

SUPPLEMENTARY INFORMATION

**Dietary supplementation with popped amaranth
modulates the gut microbiota in low height-for-age
children: A nonrandomized pilot trial**

Supplementary Table S1. Proximal composition of popped amaranth (*Amaranthus hypochondriacus*)

| Amaranth | Popped grain |
|----------------------|---------------------|
| Protein | 15.8 ±0.6 |
| Fat | 6.7 ±1.4 |
| Fiber | 3.8 ±0.9 |
| Ashes | 2.2 ±0.3 |
| Carbohydrates | 63.4 ±3.9 |

Mean of triplicates ± standard deviation

Supplementary Table S2. Hematic cytometry of participant's children with low-height for age according to HAZ index

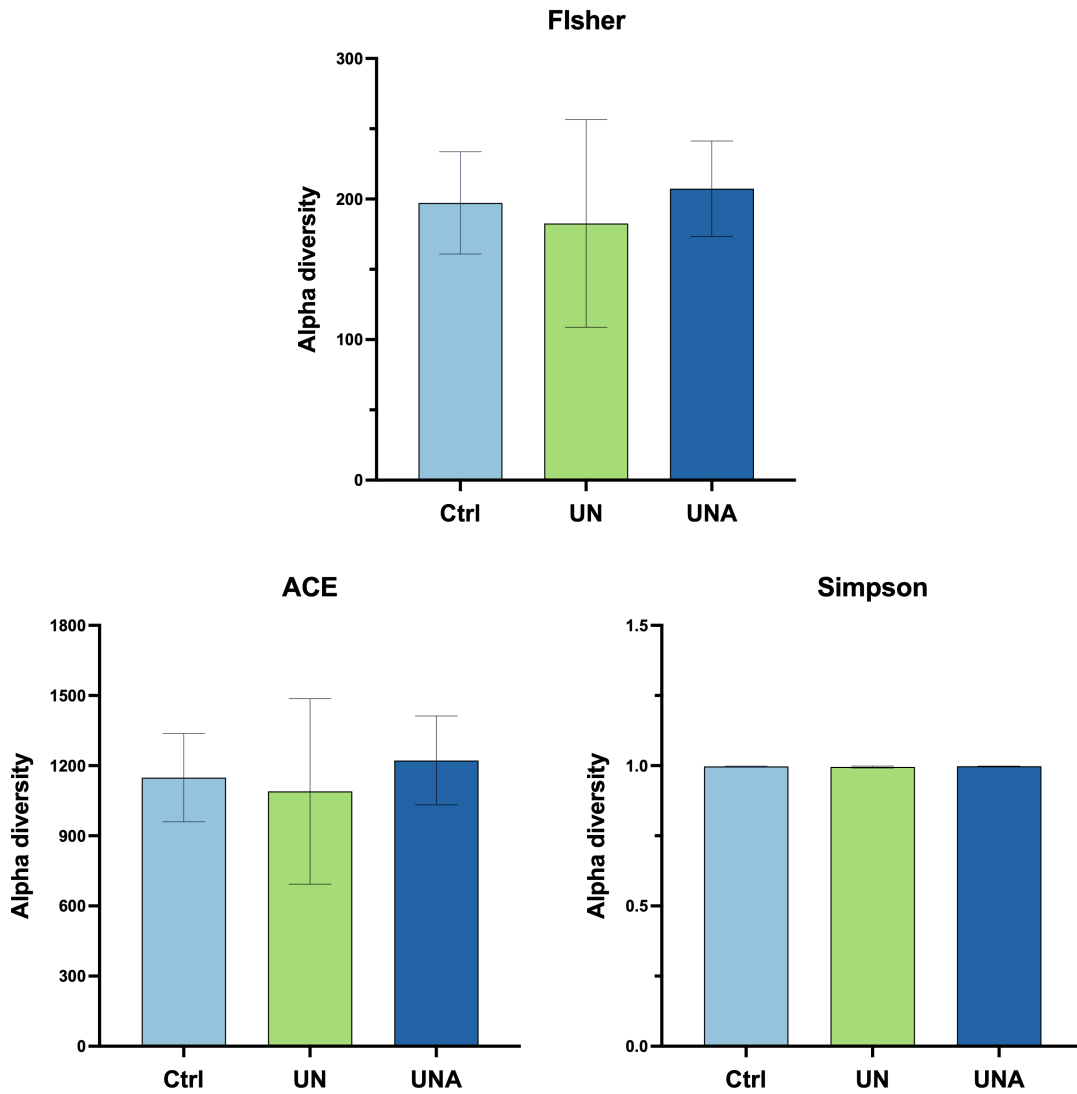
| Determination | Normal | Undernutrition | | Biological limits |
|--|----------------|----------------|----------------------------------|-------------------|
| | (n = 21) | (n = 9) | (n = 7) | |
| Red blood cells | | | | |
| Erythrocytes ($\times 10^6$) | 4.9 ± 0.1 | 4.8 ± 0.1 | 4.7 ± 0.1 | 4.3 - 5.2 |
| Hemoglobin (g/dL) | 13.2 ± 0.1 | 13.2 ± 0.4 | 13.6 ± 0.3 | 12.5 – 15 |
| Hematocrit (%) | 40.7 ± 0.4 | 40.9 ± 0.9 | 42.4 ± 0.7 | 37.5 – 48 |
| Mean corpuscular volume MCV (fL) | 83.6 ± 0.8 | 84.9 ± 0.9 | 89.7 ± 1.1 | 83 – 100 |
| Corpuscular hemoglobin (pg) | 27.1 ± 0.3 | 27.4 ± 0.6 | 28.9 ± 0.4 | 27 – 32 |
| Mean corpuscular Hb concentration (g/dL) | 32.4 ± 0.2 | 32.3 ± 0.4 | 32.0 ± 0.2 | 32 – 34.5 |
| Platelets | | | | |
| Platelet (miles) | 282 ± 15 | 338 ± 33 | 277 ± 35 | 150 - 400 |
| White blood cells | | | | |
| Total Leukocytes ($\times 10^3$) | 7.6 ± 0.5 | 6.7 ± 0.6 | 6.0 ± 0.4 | 4.5-13.5 |
| Total Neutrophils (%) | 57 ± 2 | 49 ± 3 | 48 ± 4 | |
| Segmented (%) | 57 ± 2 | 49 ± 3 | 48 ± 4 | |
| Band (%) | 0 | 0 | 0 | |
| Metamyelocytes (%) | 0 | 0 | 0 | |
| Myelocitos (%) | 0 | 0 | 0 | |
| Promyelocytes (%) | 0 | 0 | 0 | |
| Blasts (%) | 0 | 0 | 0 | |
| Eosinophils (%) | 0 | 0 | 2 ± 1 | |
| Basophils (%) | 0 | 0 | 1 ± 0 | 0-3 |
| Monocytes (%) | 3 ± 0 | 4 ± 0 | 6 ± 0 | 2-8 |
| Lymphocytes (%) | 40 ± 2 | 47 ± 3 | 44 ± 4 | 20-40 |

