APPENDIX I

PROXIMATE ANALYSIS

1.1 Total solid (ST)

Moisture is evaporated from the sample by oven drying. Dry matter is determined gravimetrically as the residue remaining after drying.

Procedure:

- Dry weighing bottles at 100^0c for 15 hours. In an Air Oven and cool I a desiccators.
- Weigh pre-dried bottles (W1).
- Add 3 ml of colostrum (weighed to the nearest 0.01 g) (Ws) and distribute uniformly.
- Dry sample to a constant weight at 60^0c for 24 hours.
- Remove bottle with diet after drying and place in desiccators to cool.
- Weigh the sample after cooling (W2).
- Calculation.

Total solid % (w/w) is calculated as follows:

$$\% \text{ Dry matter} = \frac{W2-W1}{Ws}$$

1.2 Crude Protein

Crude protein is assayed by Kjeldahl method, the official method. In this method, the protein and other organic substances are digested with concentrated sulfuric acid in the presence of selenium reagent mixture as catalyst. The present nitrogen is

converted into ammonium sulfate ($(NH_3)_2SO_4$). Concentrate NaOH is added to release NH_3 that is distilled, collected in boric acid solution, and quantities by titration method.

Reagents

Sulfuric acid, selenium reagent mixture, sodium hydroxide solution, tashiro indicator, 40% boric acid solution, and hydrochloric acid standard solution, 0.1000 N.

Procedure

- Transfer sample (1 g) into a kjeldahl tube.
- Add selenium reagent mixture (0.5 g) and mix thoroughly.
- Add H_2SO_4 (20 ml) rinse anything in neck of flask down into tube.
- Digestion: Place kjeldahl tubes in block digestion unit. At the end of digestion, digest should be closer and free undigested material. Cool the digest to room temperature; add 30 ml H_2O to each tube and mix.
- Distillation: Place kjeldahl tubes to distillation unit. Add boric acid (25 ml) solution with indicator to Erlenmeyer flask (250 ml). Place on the receiving platform, with tube from condenser extending below surface of boric acid solution. At the end of distillation, distillate should be light green solution.
- Titration: Titrate boric acid receiving solution with standard 0.1000 N HCL solutions to first trace of pink. Lighted stir may aid visualization of end point.
- Calculation

Total nitrogen (% (v/v) or % (w/v)) was calculated as follows:

$$\% \text{ Total Nitrogen} = \frac{1.40 \times (\text{ml HCL, sample} - \text{ml HCL, blank}) \times \text{Normality HCL}}{\text{g sample}}$$

Total calculate percent “protein” on a total nitrogen basis, multiply percent nitrogen by factor 6.25.

1.3 Ether extracts

Fat is extracted from a dry sample with petroleum ether using a special Soxhlet apparatus. The ether extract is collected in a flask. The percentage of crude fat is determined by weight difference.

Procedure

- Dry round bottom flask with 2-3 piece of boiling chip at 100^0C for 15 hours. in an air oven and cool in a desiccators.

- Weight pre-dried flask (W1).

- Weight approximately 3 g of ground dry milk (to the nearest 0.01 g) on sugar filter paper and transfer to an extraction thimble (Ws).

- Place the thimble inside percolator of the Soxhlet apparatus. Assemble Soxhlet apparatus and extract the sample with petroleum ether for 15 hours. At a condensation rate of at least 5-6 drops per second.

- Remove the thimble from the percolator and place it in a beaker and let it dry in the hood for 30 min.

- Stand the flask in the hood for overnight, dry at 100^0C for 60 min, to constant weight. Excessive drying may oxidize fat and give erroneous result.

- Remove desiccators, cool and weight accurately (W2).

- Calculation

% Ether extract content was calculated as follows:

$$\% \text{ Ether extract} = \frac{W2-W1}{Ws} \times 100$$

1.4 Ash

Ash was assay by oxidizing all organic matter in a weight sample of the material by incineration and determining the weight of the ash remaining.

