

## Fermentation Optimization of Macro-Fungus *Pleurotus Sajor-Caju* on Soymeal

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### Abstract

An investigation was undertaken to evaluate the impact of edible mushroom *Pleurotus sajor-caju* fermentation on the nutritional profile of soymeal under high solid submerged fermentation. Eight day fermentation resulted in changes in the nutritional profile of soymeal. A statistically significant enhancement in fermented sample was seen for crude protein, crude fiber and total amino acid. Except for hydroxyproline and hydroxylysine all amino acids showed significant increase in fermented samples. Specifically, amino acids such as glutamic acid and lysine which are important in animal feed showed significant increase in fermented samples. The overall increase of amino acids ranged from 10% to 200%. Response Surface Methodology (RSM) is an effective tool to optimize submerged fermentation of macro-fungi like *Pleurotus*. The results of the current study can serve as a basis of optimization of other macro-fungal submerged fermentation.

**Keywords:** Optimization; Macro-fungi; Mushrooms; Profiling; Nutritional; Animal feed; Soymeal

### Introduction

Mushrooms have been an integral part of various culinary cultures all over the world since several centuries. There has been a reported documents that it utilization started in oriental medicine and has its origin in Chinese culture. The large scale production of shiitake mushrooms on logs have been initiated in China, which is popular in many western countries [1-4]. In many countries traditional foods contained mushroom as an ingredient. When people immigrated from one country to another they brought the culture of mushroom with their food preparation. Though over 2000 different types of mushrooms have identified as edible, most of them are wild and only a few are commercially produced. Example, portobello mushroom (*Agaricus bisporus*), Shiitake (*Lentinula edodes*) and Oyster mushroom (*P. ostreatus*) to name a few, which are commercially cultivated for consumption [5]. Generally mushrooms are saprophytic macro-fungi which grow on dead and decaying biomass under abundant moisture and relative humidity. Mushrooms are classified under class Basidiomycete [6,7]. Naturally growing mushrooms are a part of ecosystem that are involved in vital nutrient recycling [8].

Mushrooms are well documented to provide a suite of biochemicals that are important in human and animal nutrition and health. Mushrooms are rich source of dietary fiber (DF). Mushroom cell walls are rich in chitin and polysaccharides such as glucans and mannans [9]. Further a review by Cheung [10] lists a series documented health benefits of mushroom DF. Mushrooms are rich source of high quality protein that can be produced relatively inexpensively in a short span of time using agricultural wastes such as crop residues [10-13]. Mushrooms are also rich in unsaturated fatty acids, vitamin C, thiamine, riboflavin and do not contain cholesterol [1]. Mushrooms are also known to produce variety of pharmacological, and immunomodulating compounds [2,14-17]. Mushrooms are known to

induce special flavor to food ranging from fruity flavor to meaty flavor [4,18,19]. A 2015 Zion Market Research report indicated the world over mushroom market was valued at US \$35.08 billion and projected to reach \$59.48 billion by 2021 at an annual rate of 9.2% (<https://www.zionmarketresearch.com/news/global-mushroom-market>). Due to the antioxidant and immunomodulatory effects of Mushrooms (Oyster mushrooms) they are becoming most popular in modern western diet. Exhaustive reports indicate the use of mushroom spent as animal feed which provide easily digestible carbohydrates, proteins and minerals [20-24].

Soybean is the second most important commercial crop after corn in the United States [25]. Extensive reviews [26,27] dealing with various fermented products from soybean co-products have been reported. Some of the soy co-products used in fermentation process are soymeal, soy hull and soy-isolate apart from whole soy flour. Soymeal is extensively used in bacterial and fungal fermentation for production of enzymes to reduce anti-nutritional factors in soymeal [26,27].

Though large scale production of mushrooms are produced on solid state fermentation (SSF) of cheap agricultural waste such as wheat and rice straw, it leaves a lot of post-harvest waste such as spent in commercial production that leads to a lot of landfill induced environmental problems [24,28]. Also SSF comes with set of banes such as contamination, fluctuation in quality and high labor. Submerged fermentation (SmF) is often an alternative to SSF which bears some of the salient features such as quick turnaround time, low contamination, consistency in quality and excellent space utilization [29]. *Pleurotus* has been studied under SmF for production of bioactives by various researches [6,29-31]. Since various agricultural coproducts/wastes such as wheat straw, rice straw, wheat bran and soybean products are primarily used as growth medium along with CaSO<sub>4</sub>, the present investigation choose soymeal and CaSO<sub>4</sub> as primary ingredients to optimize submerged fermentation. CaSO<sub>4</sub> is primarily used to adjust the pH that favors macro-fungal growth. The

overall objective of the study was to develop a SmF of Pleurotus sajor-caju using soymeal and CaSO<sub>4</sub>. Response Surface Methodology (RSM) statistical method was used to optimize the media ingredients. RSM design especially important in process optimization where interaction of parameters influence the growth of microbes [32-34]. The optimization process will serve as a blueprint for any macro-fungal growth optimization using soymeal as primary substrate.