One-way ANOVA was carried out followed by Tukey's post-hoc test. A p -value <0.05 was considered as statistically significant.

Supplementary Table S3. Serum biochemical profile of participant children

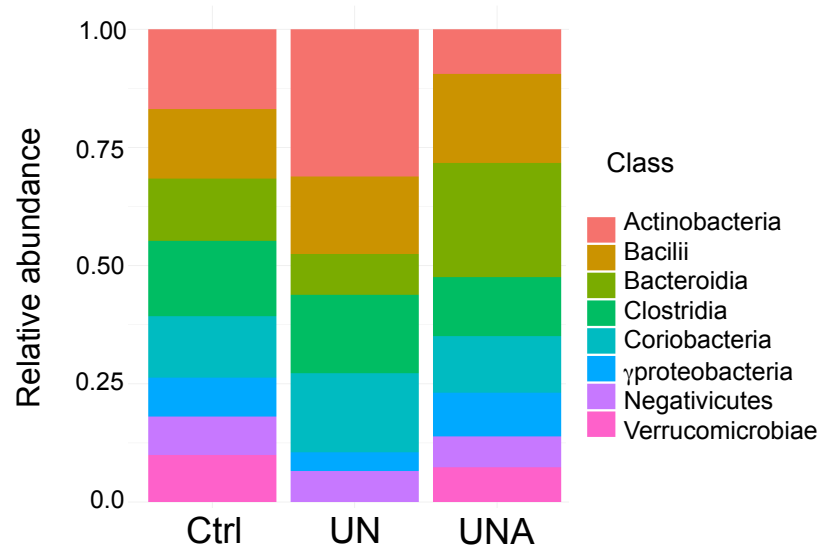
| Determination | Normal size n = 21 | Undernutrition | |
|----------------------------|-----------------------|----------------|-------------------------|
| | | start n = 9 | after 3 months n = 7 |
| Glucose (mg/dL) | 87 ±10 | 82 ±20 | 95 ±6.5 |
| Triglycerides (mg/dL) | 105 ±17 | 115 ±18 | 121 ±12 |
| Total cholesterol (mg/dL) | 133 ±19 | 146 ±31 | 151 ±28 |
| Urea (mg/dL) | 23 ±7.9 | 15.6 ±6.3 | 24.0 ±9.0 |
| Uric Acid (mg/dL) | 3.3 ±0.8 | 3.1 ±0.4 | 3.2 ±0.6 |
| Creatinine (mg/dL) | 0.7 ±0.1 | 0.70 ±0.1 | 0.70 ±0.1 |
| Total protein (g/dL) | 8.1 ±0.4 | 8.5 ±0.3 | 8.3 ±0.6 |
| Albumin (g/dL) | 4.8 ±0.4 | 5.0 ±0.3 | 5.2 ±0.6 |
| LDH (U/L) | 84 ±13 | 92 ±12 | 97 ±13 |
| ALKP (U/L) | 298 ±80 | 301 ±85 | 347 ±127 |
| AST (U/L) | 6.5 ±1.5 | 6.6 ±0.9 | 6.9 ±0.6 |
| ALT (U/L) | 2.9 ±0.9 | 2.0 ±0.7 | 2.6 ±1.9 |
| GGT (U/L) | 4.7 ±1.6 | 5.9 ±1.3 | 7.6 ±1.9 |
| Total bilirubin (mg/dL) | 0.5 ±0.3 | 0.5 ±0.2 | 0.6 ±0.2 |
| Direct bilirubin (mg/dL) | 0.1 ±0.03 | 0.1 ±0.03 | 0.1 ±0.03 |
| Indirect bilirubin (mg/dL) | 0.4 ±0.3 | 0.4 ±0.2 | 0.5 ±0.2 |