- Ignite porcelain crucibles in a muffle furnace at around 450-550^{o}C for overnight, cool in desiccators and weight after reaching room temperature (W1).

- Add 3 g of diet to the pre-ignite crucible (weighted to the nearest 0.01g) (Ws).

- Place crucibles with diets on the heater to remove smoke.

- After moving smoke, place crucibles with dry milks in the cooled muffle furnace.

- Ignite for 12-18 h at about 450-550^{o}C overnight.

- Turnoff the muffle furnace and open after temperature has reached about 250^{o}C.

- Using tongs transfer the crucibles to the desiccators, cool in a desiccators and weigh after reaching room temperature (W2).

- Calculation

% Ash content was calculated as follows:

$$\% \text{ Ash} = \frac{W2-W1}{Ws} \times 100$$

1.5 Crude fiber

Two boiling processes simulate the pH conditions of the digestive tract, acidic in the stomach and alkaline in the small intestine, but nothing more. However, the enzymatic digestion is not simulated.

Reagents

- Sulfuric acid (H2SO4) 1.25% - 0.255 ± 0.005 N. 12, 5g, 98% concentrated to 1000 ml with distilled water. Control the concentration by titration.
- Potassium hydroxide (KOH) 1.25% - 0.223 ± 0.005 N, free from carbonate. 12.5 g to 1000 ml with distilled water. Control the concentration by titration.
- n-octanol as antifoam.
- Anhydrous acetone

Procedure

1. Determine separately the sample moisture by heating in an oven at 105 °C to constant weight. Cool in a desiccator.
2. Weight accurately 1 g about of grinded sample (1 mm about) approximately with 1 mg. ==> W1
3. Add 1.25% sulfuric acid up to the 150 ml notch, after preheating by the hot plate in order to reduce the time required for boiling.
4. Add 3-5 drops of n-octanol as antifoam agent.
5. Boil 30 minutes exactly from the onset of boiling.
6. Connect to vacuum for draining sulfuric acid.

7. 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.
8. After draining the last wash, add 150 ml of preheated potassium hydroxide (KOH) 1.25% and 3-5 drops of antifoam.
9. Boil 30 minutes.
10. Filter and wash as point 7.
11. Perform a last washing with cold deionized water aimed to cool the crucibles and then wash three times the crucible content with 25 ml of acetone, stirring each time by compressed air.
12. Remove the crucibles 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 (W2)represents the crude fiber plus ash content in comparison to initial weight.

Calculation

Calculate the percentage crude fiber (wet weight basis)as follows:

$$\% \text{ Crude fiber (wet)} = \frac{(W2 - W1)}{W1} \times 100$$

Possible errors This is the most unsatisfactory principle of the Proximate Analysis. Major problem:

1. acid and base solubilize some of the true fiber (particularly hemicellulose, pectin and lignin).
2. Cellulose too is partially lost. Hence, crude fiber underestimates true fiber.

1.6 Nitrogen Free Extract (NFE)

A very inaccurate name indeed. This fraction has nothing to do with nitrogen and it's not an extract either. NFE supposedly represents the soluble carbohydrate of the feed, such as starch and sugar. Crude fiber represents insoluble carbohydrate.

Calculation

% NFE = % DM - (% EE + % CP + % ash + % CF)

where: NFE = nitrogen free extract

DM = dry matter

EE = ether extract or crude lipid

CP = crude protein

CF = crude fiber

This is the ONLY component in the Proximate Analysis which is not determined ANALYTICALLY, but is calculated by difference. Therefore, NFE accumulates all of the errors that existe in other proximate analysis components (CF is the biggest error)

Possible errors

This is the ONLY component in the Proximate Analysis which is not determined ANALYTICALLY but is calculated by difference. Therefore, NFE accumulates all of the errors that existed in other proximate analysis components (CF is the biggest error)

