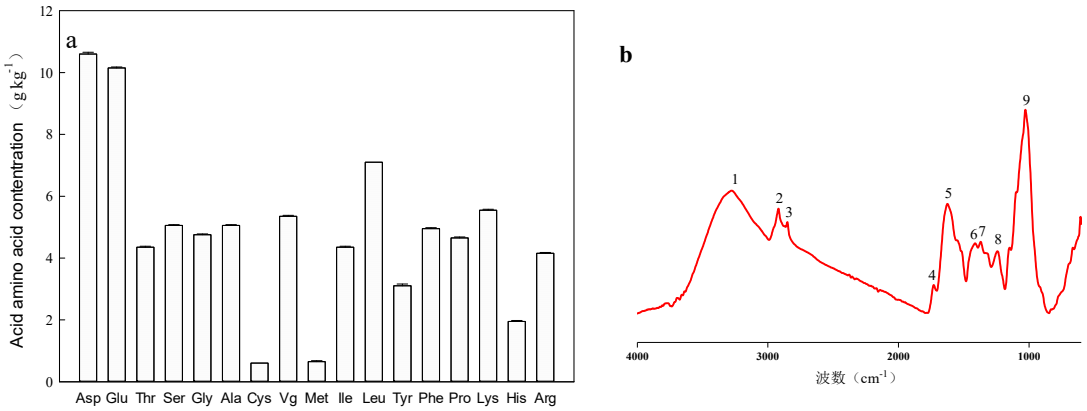

Figure S1. Acidolysis amino acids content (a) and infrared spectra (b) of the tested Chinese milk vetch.

The content of acid hydrolyzed amino acids in Chinese milk vetch(CMV) was 82.35 mg kg^{-1}. In terms of acid-hydrolyzed amino acid composition, the contents of aspartic acid and glutamate in CMV were higher, which were 10.60 mg kg^{-1} and 10.15 mg kg^{-1}, respectively. There were 9 obvious absorption peaks in the infrared spectrum of CMV. Peak 1 appears at 3277 cm^{-1}(N-H stretching vibration of amide functional groups and -OH of carbohydrates, carboxylic acids, phenols, etc.), peak 2 appears at 2719 cm^{-1}(stretching vibration of - CH_3, - CH_2 in aliphatic and alicyclic groups), peak 3 appears at 2851 cm^{-1} (stretching vibration of -CH2 in carbohydrate), peak 4 appears at 1730 cm^{-1} (the C=O stretching vibration of the lipid carbonyl group in fatty acid compounds), peak 5 appears at 1625 cm^{-1} (the C = O stretching vibration connected with aromatic ring and the C = O stretching vibration of amide compound in lignin, namely the amide I absorption band), peak 6 appears at 1413 cm^{-1}(Lignin, aliphatic compounds and C-N stretching vibration, namely amide III absorption band), peak 7 appears at 1370 cm^{-1}(the methyl group in lipids), peak 8 appears at 1242 cm^{-1}(the C-O stretching vibrations in phenolic, cellulose esters and acetate compounds), peak 9 appears at 1028 cm^{-1} (the Si-O stretching vibration, C-O stretching vibration, carbohydrate or polysaccharide).

Table S1. Concentration of amino acid standard.