## Materials and Methods

### Mushroom culture

Pleurotus sajor-caju (707) was obtained from the Penn State Mushroom culture collection and was maintained on potato glucose agar (PGA) medium at room temperature.

### Soymeal and other chemicals

Soybean meal was obtained from National Oil Seed Processors Association (NOPA). All the other chemicals used were AR grade and obtained from VWR Scientific.

### Experimental design for optimization

Media optimization was carried out using optimal design (OD) where two independent variable used were soymeal and CaSO<sub>4</sub>. Design expert 7.1.6 (Stat-Ease Inc., Minneapolis, MN, USA) was used to generate experimental designs, estimate the responses of dependent variables and also generate the contour and/or response surface plots.

The two independent variables and their levels for Optimal Design was given in Table 1. The OD consisted of six central points and 14 non-central points. The experiment consisted of 16 runs with no blocking. The upper and lower limits of the variables are given in the Table 2.

The relation between coded and actual values is according to the following equation

$$xi = \frac{X_i - X_0}{\Delta X} \rightarrow (1)$$

where  $x_i$  is the coded value of the independent variable ( $X_1$ =Soymeal,  $X_2$ =CaSO<sub>4</sub>),  $x_i$  is the real value of the independent variable,  $X_0$  is the real value of the independent variable at the center point and  $\Delta X$  is the step change value.

The relationship between independent variables and dependent variables was obtained as the sum of the contributions of the three factors through first order, second order and interaction terms according to the quadratic polynomial function in equation 2. Where  $Y$  is the predicted response,  $\beta_1$  is the linear coefficient,  $\beta_{ii}$  the squared coefficient and  $\beta_{ij}$  the interaction coefficient and  $k$  the number of factors.

$$Y = \beta_0 + \sum_{i=1}^k \beta_i X_i + \sum_{i=1}^k \beta_{ii} X_i^2 + \sum_{i < j} \beta_{ij} X_i X_j \rightarrow (2)$$

All RSM experiments were conducted in 250 mL Erlenmeyer flasks. The total volume in each flask was maintained at 50 mL. The flasks were sterilized at 120°C for 30 min and cooled to room temperature.

About 2.5 mm block of actively growing culture was added to the flask and incubated for 8 days at 200 rpm and 30°C.

### Validation of RSM

The fermentation medium contained 60.50 g of soymeal in a 2 L flask with 200 mL de-ionized water along with 7.9 g of CaSO<sub>4</sub>. The flasks were sterilized at 120°C for 30 min and cooled to room temperature. About 5 mm block of actively growing culture was added to the flask and incubated for 8 days at 200 rpm and 30°C. Four replicates were maintained. Samples from two flasks were pooled and finally two replicates were used for nutritional profiling. All samples were freeze dried before analysis.

Run#	Soymeal %	CaSO <sub>4</sub>	CFU
12	35.00	7.08	3000
4	35.00	1.00	180000
3	23.38	1.00	500000
2	10.00	1.00	300000
9	20.88	4.87	6.00E+06
8	20.88	4.87	5.80E+06
5	14.75	3.18	1.20E+06
16	27.88	10.00	2100
13	18.90	8.47	2500
7	20.88	4.87	380000
1	10.00	1.00	210000
15	27.88	10.00	12000
14	10.00	10.00	3200
6	30.13	3.97	4.00E+07
10	10.00	6.36	26000
11	35.00	7.08	2100

Table 1: Experimental design matrix with soymeal and CaSO<sub>4</sub>.

Factor	Name	Units	Type	Subtype	Minimum	Maximum
A	Soymeal	%	Numeric	Continuous	10	35
B	CaSO <sub>4</sub>	%	Numeric	Continuous	1	10
Response	Name	Units	Obs	Analysis	Minimum	Maximum
R1	CFU	CFU/G	16	Polynomial	2100	4.00E+07

Table 2: Experimental design with upper limit and lower limit for soymeal and CaSO<sub>4</sub>.

