water and 120 ml of 40% sodium hydroxide (E. Merk, Darmstadt, Germany), distill for 8 min.
- 1.2.11. Titrate the ammonium borate solution formed with 0.1 N sulfuric acid to a purplish-gray end point.
- 1.2.12. Carry out a blank determination using the same method but without sample to be tested.
- 1.2.13. Calculate the nitrogen content and hence the protein content of the sample given that:

% Nitrogen content =  $(v_2 - v_1) / w \times N \times 1.4$ 

where :  $v_1$  = volume (ml) of sulfuric acid solution required for the blank test  $v_2$  = volume (ml) of sulfuric acid solution required for the sample w = weight (g) of the sample

N = normality of sulfuric acid

and:

% Crude protein = % nitrogen x F

where:

F = conversion factor (for soya = 5.71)

- 1.3. Determination of crude fat by the Soxhlet method (Osborne and Voogt, 1972; James, 1995)
- 1.3.1. Set up a Soxhlet extractor with reflux condenser and a distillation flask which has been previous dried and weighed.
  - 1.3.2. Dry the sample according to method in 1.1.
- 1.3.3. Weigh accurately 2 3 g of dried sample into a fat-free extraction thimble, plug lightly with cotton wool.
- 1.3.4. Place the thimble in the extractor and connect a weighed flask containing 120 ml petroleum ether (Mallinckrodt Chemical, USA). Connect the extraction to a reflux condenser.
- 1.3.5. Extract the sample, under reflux, on Electromantle EMO 500/C (Electrothermal, England) for 12 h.
  - 1.3.6. Evaporate the petroleum ether extract to dryness.
- 1.3.7. Dry the flask containing the fat residue in an hot-air oven at 100°C for 1 h, cool in a desiccator, and weigh.
- 1.3.8. Crude fat is calculated as a percentage of the sample taken given that :

% Crude fat = 
$$(w_2 - w_1) / w_3 \times 100$$

where:

w<sub>1</sub> = weight of empty flask (g)

 $w_2$  = weight of flask + fat (g)

w<sub>3</sub> = weight of sample taken (g)

1.4. Determination of ash by dry ashing method (Osborne and Voogt, 1972; James, 1995)

- 1.4.1. Weigh accurately 4 6 g of the sample into a previously ignited, cooled and weighed crucible.
- 1.4.2. If the sample is liquid, pre-dry on a steam bath to prevent splitting during the charring stage.
- 1.4.3. Place the crucible on a hot plate under a fume hood and slowly increase the temperature until smoking ceases and the sample becomes thorough charred.
- 1.4.4. Transfer the crucible to a muffle furnace at about 550°C and leave until a white or light gray ash results. If the residue is black in color, moisten with a small amount of water, to dissolve salts, dry in an hot-air oven and repeat the ashing process.
  - 1.4.5. Cool in a desiccator and reweigh.
- 1.4.6. Calculate the total ash as a percentage of original sample given that :

$$% Ash = (w_3 - w_1) / (w_2 - w_1) \times 100$$

where:

 $w_1$  = weight of empty crucible

w<sub>2</sub> = weight of crucible + sample before drying and/or ashing

 $w_3$  = weight of crucible + ash

- 1.5. Determination of crude fiber by extraction unit for determining raw fiber content (Fiwe, VELP Scientific) (Osborne and Voogt, 1972; VELP Scientifica, 1994).
- 1.5.1. Weigh accurately 1-2 g of sample into a crucible (glass filter, Robu-glass, Germany).
- 1.5.2. Add 1.25% sulfuric acid up to 150 ml notch, after preheating by the hot plate in order to reduce the time required for boiling.
  - 1,5.3. Boil 30 min exactly from the onset of boiling.
  - 1.5.4. Connect to vacuum for draining sulfuric acid.

- 1.5.5. Wash three times with 30 ml (crucible filled up to the top) of hot deionized water, connecting each time to compressed air for stirring the content of crucible.
- 1.5.6. After draining the last wash, add 150 ml of preheated sodium hydroxide (NaOH) 1.25%.
  - 1.5.7. Boil 30 min.
  - 1.5.8. Filter and wash as point 1.5.5.
- 1.5.9. Perform a last washing with cold deionized water aimed to cool the crucibles and then wash the crucible content three times with 25 ml of 95% ethyl alcohol, stirring each time by compressed air.
- 1.5.10. Remove the crucible and determine the dry weight after drying in an oven at 105°C for an hour or up to constant weight. Let cool in a desiccator. This weight represents the crude fiber plus ash content in comparison to initial weight.
- 1.5.11. When ash content is also required, the crucible are placed in a muffle at 500°C for 3 h and reweighed after cooling in a desiccator. The difference in weight in comparison to point 1.5.10 represents the crude fiber content without ash.
- 1.5.12. Calculate the crude fiber content as a percentage of sample given that:

% crude fiber = 
$$(w_2-w_3)/w_1 \times 100$$

where:

w<sub>1</sub> = weight of sample in the crucible (g)

 $w_2$  = weight of the residue in the crucible (g)

 $w_3$  = weight of ash in the crucible (g)

# 1.6. Determination of carbohydrates (James, 1995)

Carbohydrates content is calculated by difference method, estimating all the other fractions by proximate analysis, i.e.

# 2. Analysis of amino acid composition

Amino acid composition is determined by amino acid analyzer, Beckman system 6300 series (Osborne and Voogt, 1972; Matheson,1974; Meason et al., 1980)

- 2.1. Analysis of acid stable amino acids (except cystine and tryptophan)
- 2.1.1. Weigh accurately the sample containing 5-10 mg protein into hydrolysate tube.
- 2.1.2. Add 6 N hydrochloric acid (hydrochloric acid 1 ml per 1.5 mg protein) for hydrolyzing protein, then freeze.
  - 2.1.3. Vacuum and stopper the tube.
  - 2.1.4. Place the tube on the heating block, heat at 110°C for 24 h.
  - 2.1.5. Cool and dry at 40°C by rotary vacuum evaporator.
  - 2.1.6. Dissolve the residue in 20 ml of pH 2 sodium citrate buffer.
- 2.1.7. Separate the residue by centrifugation at 15,000 rpm for 5 min.
- 2.1.8. Transfer the supernatant solution into sample coil, place in autoinjection part of amino acid analyzer.