APPENDIX II

ANALYSIS OF SERUM LYSOZYME ACTIVITY

2.1 Equipment

96-well microtiter plate

Microplate reader

Micro-pipette

Eppendorf tubes (1.5 ml)

Micro tips

2.2 Reagents

Citric acid

Dibasic sodium phosphate ($Na_2HPO_4.7H_2O$)

Citrate Phosphate Buffer (0.1 M, pH 5.8)

Sodium Chloride (NaCl)

Lyophilyzed *Micrococcus lysodeikticus* (Sigma)

Hen Egg White Lysozyme (Sigma)

2.3 Solution preparation

2.3.1 Citrate phosphate Buffer (0.1 M, pH 5.8 – 100 mL)

Solution A: 0.1 M solution of citric acid (). Solution B: 0.2 M solution of dibasic sodium phosphate (). Place19.7 mL of A + 30.3 mL of B, diluted to a total of 100 ml. Adjust pH to 5.8 with sodium hydroxide (NaOH 1N) or hydrogen chloride (HCl 1N)

2.3.2 Bacterial suspension (10 mL)

The needed concentration of *Micrococcus lysodeikticus* is 300µg ml^{-1}. Dissolved 3 mg of *M. lysodeikticus* in 1 ml of normal saline solution (NSS - 0.85%).Using the formula C1V1 = C2V2 -> V1 = C2xV2/C1. V1 = 300 µg x10 ml/3000 µg -> V1 = 1 ml (bacterial suspension in 1 ml of NSS. So V2 = 10 – 1 = 9 ml (0.01 Citrate Phosphate Buffer - CPB)

Note: Bacterial suspension was prepared prior to use

2.3.3 Hen egg white lysozyme solution (HWL)

The needed concentration of HWL is 100 µg ml^{-1}. Dissolved 1 mg of HWL in 10 mL of CPB the make aliquot 500 µl/Eppendorf and keep at -20 for further using

2.4 Procedure

2.4.1 Standard curve

Hen-egg white lysozyme (Sigma) ranged from 0 to 20 µg ml^{-1} at 2 unit intervals was used to prepare a standard curve**.** The standard curve preparation is as follow:

Concentration of HWL (µg ml^{-1})	HWL suspension (µl)	CPB (µl)	Total volume (µl)
0	0	200	200
2	4	196	200
4	8	192	200
6	12	188	200
8	16	184	200
10	20	180	200
12	24	176	200
14	28	172	200
16	32	168	200
18	36	164	200
20	40	160	200

Place 25 µl of each HWL suspension into 96-well microtiter plate in triplicate number. After a rapid mixing, the change in turbidity was measured every 30 seconds for 10 minutes at 540 nm at approximately 25^0 C, using a micro-plate reader (Sunrise, TECAN; Germany).

2.4.2 Sample preparation

Blood samples were collected through the caudal vein from 1 fish tank^{-1} using a 1 ml syringe. They were immediately withdrawn into the Eppendorf tubes without anticoagulant, and allowed to clot for 4 hours at room temperature. They were then centrifuged at 1500 x g, 5 minutes, and 4^{0}C. The serum was finally collected and stored at minus 20^{0}C until assay.