Data is the mean of triplicates ± standard deviation. *After 3 months of amaranth consumption. One-way ANOVA was carried out followed by Tukey's post-hoc test. A *p*-value <0.05 was considered as statistically significant.

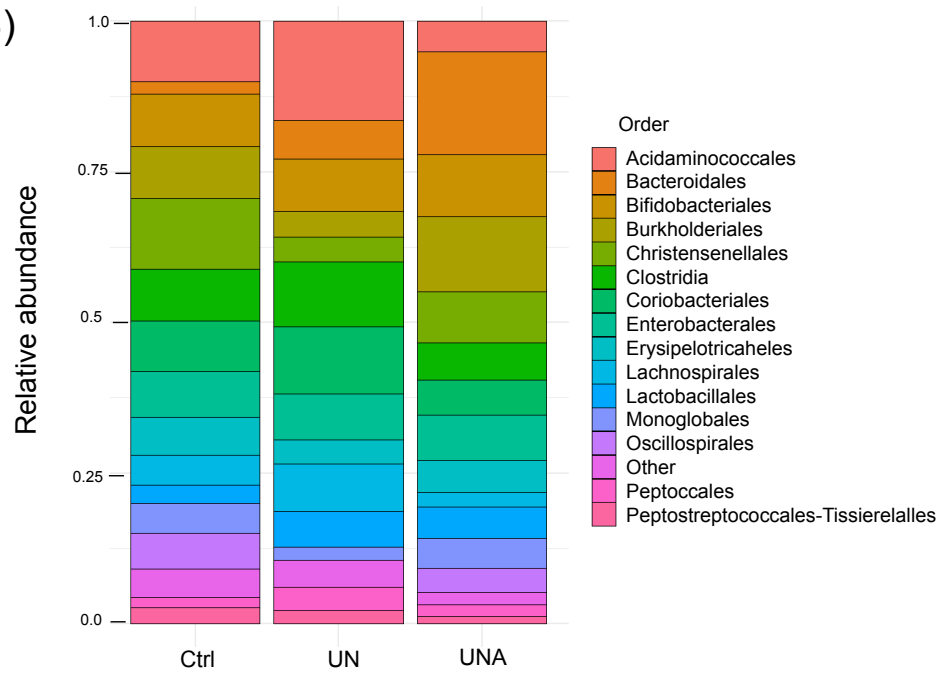


Supplementary Figure S1. Alpha-diversity differences amongst child's groups. Fisher, ACE (abundance-based coverage estimators), and Simpson values. Columns shows the means values and bars the standard deviation. ONE-way ANOVA was carried out followed by Tukey's post-hoc test at $p < 0.05$. Ctrl=control group of children with normal weight-high for age; UN=undernutrition children; UNA=undernutrition group after three months of amaranth consumption.

A)



B)



Supplementary Figure S2. Distribution of gut microbiota at A) class and B) order levels. Data showed the top-ten groups in each taxonomy clade.