## 2.2. Analysis of cystine

Cystine is labile under acid hydrolysis condition, and require separate methods of analysis. It is therefore first oxidized with performic acid, to convert into cysteic acid and then freed from the protein by hydrolysis with hydrochloric acid.

2.2.1. Weigh accurately 20-30 mg (containing 10 mg of nitrogen content) into the tube.

- 2.2.2. Add performic acid (mix formic acid and hydrogen peroxide together to the ratio of formic acid to hydrogen peroxide 9:1, allow to stand for 1 h, then cool to 0°C).
- 2.2.3. Mix the sample with performic acid (point 2.2.2) thoroughly, stopper and leave to stand at 0°C for 16 h.
  - 2.2.4. Follow the steps in 2.1.2 to 2.1.8.

# 2.3. Analysis of tryptophan

Tryptophan is determined by measuring the atomic absorption of the sample after hydrolysis of protein with barium hydroxide and dimethylamino benzaldehyde, according to the method of Matheson (1974).

## 2.4. Chemicals and working condition

## 2.4.1. Chemicals

- Sodium column 12 cm (Beckman No. 338052)
- Buffer pH 2.0, 3.0, 4.0, and 6.0
- Ninhydrin reagent
- 0.1 N Sodium hydroxide

# 2.4.2. Working condition for amino acid analyzer

- Temperature of column : 48, 75, and 77°C

- Buffer flow rate: 14 ml/h

- Ninhydrin flow rate: 7 ml/h

- Detector detect at 570 nm

# 3. Vitamin analysis

3.1. Vitamin B<sub>1</sub> (thiamin) (Kaew Kangsadalampai and Pongtom Sungpuag, 1984)

#### inoculum and standard:

Microorganism: Lactobacillus fermini ATCC 9338

Assay medium: add 0.7% D-xylose to Bacto-Thiamin Assay medium (Difco)

# Preparation of standards:

- 1. Weigh 50 mg of thiamin into 500 ml volumetric flask and dilute to mark (solution a).
- 2. Pipette 5 ml of "solution a" into 500 ml volumetric flask and dilute to mark (solution b).

Standard a: Pipette 5 ml of "solution b" into 250 ml volumetric flask and dilute to mark (conc. 8 ng/ml).

Standard b: Pipette 2 ml of "solution b" into 100 ml volumetric flask and dilute to mark (conc. 20 ng/ml).

3. Pipette into 8 test tubes (in triplicate) according to the following:

conc.thiamin (ng/tube)	medium (ml)	dist. water (ml)	standard (ml)
0	2	2	0
4	2	0.5	1.5a
8	2	1	1.0a
12	2	0,5	1.5a
12	2	0	2a
20	2	1	1b
20 30	2	0.5	1.5b
40	2	0	2b

## **Procedure**

- 1. weigh x g of sample into a flask.
- 2. Add 80 ml of distilled water and add 3 ml of 3N sulfuric acid.
- 3. Place on waterbath (100°C) for 30 min.
- 4. Cool, adjust pH to 4.5 with 3M sodium acetate.
- 5. Add 100 mi of Takadiastase (fungal enzyme) and keep overnight in incubator at 37°C.
  - 6. Place into autoclave (120°C) for 5 min.
  - 7. Cool and dilute according to the weight of sample.
  - 8. Filter, adjust the filtrate to pH 6.1 with sodium hydroxide.
  - 9. Dilute to concentration about 5 ng/ml.
  - 10. Pipette in duplicate according to the following:

sample (ml)	dist.water (ml)	medium (ml)
0,5	1.5	2.0
1.0	1.0	2.0
2.0	0	2.0

- 11. Sterilize in autoclave at 100 °C for 15 min.
- 12. Cool, add one drop of inoculum.
- 13. Incubate at 37°C for 18 h.
- 14. Read in a spectrophotometer at 620 nm.

## Calculation

Draw a standard curve by plotting the concentration of the standard on the x axis vs its corresponding absorbance (OD) on the y axis and determine the slope. Then calculate the thiamin concentration in the sample as follows:

3.2. Vitamin B<sub>2</sub> (riboflavin) (Kaew Kangsadalampai and Pongtorn Sungpuag, 1984)

# Inoculum and standard:

Microorganism: Lactobacillus casei ATCC 7469

Assay medium: Bacto - Riboflavin Assay medium (Difco)

Preparation of standards

- 1. Weigh 25 g of riboflavin into a beaker.
- 2. Add small amount of 0.02 N acetic acid.
- 3. Heat on waterbath until dissolved, dilute to 500 ml (solution a).
- 4. Pipette 10 ml of "solution a" into 500 ml volumetric flask and dilute to mark (solution b).

standard a : Pipette 2 ml of "solution b" into 100 ml volumetric flask and dilute to mark (conc. = 20 ng/ml).

standard b: Pipette 5 ml of "solution b" into 100 ml volumetric flask and dilute to mark (conc. 50 ng/ml).

5. Pipette into 8 test tubes (in triplicate) according to the following:

conc. riboflavin (ng/tube)	medium (ml)	dist, water (ml)	standard (ml)
0	2	2	0
10	2	1.5	0.5 <b>a</b>
20	2	1	1a
30	2	0.5	1.5a
40	2	0	2a
50	2	1	1b
75	2	0.5	1.5b
100	2	0	2b

## **Procedure**

- 1. Weigh x g of sample into a flask.
- 2. Add 100 ml 0.1 N hydrochloric acid.
- 3. Place in autoclave (120°C) for 15 min.
- 4. Cool, adjust pH to 4.5 with 3 M sodium acetate.
- 5. Dilute according to the weight of sample.
- 6. Filter, adjust filtrate to pH 6.6 with sodium hydroxide.
- 7. Dilute to concentration about 20 ng/ml.
- 8. Pipette in duplicate according to the following:

sample (ml)	dist. water (ml)	medium (ml)
0.5	1 1.5	2.0
1.0	- 1.0	2.0
2.0	080000000000000000000000000000000000000	2.0

- 9. Sterilize in autoclave (120°C) for 10 min.
- 10. Cool, and add one drop of inoculum
- 11. Incubate at 37°C overnight
- 12. Read in spectrophotometer at 620 nm.