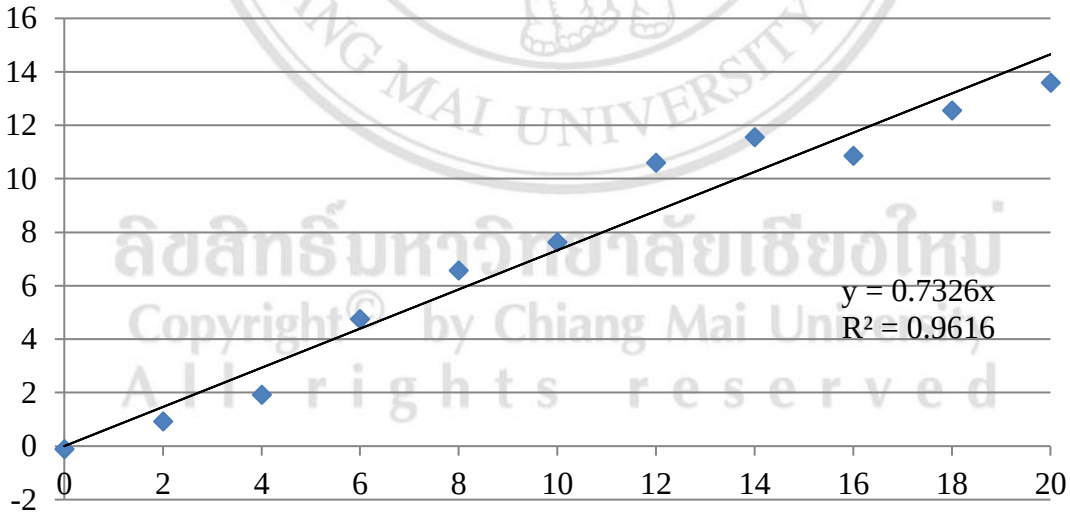
2.4.3 Assay

Twenty five µl of undiluted serum sample was added to 175 µl of *M. lysodiekticus* suspension 0.3 mg ml^{-1} (Sigma) in 0.1M phosphate citrate buffer, pH 5.8. After a rapid mixing, the change in turbidity was measured every 30 seconds for 5 minutes at 540 nm at approximately 25^0 C using a micro-plate reader(Sunrise, TECAN; Germany).

2.4.4 Calculation

The equivalent unit of the activity of the sample (compared with the standard) were determined and expressed in µg ml^{-1} serum.

Delta T% (y) = [Abs (0 second) – Abs (300 second)] x 100



Using the equation y = 0.7326 x. where y = Delta T%, x = µg/ml of serum.

APPENDIX III

Experimental statistic analysis

ANOVA of growth parameters of red-tail catfish

		Sum of Squares	df	Mean Square	F	Sig.
Replication	Between Groups	.000	3	.000	.000	1.000
	Within Groups	8.000	8	1.000		
	Total	8.000	11			
feed	Between Groups	120.706	3	40.235	478.992	.000
	Within Groups	.672	8	.084		
	Total	121.378	11			
weight	Between Groups	112.774	3	37.591	225548.133	.000
	Within Groups	.001	8	.000		
	Total	112.775	11			
SGR	Between Groups	.014	3	.005	70.792	.000
	Within Groups	.001	8	.000		
	Total	.015	11			
ADG	Between Groups	.012	3	.004	68.714	.000
	Within Groups	.000	8	.000		
	Total	.012	11			
FCR	Between Groups	.012	3	.004	38.750	.000
	Within Groups	.001	8	.000		
	Total	.012	11			
PER	Between Groups	.010	3	.003	46.333	.000
	Within Groups	.001	8	.000		
	Total	.011	11			
survival	Between Groups	.941	3	.314	.627	.618
	Within Groups	4.001	8	.500		
	Total	4.942	11			
Length	Between Groups	.642	3	.214	83.146	.000
	Within Groups	.021	8	.003		
	Total	.663	11			