Amino acids	Abbreviation	Molarity umol mL^{-1}	Wavelength nm
Phosphoserine	Phser	0.5	570
Taurine	Taur	0.5	570
Phosphoethanolamine	Pea	0.5	570
Urease	urease	0.5	570
Aspartic acid	Asp	0.5	570
Hydroxyproline	Hypro	0.5	440
Threonine	Thr	0.5	570
Serine	Ser	0.5	570
Asparagine	Asn	0.5	570
Glutamate	Glu	0.5	570
Sarcosine	Sarc	0.5	570
a-aminoadipate	Aaaa	0.5	570
Proline	Pro	0.5	440
Glycine	Gly	0.5	570
Alanine	Ala	0.5	570
Citrulline	Citr	0.5	570
a-aminobutyric acid	Aaba	0.5	570
Valine	Val	0.5	570
Cystine	Cys	0.25	570
Methionine	Met	0.5	570
Cystathionine	Cysth	0.5	570
Isoleucine	Ile	0.5	570
Leucine	Leu	0.5	570
Tyrosine	Tyr	0.5	570
b-alanine	Bala	0.5	570
Phenylalanine	Phe	0.5	570
b-aminoisobutyric acid	Baiba	0.5	570
Homocysteine	Homocys	0.5	570
g-aminobutyric acid	Gaba	0.5	570
Ethanolamine	Ethan	0.5	570
Ammonia	Amm	0.5	570
Hydroxylysine	Hylys	0.5	570
Ornithine	Orn	0.5	570
Lysine	Lys	0.5	570
1-methylhistidine	1-mhis	0.5	570
Histidine	His	0.5	570
Tryptophan	Trp	0.5	570
3-methylhistidine	3-mhis	0.5	570
Anserine	Ans	0.5	570
Carnosine	Car	0.5	570
Arginine	Arg	0.5	570

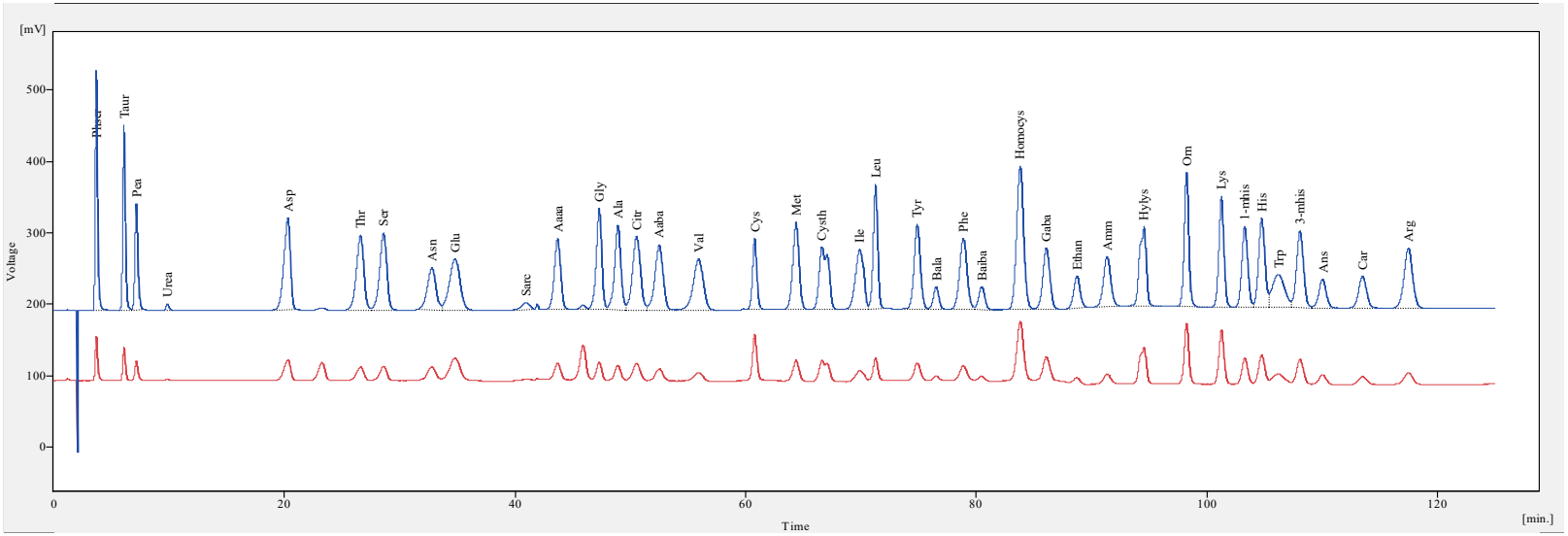

Figure S2. Standard spectrum of free amino acids.