## calculation

Draw a standard curve by plotting the concentration of the standard on the x axis vs its corresponding absorbance (OD) on the y axis and determine the slope. Then calculate the riboflavin concentration in the sample as follows;

3.3. Niacin (Kaew Kangsadalampai and Pongtorn Sungpuag, 1984)

## inoculum and standard:

Microorganism: Lactobacillus plantarum ATCC 8014

Assay medium: Bacto-Niacin Assay Medium (Difco)

Preparation of standards

1. Weigh 50 mg of nicotinic acid into a beaker.

- 2. Dissolve with a little water and dilute 500 ml with 500 volumetric flask (solution a).
- 3. Pipette 1 ml of "solution a" into 100 ml volumetric flask and dilute to mark (solution b).

Standard a: Pipette 2 ml of solution b into 100 ml volumetric flask and dilute to mark (20 ng/ml).

Standard b: Pipette 5 ml of solution b into 100 ml volumetric flask and dilute to mark (50 ng/ml).

4. Pipette into 8 test tubes in triplicate according to the following:

conc. niacin (ng/ml)	medium (ml)	dist, water (ml)	standard (ml)
0	2	2	0
10	2	1.5	0.5a
20	2	1 1	1.0a
30	2	0.5	1.5a
40	2	0	2.0a
50	2	1	1.0b
75	2	0.5	1.5b
100	2		2.0b

#### Procedure

- 1. Weigh x g of sample into a flask.
- 2. Add 80 ml of 1 N hydrochloric acid.
- 3. Place in autoclave (120°C) for 20 min.
- 4. Cool, adjust pH to 6.8 with sodium hydroxide.
- 5. Dilute according to the weight of sample.
- 6. Filter, dilute clear filtrate to a concentration of about 20 ng/ml.
- 7. Pipette in duplicate according to the following:

sample (ml)	dist. water (ml)	medium (ml)
0.5	1.5	2
1	7 / 9 200 10	2
2	0	2

- 8. Sterilize in an autoclave (120°C) for 10 min.
- 9. Cool, add one drop of inoculum and mix thoroughly.
- 10. Incubate at 37°C for 18 h.
- 11. Read in a spectrophotometer at 620 nm.

#### Calculation

Draw a standard curve by plotting the concentration of the standard on the x axis vs its corresponding absorbance (OD) on the y axis and determine the slope. Then calculate the niacin concentration in the sample as follows;

# 3.4. Vitamin B<sub>6</sub> (pyridoxine) (Osborne and Voogt, 1978)

#### **Procedure**

# Extraction

- 1. Weigh between 0.5 g and 15 g into a 400 ml beaker, containing not more than 12.5  $\mu g$  vitamin B<sub>6</sub>.
  - 2. Add 180 ml of 0.44 N sulfuric acid.
  - 3. Cover the beaker with an aluminium foil cap.
  - 4. Autoclave for 5 min at 121°C.
  - 5. Remove from autoclave and cool in waterbath.
  - 6. Add 20 ml of 4 N sodium hydroxide, using a measuring cylinder.
- 7. Adjust to pH 4.5 on a pH meter, using 1 N and 0.1 N sodium hydroxide solution.
  - 8. Rinse electrode with water.
- 9. Transfer contents of beaker to volumetric flask and dilute to 250 ml with water.
- 10. Filter through Whatman No. 42 paper (or No. 541 paper if samples contain no fat).
- 11. Store the filtrate in the refrigerator until needed (extracts may be stored for up to 36 h).
- 12. Dilute the filtrate if necessary to given pyridoxine concentration of approximately 50 ng/ml.

Reagent blanks are taken through the same procedure in duplicate.

# Praparation of assay solution

- 1. Serially dilute the pyridoxine stock standard solution 5 ml to 500 ml and 5 ml to 100 ml to given a pyridoxine working solution (50 ng/ml). Pipette 0, 0.04, 0.08, 0.12, 0.16, and 0.2 ml of working standard solution in duplicate into assay tubes.
- 2. Pipette 0.05, 0.10, and 0.20 ml aliquots of each sample extraction in duplicate into assay tubes.

- 3. Using a suitable dispenser add 5 ml of double strength medium to each assay tube.
- 4. Dipense 5 ml aliquots of medium into a further set of assay tubes to act as blanks.
  - 5. Cap each tube with polypropylene cap.
  - 6. Autoclave the assay for 5 min at 121°C.
  - 7. Remove from autoclave and cool to below 30°C in waterbath.

# Preparation of the inoculum

- 1. Transfer cells of Saccharomyces carlsbergensis from the agar slope to a tube containing 5 ml of sterile double strength pyridoxine Y medium.
- 2. Incubate for 20 h at a temperature between 28 and 30°C with the loosely capped tube inclined at an angle of 45°C.
- 3. Prepare inoculum by diluting the subculture aseptically with sterile double strength medium until a reading of 50 is obtained on the standard perpex scale.

## Inoculation and incubation of tubes

- 1. Fill a sterile 10 ml pipette with the inoculum.
- 2. Remove the cap from the first assay tube.
- 3. Immediately add 1 drop only of the inoculum to the tube and replace the cap loosely.
- 4. Repeat the process for each tube in the assay except the uninoculated blank tubes.
  - 5. Place the assay in an incubator with each tube in an inclined position.
  - 6. Incubate at 30°C for 2 to 22 h.
  - 7. Remove tubes from the incubator and add 7 ml of water to each.