Multiple Comparisons

Dependent Variable		(I) Treatment	(J) Treatment	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
				Lower Bound	Upper Bound	Lower Bound	Upper Bound	Lower Bound
Replication	Tukey HSD	1.00	2.00	.00000	.81650	1.000	-2.6147	2.6147
			3.00	.00000	.81650	1.000	-2.6147	2.6147
			4.00	.00000	.81650	1.000	-2.6147	2.6147
		2.00	1.00	.00000	.81650	1.000	-2.6147	2.6147
			3.00	.00000	.81650	1.000	-2.6147	2.6147
			4.00	.00000	.81650	1.000	-2.6147	2.6147
		3.00	1.00	.00000	.81650	1.000	-2.6147	2.6147
			2.00	.00000	.81650	1.000	-2.6147	2.6147
			4.00	.00000	.81650	1.000	-2.6147	2.6147
		4.00	1.00	.00000	.81650	1.000	-2.6147	2.6147
			2.00	.00000	.81650	1.000	-2.6147	2.6147
			3.00	.00000	.81650	1.000	-2.6147	2.6147
feed	Tukey HSD	1.00	2.00	-.49667	.23664	.232	-1.2545	.2611
			3.00	6.06333(*)	.23664	.000	-6.8211	-5.3055
			4.00	7.02667(*)	.23664	.000	-7.7845	-6.2689
		2.00	1.00	.49667	.23664	.232	-.2611	1.2545
			3.00	5.56667(*)	.23664	.000	-6.3245	-4.8089
			4.00	6.53000(*)	.23664	.000	-7.2878	-5.7722
		3.00	1.00	6.06333(*)	.23664	.000	5.3055	6.8211
			2.00	5.56667(*)	.23664	.000	4.8089	6.3245
			4.00	-.96333(*)	.23664	.015	-1.7211	-.2055
		4.00	1.00	7.02667(*)	.23664	.000	6.2689	7.7845
			2.00	6.53000(*)	.23664	.000	5.7722	7.2878

			3.00	.96333(*)	.23664	.015	.2055	1.7211
weight	Tukey HSD	1.00	2.00	-.21333(*)	.01054	.000	-.2471	-.1796
			3.00	6.81667(*)	.01054	.000	-6.8504	-6.7829
			4.00	5.51667(*)	.01054	.000	-5.5504	-5.4829
		2.00	1.00	.21333(*)	.01054	.000	.1796	.2471
			3.00	6.60333(*)	.01054	.000	-6.6371	-6.5696
			4.00	5.30333(*)	.01054	.000	-5.3371	-5.2696
		3.00	1.00	6.81667(*)	.01054	.000	6.7829	6.8504
			2.00	6.60333(*)	.01054	.000	6.5696	6.6371
			4.00	1.30000(*)	.01054	.000	1.2662	1.3338
		4.00	1.00	5.51667(*)	.01054	.000	5.4829	5.5504
			2.00	5.30333(*)	.01054	.000	5.2696	5.3371
			3.00	1.30000(*)	.01054	.000	-1.3338	-1.2662
SGR	Tukey HSD	1.00	2.00	.00000	.00667	1.000	-.0213	.0213
			3.00	-.07333(*)	.00667	.000	-.0947	-.0520
			4.00	-.06333(*)	.00667	.000	-.0847	-.0420
		2.00	1.00	.00000	.00667	1.000	-.0213	.0213
			3.00	-.07333(*)	.00667	.000	-.0947	-.0520
			4.00	-.06333(*)	.00667	.000	-.0847	-.0420
		3.00	1.00	.07333(*)	.00667	.000	.0520	.0947
			2.00	.07333(*)	.00667	.000	.0520	.0947
			4.00	.01000	.00667	.480	-.0113	.0313
		4.00	1.00	.06333(*)	.00667	.000	.0420	.0847
			2.00	.06333(*)	.00667	.000	.0420	.0847
			3.00	-.01000	.00667	.480	-.0313	.0113
ADG	Tukey HSD	1.00	2.00	-.00333	.00624	.948	-.0233	.0166
			3.00	-.07333(*)	.00624	.000	-.0933	-.0534
			4.00	-.05333(*)	.00624	.000	-.0733	-.0334
		2.00	1.00	.00333	.00624	.948	-.0166	.0233
			3.00	-.07000(*)	.00624	.000	-.0900	-.0500