Performance of structural equation model

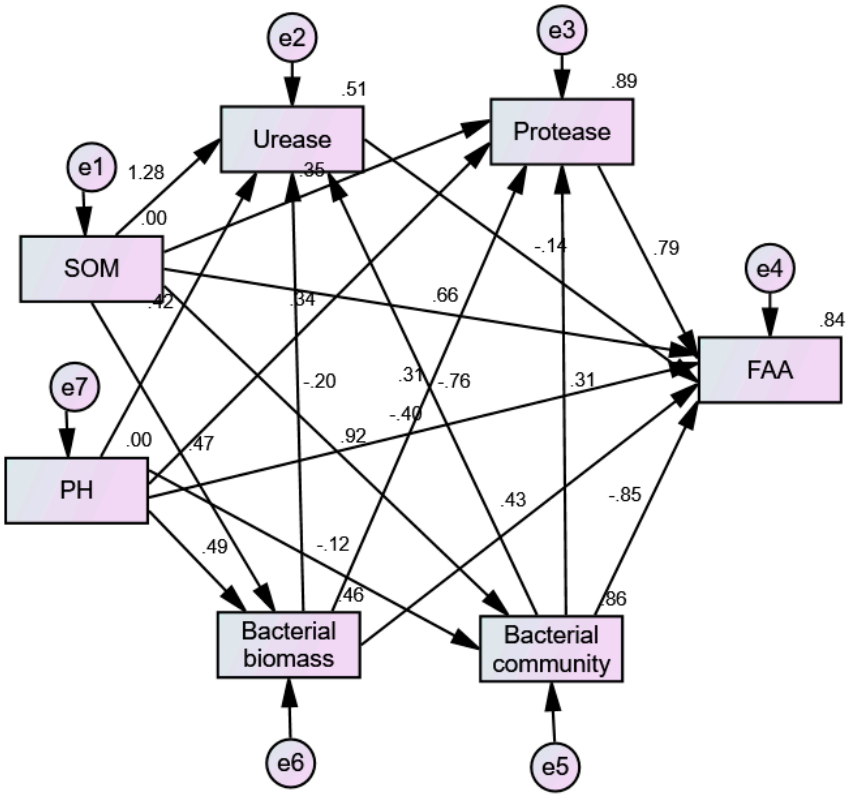

Figure S3. Conceptual model demonstrating the relationship between FAAs and its impact factors.

Some hypotheses could be made as follows:

i) pH, SOM, protease, urease, MBN, bacterial biomass and bacterial community have a direct impact on FAAs

ii)Bacterial biomass can have an indirect effect on FAAs through SOM, protease, urease

iii)Bacterial community can have an indirect effect on FAAs through SOM, protease, urease

iv)pH can have an indirect effect on FAAs through protease, urease, bacterial biomass, bacterial community

v)SOM can have an indirect effect on FAAs through protease, urease, bacterial biomass, bacterial community

Table S2. Estimates of conceptual model coefficients for FAAs and its impact factors.

Item	Estimate [a)]	S.E.[b)]	C.R. [c)]	P[d)]
bacterial biomass<---SOM	10045610.972	2527473.198	3.975	***
bacterial community<---SOM	0.971	0.065	15.043	***
bacterial biomass<---pH	133198688.758	31844847.118	4.183	***
bacterial community<---pH	-1.627	0.814	-2.000	.045
urease<---SOM	-.115	0.060	-1.917	***
protease<---SOM	0.698	0.281	2.489	0.013
urease<---pH	0.141	0.366	0.387	0.004
protease<---pH	8.550	1.715	4.986	***
urease<---bacterial biomass	0.000	0.000	-0.343	0.186
protease<---bacterial biomass	0.000	0.000	4.211	***
urease<---bacterial community	0.089	0.057	1.561	0.011
protease<---bacterial community	0.581	0.268	2.172	0.030
FAA<---SOM	7.487	2.689	2.784	0.001
FAA<---pH	-73.565	18.498	-3.977	***
FAA<---bacterial biomass	0.000	0.000	4.481	***
FAA<---bacterial community	-9.419	2.429	-3.878	***
FAA<---urease	2.987	6.391	0.467	0.151
FAA<---protease	4.744	1.363	3.481	***

a): Non standardized regression coefficients of estimate.

b):Standard error of estimate.

c): critical ratio is the t values of T-test, C.R.>1.96 *represents significant at 0.05* probability *levels.*

d): P value represents the significance level, ***significant at 0.001 probability levels, $P > 0.05$ implied causal hypothetical pathways were false.