## Measurement of growth

- 1. Mix the contents of each assay tube on a Vortex mixer immediately before reading the nephelometer.
- 2. Place an uninoculated blank tube in the instrument and adjust the reading to zero.

- 3. Place an assay tube containing 0.2 ml of standard in the instrument and set the reading to approximately 95-100% full scale deflection.
- 4. Read the remaining assay solution, mixing each before placing in the instrument and record the galvanometer readings.

## Calculation

- 1. Draw a standard curve by plotting nephelometer reading against nanogram pyridoxine per tube for standards.
- 2. From the graph obtain the amount of pyridoxine (ng) in each pair of assay tubes,  $x_1$ ,  $x_2$ ,  $x_3$ .

Let: Aliquots (ml) taken for the assay be v<sub>1</sub>, v<sub>2</sub>, v<sub>3</sub> respectively.

Then: Concentration of pyridoxine in sample extract =  $(x_1/v_1 + x_2/v_2 + x_3/v_3)/3$  ng/ml = a ng/ml.

Let: Weight (g) of sample = w

Volume (ml) of extract = v

Then: Pyridoxine content (mg/100 g) =  $(a \times v \times 10^2) / (w \times 10^6)$ =  $(a \times v) / (w \times 10^4)$ 

3.5. Vitamin B<sub>12</sub> (cobalamine) (Osborne and Voogt, 1978)

## Procedure

# Extraction

- 1. Weigh out between 0.25 g and 5.0 g of sample into 25 mm x 150 mm assay tubes containing not more than 40 ng  $B_{12}$ .
- 2. Add 20 ml of acetate buffer solution and 2 drops of sodium cyanide solution.
  - 3. Cover the tubes with aluminium foil caps,
  - 4. Immerse in a boiling water bath for 30 min.
  - 5. Cool and dilute the extracts to 50 ml with water.

- 6. Filter through Whatman No. 42 paper (or No. 541 paper if samples do not contain fat).
  - 7. If necessary the filtrate can be stored in refrigerator overnight.

# Preparatiopn of inoculum

- 1. Subculture the organism overnight from the *Lactobacilus leichmanii* culture and transfer to a tube containing 5 ml sterile micro inoculum broth.
  - 2. Incubate overnight at 37°C.
- 3. Mix and transfer 1 drop aseptically to a tube containing 5 ml of single strength vitamin  $B_{12}$  medium fortified with vitamin  $B_{12}$ .
  - 4. Incubate for 6 h at 37°C.
- 5. Prepare the inoculum by transferring 1 drop with a sterile pipette to an assay tube containing 10 ml of single strength assay media.

# Preparation of assay solutions

- 1. From the stock solution A, dilute 2 ml + 2 drops of sodium cyanide to 1000 ml with water to give standard B (20 ng/ml).
  - 2. From standard B dilute 4 ml to 100 ml to give standard C (0.8 ng/ml).
- 3. Pipette 0, 0.05, 0.1, 0.15, 0.2, and 0.25 ml aliquots of standard solution C in duplicate into assay tubes.
- 4. Dilute sample extracts, if necessary, to give a concentration of approximately 0.80 ng/ml.
- 5. Pipette 0.05, 0.1, and 0.2 ml aliquots of each extract in duplicate into assay tubes.
- 6. Using a suitable dispenser, add 10 ml of single strength media to each assay tube.
- 7. Add 10 ml of media into a further 5 assay tubes to act as blanks or to use in the preparation of inoculum.
  - 8. Cap all the tubes.
  - 9. Autoclave the whole assay for 5 min at 121°C (15 lb/in²).
  - 10. Remove from autoclave and cool to below 30°C in a waterbath.

# Inoculation and incubation of tubes

- 1. Loosen all caps, but leave tubes covered.
- 2. Fill a sterile 10 ml pipette with the inoculum.
- 3. Remove cap from first assay tube, then add 1 drop only of inoculum and rapidly replace the cap.
- 4. Repeat the process for each tube in the assay except the 5 blanks (uninoculated blanks).
  - 5. Place the assay in the incubator for 22 h at 37°C.

# Measurement of growth

- 1. Mix contents of each set of tubes using a Vortex mixer, just before reading. Read the assay an EEL nephelometer.
- 2. Place an inoculated blank tube in nephelometer and adjust the reading to zero.
- 3. Place an assay tube containing the top level of standard in the instrument and set the readings to approximately 95-100% full scale deflection.
- 4. Repeat the previous two procedure until the instrument is stable at 0 and a point between 95-100% full scale deflection.
- 5. Read the remaining assay tubes and record the galvanometer readings.

## calculation

- 1. Draw a standard curve by plotting nephelometer readings against picogram vitamin  $B_{12}$  per tube for standards.
- 2. From the graph obtain the amount of vitamin  $B_{12}$  (pg) in each pair of assay tubes  $x_1, x_2, x_3$ .

Let : Aliquots (ml) taken for the assay be  $v_1$ ,  $v_2$ ,  $v_3$  respectively.

Then: Concentration of vitamin  $B_{12}$  in sample extract  $(x_1/v_1 + x_2/v_2 + x_3/v_3)/3 = a pg/ml$ .

Let: Weight (g) of sample = w

Volume (ml) of extract = v

Then: Vitamin B<sub>12</sub> content (
$$\mu$$
g/100 g) = (a x v x 10<sup>2</sup>) / (w x 10<sup>6</sup>)  
= (a x v) / (w x 10<sup>4</sup>)

# 3.6. Pantothenic acid (Murata et al.,1967)

Samples are homogenized with water, then heated for 30 min in boiling waterbath. The extracts are treated with intestinal alkaline phosphatase and pigeon liver enzyme in pH 8.3 Tris buffer for 4 h at 37°C (Novelli et al.,1951), heated in an autoclave, cooled, adjusted to pH 5.0, and centrifuged. The assay is run on the supernatant, according to the method of Hoag et al. (1945), using Lactobacillus arabinosus. ATCC 8014, as test organism. The tubes are incubated for 15 h at 37°C, and the turbidity is read in a photoelectric colorimeter using 620 mµ filter.