			4.00	-.05000(*)	.00624	.000	-.0700	-.0300
		3.00	1.00	.07333(*)	.00624	.000	.0534	.0933
			2.00	.07000(*)	.00624	.000	.0500	.0900
			4.00	.02000(*)	.00624	.050	.0000	.0400
		4.00	1.00	.05333(*)	.00624	.000	.0334	.0733
			2.00	.05000(*)	.00624	.000	.0300	.0700
			3.00	-.02000(*)	.00624	.050	-.0400	.0000
FCR	Tukey HSD	1.00	2.00	.01000	.00816	.630	-.0161	.0361
			3.00	.08000(*)	.00816	.000	.0539	.1061
			4.00	.04000(*)	.00816	.005	.0139	.0661
		2.00	1.00	-.01000	.00816	.630	-.0361	.0161
			3.00	.07000(*)	.00816	.000	.0439	.0961
			4.00	.03000(*)	.00816	.026	.0039	.0561
		3.00	1.00	-.08000(*)	.00816	.000	-.1061	-.0539
			2.00	-.07000(*)	.00816	.000	-.0961	-.0439
			4.00	-.04000(*)	.00816	.005	-.0661	-.0139
		4.00	1.00	-.04000(*)	.00816	.005	-.0661	-.0139
			2.00	-.03000(*)	.00816	.026	-.0561	-.0039
			3.00	.04000(*)	.00816	.005	.0139	.0661
PER	Tukey HSD	1.00	2.00	.00000	.00707	1.000	-.0226	.0226
			3.00	-.07000(*)	.00707	.000	-.0926	-.0474
			4.00	-.04000(*)	.00707	.002	-.0626	-.0174
		2.00	1.00	.00000	.00707	1.000	-.0226	.0226
			3.00	-.07000(*)	.00707	.000	-.0926	-.0474
			4.00	-.04000(*)	.00707	.002	-.0626	-.0174
		3.00	1.00	.07000(*)	.00707	.000	.0474	.0926
			2.00	.07000(*)	.00707	.000	.0474	.0926
			4.00	.03000(*)	.00707	.012	.0074	.0526
		4.00	1.00	.04000(*)	.00707	.002	.0174	.0626
			2.00	.04000(*)	.00707	.002	.0174	.0626

			3.00	-.03000(*)	.00707	.012	-.0526	-.0074
survival	Tukey HSD	1.00	2.00	.00000	.57742	1.000	-1.8491	1.8491
			3.00	.56000	.57742	.770	-1.2891	2.4091
			4.00	.56000	.57742	.770	-1.2891	2.4091
		2.00	1.00	.00000	.57742	1.000	-1.8491	1.8491
			3.00	.56000	.57742	.770	-1.2891	2.4091
			4.00	.56000	.57742	.770	-1.2891	2.4091
		3.00	1.00	-.56000	.57742	.770	-2.4091	1.2891
			2.00	-.56000	.57742	.770	-2.4091	1.2891
			4.00	.00000	.57742	1.000	-1.8491	1.8491
		4.00	1.00	-.56000	.57742	.770	-2.4091	1.2891
			2.00	-.56000	.57742	.770	-2.4091	1.2891
			3.00	.00000	.57742	1.000	-1.8491	1.8491
Length	Tukey HSD	1.00	2.00	-.05000	.04143	.640	-.1827	.0827
			3.00	-.51000(*)	.04143	.000	-.6427	-.3773
			4.00	-.46000(*)	.04143	.000	-.5927	-.3273
		2.00	1.00	.05000	.04143	.640	-.0827	.1827
			3.00	-.46000(*)	.04143	.000	-.5927	-.3273
			4.00	-.41000(*)	.04143	.000	-.5427	-.2773
		3.00	1.00	.51000(*)	.04143	.000	.3773	.6427
			2.00	.46000(*)	.04143	.000	.3273	.5927
			4.00	.05000	.04143	.640	-.0827	.1827
		4.00	1.00	.46000(*)	.04143	.000	.3273	.5927
			2.00	.41000(*)	.04143	.000	.2773	.5427
			3.00	-.05000	.04143	.640	-.1827	.0827

* The mean difference is significant at the .05 level.