The release the path of $P>0.05$, delete urease to FAAs, bacterial biomass to urease, and get the modified model

Table S3. Estimates of modified model coefficients for FAAs and its impact factors.

Item	Estimate [a)]	S.E.[b)]	C.R. [c)]	P[d)]
bacterial biomass<---SOM	10045610.972	2527473.198	3.975	***
bacterial community<---SOM	0.971	0.065	15.043	***
bacterial biomass<---pH	133198688.758	31844847.118	4.183	***
bacterial community<---pH	-1.627	0.814	-2.000	0.045
protease<---SOM	0.698	0.281	2.489	0.013
protease<---pH	8.550	1.715	4.986	***
protease<---bacterial biomass	0.000	0.000	4.211	***
protease<---bacterial community	0.581	0.268	2.172	0.030
FAA<---SOM	7.080	2.552	2.775	0.006
FAA<---pH	-73.928	18.534	-3.989	***
FAA<---bacterial biomass	0.000	0.000	4.446	***
FAA<---bacterial community	-9.207	2.393	-3.848	***
FAA<---protease	4.836	1.352	3.576	***

Table S4. Fitting coefficients of the FAAs and its impact factors model.

Indices name	χ^2/ df	RFI	RMSEA	NFI	TLI	CFI	IFI
Evaluation criterion	<3	close to 1	<0.05	close to 1	close to 1	close to 1	close to 1
Results	0.500	0.971	0	0.996	1.031	1	1.004

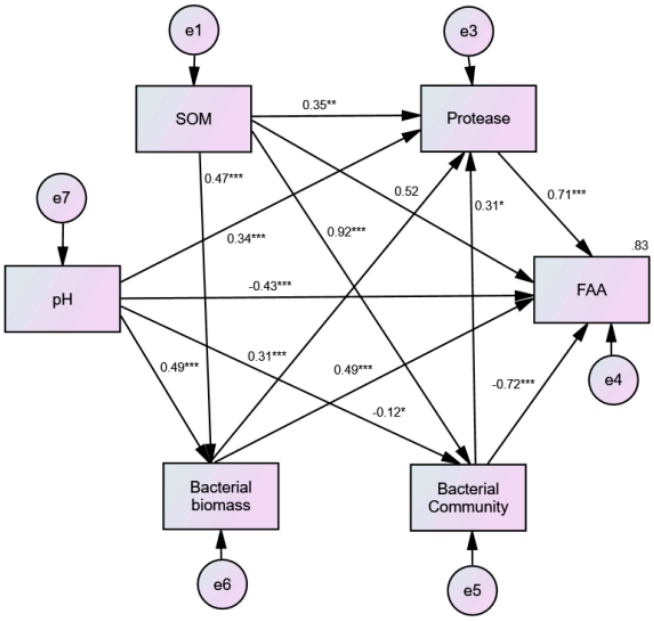

Figure S4. Modified model for FAAs and its impact factors.

Table S5. Total effects of factors contributing to the variability of FAAs content.

Item	Direct Effects[a)]	Indirect Effects[b)]	Total Effects[c)]
FAA <--- pH	-0.43	0.65	0.22
FAA <--- SOM	0.52	0.12	0.64
FAA <--- bacterial biomass	0.49	0.22	0.71
FAA <--- bacterial community	-0.72	0.22	-0.50
FAA <--- protease	0.71	0	0.71

Note：a): Standard path coefficients

b): The product of the direct effects path coefficients

c): The sum of direct effects and indirect effects

The absolute value of the path coefficient represents the size of the correlation, "-" represents a negative correlation