Table A.1 : Standard protein of FAO/WHO 1973

(Joint FAO/WHO Ad Hoc Expert Committee 1973)

Amino acid	mg/g protein
Isoleucine	40
Leucine	70
Lysine	55
Methionine + Cystine	35
Threonine	40
Phenylalanine + Tyrosine	60
Valine	50
Tryptophan	10



# APPENDIX II

## **TECHNIQUES IN MICROBIOLOGY**

# Microbiological culture media

1. Potato dextrose agar (PDA)

Potato, peeied and cut up 200.0 g

Dextrose 10.0 g

Agar 15.0 g

Distilled water 1.0 l

# 2. Nutrient agar (NA) Nutrient agar 31.0 g Distilled water 1.0

# Microorganisms

- 1. Rhizopus oligosporus TISTR 3001 was obtained from Microbiological Resources Center (Bangkok MIRCEN), Thailand Institute of Scientific and Technological Research (TISTR). Stock of strain was maintained on PDA slopes at 5°C.
- 2. Bacillus subtilis TISTR 1 was furnished from Microbiological Resources Center (Bangkok MIRCEN), Thailand Institute of Scientific and Technological Research (TISTR). Stock of strain was maintained on NA slopes at 5°C.

## Subculturing

At bimonthly intervals, a subculture was made of a stock strain kept. This was done by using a sterile loop to pick up a few cells of the microorganisms and then making a streak of these on an agar slope in a test tube.

## The determination of microbial numbers

1. Total spore count of *Rhizopus oligosporus* TISTR 3001 (Gerhardt,1981; วัฒนาลัย ปานบ้านเกร็ค และ สรวง อุคมวรภัณฑ์, 2536)

A spore suspension of *Rhizopus oligosporus* TISTR 3001 on PDA slant was prepared by introducing 5 ml sterile 0.02% tween 80 in distilled water onto 3-day-old culture incubated at 30°C. Dilute the suspension so that 1 ml would be expected to yield 1 x 10<sup>7</sup> spores. The number of spores in the suspension was \*determined by haemocytometer.

## Procedure

- 1. Clean the chamber and the cover slip and let it air dry.
- 2. Make preliminary estimation of the concentration of spores. Proceed to the next step if the concentration is less than  $3 \times 10^8$  spores per ml. Otherwise, make a primary dilution of the spore suspension in 0.02% Tween 80 in distilled water.
- 3. Immediately fill the chamber with spore suspension. Let the chamber rest for 1-2 min.
  - 4. Examine with microscope under a high dry objective lens.
- 5. Count the spores lying within small squares. Optically, the number in each small square should be in the rang of 5 to 15. Score the spores that cross the bounderies of a square if they are on the upper or left side but not if they are on the lower or right side. It is best to count squares chosen in a systematic fashion, such as the four corner squares and the major diagonal squares. This prevents counting the same square twice and average a possible geometric gradient of spores in the chamber.

6. Calculate the number of spores by the following formula:

Small square counted area =  $1/5 \times 1/5 \times 1/10 \times 5$  mm<sup>3</sup> (A,B,C,D,E) = 1/50 mm<sup>3</sup> Number of spores in 1/50 mm<sup>3</sup> = X spores

Total initial spores counted =  $5X \times 10^4 \times \text{dilution factor spores/ml}$ 

Figure 5: The counting chamber of haemocytometer showing square chosen (A,B,C,D,E)

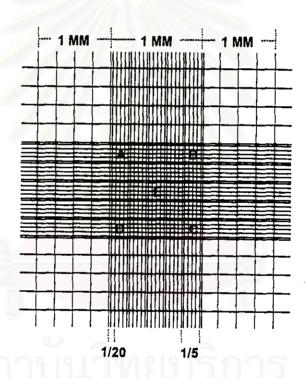
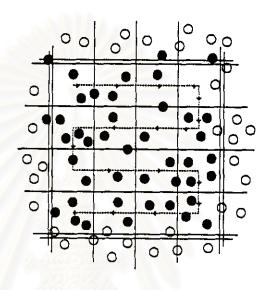


Figure 6: Method of spore counting

- score
- o unscore



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- 2. Total cells count of *Bacillus subtilis* TISTR 1 (Seeley and Demark, 1972; Poolsri Suwisuttagul, 1979)
- 2.1. Pour plate method (Seeley and Demark, 1972; Poolsri Suwisuttagul, 1979)

Bacillus subtilis TISTR 1 was grown on nutrient agar at 30°C for 2 days. The culture was suspended in sterile diluent (0.85% sodium chloride in distilled water).

#### Procedure

To dilute the culture suspension, 1-ml portion was diluted stepwise through a series of tubes containing 9 ml of 0.85% sodium chloride in distilled water. By containing this dilution stepwise through additional dilution tubes, we could dilute the culture suspension at 10<sup>-1</sup>, 10<sup>-2</sup>, 10<sup>-3</sup>, 10<sup>-4</sup>, and higher dilutions.

Pipette 1 ml of each dilution into each of two sterile petri dishes. Promptly pour the melted, cooled nutrient agar into the petri dishes and mix the culture suspension thoroughly with the agar by tilting or rotating the dishes. Allow the contents to solidify at room temperature and then incubate at 30°C for 24 h in an inverted position. Following incubation, the number of colonies developing on each dish in the range of 30 to 300 were counted. The number of bacteria of the initial culture suspension was then determined by multifying the number of colonies by the degree of dilution (dilution factor) of the dish that was being counted and express the average for the two dishes in terms of the number of cellls per ml of the initial culture suspension.