Homogeneous Subsets of:

feed

	Treatment	N	Subset for alpha = .05		
		1	2	3	1
Tukey HSD(a)	1.00	3	141.6400		
	2.00	3	142.1367		
	3.00	3		147.7033	
	4.00	3			148.6667
	Sig.		.232	1.000	1.000
Duncan(a)	1.00	3	141.6400		
	2.00	3	142.1367		
	3.00	3		147.7033	
	4.00	3			148.6667
	Sig.		.069	1.000	1.000

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

weight

	Treatment	N	Subset for alpha = .05			
		1	2	3	4	1
Tukey HSD(a)	1.00	3	79.1633			
	2.00	3		79.3767		
	4.00	3			84.6800	
	3.00	3				85.9800
	Sig.		1.000	1.000	1.000	1.000
Duncan(a)	1.00	3	79.1633			
	2.00	3		79.3767		
	4.00	3			84.6800	
	3.00	3				85.9800
	Sig.		1.000	1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

SGR

	Treatment	N	Subset for alpha = .05	
		1	2	1
Tukey HSD(a)	1.00	3	2.7867	
	2.00	3	2.7867	
	4.00	3		2.8500
	3.00	3		2.8600
	Sig.		1.000	.480
Duncan(a)	1.00	3	2.7867	
	2.00	3	2.7867	
	4.00	3		2.8500
	3.00	3		2.8600
	Sig.		1.000	.172

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

ADG

	Treatment	N	Subset for alpha = .05		
		1	2	3	1
Tukey HSD(a)	1.00	3	.8067		
	2.00	3	.8100		
	4.00	3		.8600	
	3.00	3			.8800
	Sig.		.948	1.000	1.000
Duncan(a)	1.00	3	.8067		
	2.00	3	.8100		
	4.00	3		.8600	
	3.00	3			.8800
	Sig.		.608	1.000	1.000

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

FCR

	Treatment	N	Subset for alpha = .05		
		1	2	3	1
Tukey HSD(a)	3.00	3	1.7100		
	4.00	3		1.7500	
	2.00	3			1.7800
	1.00	3			1.7900
	Sig.		1.000	1.000	.630
Duncan(a)	3.00	3	1.7100		
	4.00	3		1.7500	
	2.00	3			1.7800
	1.00	3			1.7900
	Sig.		1.000	1.000	.256

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

PER

	Treatment	N	Subset for alpha = .05		
		1	2	3	1
Tukey HSD(a)	1.00	3	1.7400		
	2.00	3	1.7400		
	4.00	3		1.7800	
	3.00	3			1.8100
	Sig.		1.000	1.000	1.000
Duncan(a)	1.00	3	1.7400		
	2.00	3	1.7400		
	4.00	3		1.7800	
	3.00	3			1.8100
	Sig.		1.000	1.000	1.000

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

Length

	Treatment	N	Subset for alpha = .05	
		1	2	1
Tukey HSD(a)	1.00	3	22.1000	
	2.00	3	22.1500	
	4.00	3		22.5600
	3.00	3		22.6100
	Sig.		.640	.640
Duncan(a)	1.00	3	22.1000	
	2.00	3	22.1500	
	4.00	3		22.5600
	3.00	3		22.6100
	Sig.		.262	.262

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

survival

	Treatment	N	Subset for alpha = .05
		1	1
Tukey HSD(a)	3.00	3	99.4400
	4.00	3	99.4400
	1.00	3	100.0000
	2.00	3	100.0000
	Sig.		.770
Duncan(a)	3.00	3	99.4400
	4.00	3	99.4400
	1.00	3	100.0000
	2.00	3	100.0000
	Sig.		.387

Means for groups in homogeneous subsets are displayed.
a Uses Harmonic Mean Sample Size = 3.000.

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