2.2. Turbidimetric estimation of cell growth (Seeley and Demark, 1972)

In the use of turbidimetry to measure cell growth, the turbidity of the bacterial culture is correlated with some other known measure of cell growth, such as the total number of bacteria as determined by the plate method. In this

experiment, we determined the turbidity of several dilutions of a 24-hour culture of *Bacillus subtilis* TISTR1 by spectronic 21 (Milton Roy Company) at 600 nm and also made plate counts on the culture to determine the cell number. From the results, we could find the correlation between turbidity and cell count and we would be able to estimate the number of cells present in the suspension which be used in inoculation step of tooa-nao production.



# APPENDIX III

# STATISTICAL ANALYSIS

1. Mean  $(\overline{x})$ 

$$\overline{x} = \frac{\sum x_i}{n}$$

where n = sample size

2. Standard Deviation (S.D.)

S.D. = 
$$\sqrt{\frac{\sum (x_i - \overline{x})^2}{n-1}}$$

3. One - way analysis of variance - ANOVA (Anderson, Sweeney, and Williams, 1981; Garcia - Diaz and Phillips, 1995)

# Basic notation and data format

			Treatmen	ts		
	j = 1	j = 2	j = 3	i	j = k-l	j = 1
i=1	$y_{11}$	$y_{12}$	$y_{13}$	$y_{1j}$	$y_{1,k}$ _	$\mathcal{Y}_{1k}$
i = 2	$y_{21}$	$y_{22}$	$y_{23}$	$y_{2j}$	$y_{2,k-1}$	$y_{2k}$
•	5101	:			•	÷
$i = n_i$	$y_{n1,1}$	$y_{n2,2}$	$y_{n3,3}$	$y_{nj,j}$	$y_{nk-1,k-1}$	$\mathcal{Y}_{nk,k}$
total	$T_{.1}$	$T_{.2}$	$T_{.3}$	$T_{.j}$	$T_{.k-1}$	$T_{.1}$
sample size	$n_{ m l}$	$n_2$	$n_3$	$n_{j}$	$n_{k-1}$	$n_k$
sample mean	$\overline{\mathcal{Y}}_{.1}$	<u> 7</u> . 2	<i>ӯ</i> .₃	$\overline{y}_{.j}$	$\overline{\mathcal{Y}}_{.k-1}$	$\overline{\mathcal{Y}}_{.k}$

The general analysis of variance table

Source of variation	df	SS	MS	F
Between treatments	k-1	SS treatment	$\frac{SS_{treatment}}{(k-1)}$	MS treatment MS error
Within treatment	N-k	SS <sub>error</sub>	$\frac{SS_{error}}{(N-k)}$	
Total variation	N-1	SS <sub>total</sub>		

$$SS_{treatment} = \sum_{j} \frac{T_{j}^{2}}{n_{j}} - \frac{T^{2}}{N}$$

$$SS_{total} = \sum_{i} \sum_{j} y_{ij}^{2} - \frac{T^{2}}{N}$$

$$SS_{error} = SS_{total} - SS_{treatment}$$
where  $i$  = number of sample in each treatment 1, 2, ...,  $n_{j}$ 
 $j$  = number of treatment 1, 2, ...,  $k$ 

$$T = \text{the grand total} \sum_{j=1}^{k} T_{j}$$

$$N = \text{the total number of observations} \sum_{j=1}^{k} n_{j}$$

# 4. Duncan's multiple range test

The Least Significant Difference (LSD) procedure is only use when the basic ANOVA test shown that at least one treatment mean is significantly different from the others i.e. when the treatment source of variation is formed to be significant by the F-Statistic.

It is easy to apply the LSD procedure, since one simply compares the observed absolute value of the difference between each pair of means. All pairs of treatment means whose difference exceeds the critical value are considered as significant.

$$R_C = \left[\frac{MS_{error}}{n}\right]^{1/2} Q'_{(r,\alpha,f)}$$

where

R<sub>C</sub> = Least Significant Difference

Q = Values of Duncan multiple range test

r = The number of steps between  $\overline{Y}_i$  and  $\overline{Y}_i$  ,that is

$$r = j - i + 1$$

 $\alpha$  = The significance level of the test

f = Degree of freedom within treatments (N-k)

n = Number of sample in each treatment

# Example

		Treatment		
Α	В	С	D	E
1.25	2.25	6.75	3.25	5,50
1.50	4.50	4.25	3,50	3.50
2.50	4.75	6.25	4.75	7.25
1.30	3.25	7.50	3.50	4.75
2.70	1.50	4.50	5.50	4.00
1.20	3.75	4.75	3.75	6.25
1.80	4.50	8.00	7.25	3.75

	A(j=1)	B(j=2)	C(j=3)	$D\left(j=4\right)$	E(j=5)	Total
$T_{i}$	12.25	24.50	31.50	35.00	42.00	T = 145.25
n.	7	7	7	7	7	<i>N</i> = 35
Y	1.75	3.50	4.50	5.00	6.00	

# Results from Duncan's test

	Y <sub>(1)</sub>	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	_ Y <sub>(5)</sub>
Y <sub>(1)</sub>	10-713	1.75*	2.75*	3.25*	4.25
Y <sub>(2)</sub>	101 41	1 0 0 1000	1.00	1.50*	2.50*
Y <sub>(3)</sub>	-		-	0.50	1.50*
Y <sub>(4)</sub>	-	•	-	-	1.00
Y <sub>(5)</sub>	-	• 1	-	-	-

<sup>\*</sup> indicate a significant difference between means.

The critical value for  $R_{\mathcal{C}}$  in this case are determined using

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,30)}$$

where the required critical value of the Q-Statistic come from values for Duncan's multiple range test,  $\alpha=0.05$ The following critical value are obtained:

 $r = 2 : Q'_{(2,0.05,30)} = 2.89$   $R_C = 1.41$   $r = 3 : Q'_{(3,0.05,30)} = 3.04$   $R_C = 1.48$   $r = 4 : Q'_{(4,0.05,30)} = 3.13$   $R_C = 1.52$  $r = 5 : Q'_{(5,0.05,30)} = 3.20$   $R_C = 1.56$ 

Table A.2: Analysis of variance table of moisture content (dry weight basis)

Source of variation	df	SS	MS	F	
			calculated	α=0.05	
Between treatments	5	20.320	4.0640	72.57*	3,11
Within treatment	12	0.673	0.0560		
Total variation	17	20.993			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

#### Results from Duncan's test

	Y <sub>(1)</sub>	Y <sub>(2)</sub>	_ Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(6)</sub>
Y <sub>(1)</sub>	• 19/1	0.20	1.31*	1.44*	1.70*	3,23*
Y <sub>(2)</sub>	-	-	1.11*	1.24*	1.50*	3.03*
Y <sub>(3)</sub>	- 4	-	-	0.13	0.39	1.92*
Y <sub>(4)</sub>	-	-	-	•	0.26	1.79*
Y <sub>(5)</sub>	-	U- c	-	-	•	1.53*
Y <sub>(6)</sub>	<b>5-</b> 91	79 19 14	19/19/19	15225	-	-

<sup>\*</sup> indicate a significant difference between means.

The critical value for  $R_{\!C}$  are as follows;

$$R_C = \left\lceil \frac{MS_{error}}{n} \right\rceil^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 0.4207$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.4412$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.4549$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.4590$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.4644$ 

 $Y_{(1)}$ = Soybean residue tempeh : 3.97°  $Y_{(2)}$ = Unfermented soybean : 4.17°  $Y_{(3)}$ = Soybean tooa-nao : 5.28 b Y(4) = Soybean tempeh : 5.41 b Unfermented soybean residue Y<sub>(5)</sub> : 5.67 <sup>b</sup> = Soybean residue tooa-nao  $Y_{(5)}$ : 7.20 ª

Table A.3: Analysis of variance table of crude protein content

Source of variation	df	SS	MS	F	
				calculated	α=0.05
Between treatments	5	834.210	166,8400	9533.71*	3.11
Within treatment	12	0.210	0.0175	,	0.,,
Total variation	17	834.420			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

# Results from Duncan's test

· <del>-</del> · · · · · · · · · · · · · · · · · · ·	Y <sub>(1)</sub>	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(6)</sub>
Y <sub>(1)</sub>	-	0.42*	0.61*	13.37*	14.09*	14.36
$Y_{(2)}$	-	10000	0.19	12.95*	13.67*	13.94
$Y_{(3)}$	-	1 ( ) He	113/11-12	12.76*	13.48*	13.75*
Y <sub>(4)</sub>	-	-	A and a	-	0.72*	0.99*
Y <sub>(5)</sub>	+	-	-	- 52	•.	0.27*
Y <sub>(6)</sub>	-	_	-	- /	-	-

<sup>\*</sup> indicate a significant difference between means.

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 0.2340$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.2450$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.2530$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.2550$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.2580$ 

= Unfermented soybean residue  $Y_{(1)}$ : 25.45 ° : 25.87 d = Soybean residue tooa-nao Y<sub>(2)</sub> : 26.06 d  $Y_{(3)}$ = Soybean residue tempeh Y<sub>(4)</sub> = Unfermented soybean : 38.82° : 39.54 b = Soybean tooa-nao  $Y_{(5)}$ : 39.81 \* = Soybean tempeh  $Y_{(6)}$ 

Table A.4: Analysis of variance table of crude fat content

Source of variation	df	SS	MS	F	
				calculated	α=0.05
Between treatments	5	449.570	89.9140	1729.12*	3.11
Within treatment	12	0.620	0.0520		
Total variation	17	450.190			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

# Results from Duncan's test

	Y <sub>(1)</sub>	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	$ Y_{(6)}$
Y <sub>(1)</sub>	-	0.21	1.74*	7.29*	9.10*	13.35*
Y <sub>(2)</sub>	•	A State	1.53*	7.08*	8.89*	13.14*
Y <sub>(3)</sub>	•	(2) 400)	112/11-12	5.55*	7.36*	11.61*
Y <sub>(4)</sub>	-	-	SA S	-	1.81*	6.06*
Y <sub>(5)</sub>	-	-	-	- 49	-	4.25*
Y <sub>(6)</sub>	-	<del>-</del>	•	-	-	-

<sup>\*</sup> indicate a significant difference between means.

The critical value for  $R_{C}$  are as follows;

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 0.4070$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.4260$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.4400$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.4440$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.4490$ 

= Soybean residue tooa-nao : 13.23 °  $Y_{(1)}$ : 13.44 \* = Soybean residue tempeh  $Y_{(2)}$ : 14.97 d = Unfermented soybean residue  $Y_{(3)}$ : 20.52° = Soybean tempeh Y<sub>(4)</sub> : 22.33 b = Unfermented soybean Y<sub>(5)</sub> : 26.58 ª = Soybean tooa-nao  $Y_{(6)}$ 

Table A.5: Analysis of variance table of ash content

Source of variation	df	SS	MS	F	
Codice of variation				caiculated	α=0.05
Between treatments	5	5.387	1.0770	828.46*	3.11
Within treatment	12	0.015	0.0010		
Total variation	17	5.402			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

## Results from Duncan's test

	Y(1)	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(5)</sub>
Y <sub>(1)</sub>	-	Ö	0.11*	1.02*	1.08*	1.24*
Y <sub>(2)</sub>	-		0.11*	1.02*	1.08*	1.24*
V.	-			0.91*	0.97*	1.13*
Y (3)	-	and the state of		-	0.06	0.22*
Y <sub>(5)</sub>	-0	-	-	-	-	0.16*
Y <sub>(6)</sub>	-	-	-	- 91	<u> </u>	

<sup>\*</sup> indicate a significant difference between means.

The critical value for  $R_{\rm C}$  are as follows;

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

 $r = 2 : Q'_{(2,0.05,12)} = 3.08$   $R_C = 0.0650$   $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.0680$   $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.0700$   $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.0706$  $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.0714$ 

Y <sub>(1)</sub>	<ul> <li>Unfermented soybean residue</li> </ul>	: 3.33 <sup>d</sup>
Y <sub>(2)</sub>	= Soybean residue tooa-nao	: 3.33 <sup>d</sup>
Y <sub>(3)</sub>	= Soybean residue tempeh	: 3.44 <sup>c</sup>
Y <sub>(4)</sub>	= Unfermented soybean	: 4.35 <sup>b</sup>
Y <sub>(5)</sub>	= Soybean tempeh	: 4.41 <sup>b</sup>
Yon	= Soybean tooa-nao	: 4.57 ª

Table A.6: Analysis of variance table of crude fiber content

Source of variation	df	SS	MS	F	
Coulds of variation				calculated	α=0.05
Between treatments	5	1008.644	201.7290	3955.471*	3,11
Within treatment	12	0.609	0.0510		
Total variation	17_	1009.253			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

# Results from Duncan's test

· · · · · · · · · · · · · · · · · · ·	Y(t)	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(6)</sub>
Y <sub>(1)</sub>		2.25*	2.95*	14.41*	17,44*	17.52*
Y <sub>(2)</sub>	· <b>-</b>	The second	0.70*	12.16*	15.19*	15.27*
Y <sub>(3)</sub>			Manager 1	11.46*	14.49*	14.57*
Y <sub>(4)</sub>	-		NA DADA	-	3.03*	3.11*
Y <sub>(5)</sub>		-	-	-	-	0.08
Y <sub>(6)</sub>	_	-	-	- 1	<u> </u>	

<sup>\*</sup> indicate a significant difference between means.

$$R_C = \left[\frac{MS_{error}}{n}\right]^{1/2} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 0.4000$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.4200$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.4330$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.4370$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.4420$ 

: 5.49 ° = Soybean tempeh  $Y_{(1)}$ : 7.74 d = Unfermented soybean  $Y_{(2)}$ : 8.44 <sup>c</sup> = Soybean tooa-nao  $Y_{(3)}$ : 19.90  $Y_{(4)}$ = Soybean residue tempeh = Unfermented soybean residue : 22.93 °  $Y_{(5)}$ : 23.01 ª = Soybean residue tooa-nao  $Y_{(6)}$ 

Table A.7: Analysis of variance table of moisture content (fresh weight basis)

Source of variation	df	SS	MS	F	
				calculated	α=0.05
Between treatments	5	127.550	25.5100	398,59*	3.11
Within treatment	12	0.770	0.0640		
Total variation	17_	128.320			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

# Results from Duncan's test

	Y <sub>(1)</sub>	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(5)</sub>
Y <sub>(1)</sub>	-	0.12	0.25	4.49*	5.07*	6.41*
Y <sub>(2)</sub>	-	and the state of t	0,13	4.37*	4.95*	6.29*
Y <sub>(3)</sub>		_	-	4.24*	4.82*	6.16*
Y <sub>(4)</sub>		-	-	-	0.58*	1.92*
Y <sub>(5)</sub>		-	-		•	1.34*
Y <sub>(6)</sub>	- (111)	-	-	-(11)	-	_

<sup>\*</sup> indicate a significant difference between means.

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 0.4497$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 0.4716$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 0.4862$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 0.4906$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 0.4964$ 

: 51.61 <sup>a</sup> = Soybean residue tooa-nao Y<sub>(1)</sub> : 51.73 d = Unfermented soybean residue  $Y_{(2)}$ : 51.86 d = Soybean residue tempeh  $Y_{(3)}$ : 56.10° = Unfermented soybean Y<sub>(4)</sub> : 56.68 b = Soybean tempeh Y<sub>(5)</sub> : 58.02 ª = Soybean tooa-nao  $Y_{(6)}$ 

Table A.8: Analysis of variance table of protein digestibility

Source of variation	df	SS	MS	F	
				calculated	$\alpha = 0.05$
Between treatments	5	374.040	74,8080	6.087*	3.11
Within treatment	12	147.470	12.2890		•
Total variation	17	521.510			

<sup>\*</sup> At least one treatment mean is significantly different from the others.

## Results from Duncan's test

<del></del>	Yan	Y <sub>(2)</sub>	Y <sub>(3)</sub>	Y <sub>(4)</sub>	Y <sub>(5)</sub>	Y <sub>(6)</sub>
Y <sub>(1)</sub>	-	5	7.27*	8.03*	8.53*	15.3*
Y <sub>(2)</sub>	-	A MEETE	2.27	3.03	3.53	10.3*
Y <sub>(3)</sub>	_	Carry Miles	118-2118-11-15	0.76	1.26	8.03*
Y <sub>(4)</sub>	•		Andrea	-	0.50	7.27*
Y <sub>(5)</sub>	<u></u>	-	-	-159	-	6.77*
Y <sub>(6)</sub>	_	-	-	•	-	-

<sup>\*</sup> indicate a significant difference between means.

$$R_C = \left[\frac{MS_{error}}{n}\right]^{\frac{1}{2}} Q'_{(r,0.05,12)}$$

$$r = 2 : Q'_{(2,0.05,12)} = 3.08$$
  $R_C = 6.2340$   
 $r = 3 : Q'_{(3,0.05,12)} = 3.23$   $R_C = 6.5380$   
 $r = 4 : Q'_{(4,0.05,12)} = 3.33$   $R_C = 6.7400$   
 $r = 5 : Q'_{(5,0.05,12)} = 3.36$   $R_C = 6.8010$   
 $r = 6 : Q'_{(6,0.05,12)} = 3.40$   $R_C = 6.8820$ 

; 59.65° = Unfermented soybean Y<sub>(1)</sub> : 64.65 bc = Soybean residue tooa-nao Y<sub>(2)</sub> : 66.92 <sup>b</sup> = Soybean tooa-nao Y<sub>(3)</sub> : 67.68 <sup>b</sup> = Unfermented soybean residue Y<sub>(4)</sub> : 68.18 <sup>b</sup> = Soybean tempeh Y<sub>(5)</sub> : 74.95 ª = Soybean residue tempeh Y<sub>(6)</sub>

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