### Determination of colony forming units (CFU) of pleurotus

Serial dilution technique was used to determine CFU which represents viable cells per gram of the final fermented samples. In brief, a serial dilution method was used and spread plate method of culturing yeast cells on PDA medium was carried out. Sample dilutions up to 10<sup>-12</sup> were carried out. After incubation of plates at 30°C for 4 days, colonies from plates with highest dilutions (where the colony numbers varied between 50-100) were counted and CFU/g of fermented samples was expressed.

### Nutritional profiling

Known quantity of freeze-dried samples were weighed and sent to the Agricultural Experiment Station Chemical Laboratories (AESCL) at the University of Missouri-Columbia for biochemical compositional analyses using the ASOS methods as described in Nanjundaswamy and Vadlani [35]. Nutrition composition analyses included total amino acid profile, crude fat and protein, crude fiber, % NDF and % ADF.

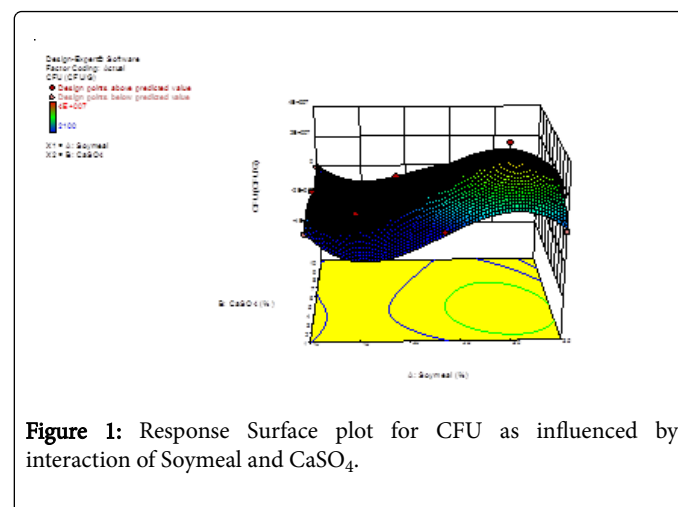
Source	Sum of squares	df	Mean Square	F Value	p-value (prob>F)	Significance
Model	1.26 × 10 <sup>15</sup>	9	1.40 × 10 <sup>14</sup>	3.69	0.0629	not significant
A-Soymeal	7.18 × 10 <sup>14</sup>	1	7.18 × 10 <sup>14</sup>	19	0.0048	
B-CaSO <sub>4</sub>	5.37 × 10 <sup>13</sup>	1	5.37 × 10 <sup>13</sup>	1.42	0.2787	
AB	2.36 × 10 <sup>14</sup>	1	2.36 × 10 <sup>14</sup>	6.24	0.0466	
A <sup>2</sup>	5.19 × 10 <sup>13</sup>	1	5.19 × 10 <sup>13</sup>	1.37	0.2861	
B <sup>2</sup>	4.67 × 10 <sup>14</sup>	1	4.67 × 10 <sup>14</sup>	12.4	0.0126	
A <sup>2</sup> B	9.65 × 10 <sup>13</sup>	1	9.65 × 10 <sup>13</sup>	2.55	0.1614	
AB <sup>2</sup>	2.37 × 10 <sup>14</sup>	1	2.37 × 10 <sup>14</sup>	6.26	0.0463	
A <sup>3</sup>	4.61 × 10 <sup>14</sup>	1	4.61 × 10 <sup>14</sup>	12.2	0.013	
B <sup>3</sup>	5.98 × 10 <sup>13</sup>	1	5.98 × 10 <sup>13</sup>	1.58	0.2555	
Residual	2.27 × 10 <sup>14</sup>	6	3.79 × 10 <sup>13</sup>			
Lack of Fit	2.07 × 10 <sup>14</sup>	1	2.07 × 10 <sup>14</sup>	50.8	0.0008	significant
Pure Error	2.03 × 10 <sup>13</sup>	5	4.07 × 10 <sup>12</sup>			
Cor Total	1.49 × 10 <sup>15</sup>	15				

**Table 3:** ANNOVA for Response Surface Cubic model for Soymeal and CaSO<sub>4</sub>.

### Results and Discussion

Optimization experiments revealed that both soymeal and CaSO<sub>4</sub> influenced the CFU of Pleurotus. From the RSM plots (Figures 1 and 2) it is clear that as the soymeal concentration increased the growth of mycelia increased while the CaSO<sub>4</sub> had the opposite effect. The desirability (Figure 2) for the optimal production of Pleurotus was about 0.89 when the concentration of Soymeal and CaSO<sub>4</sub> were 30.27% and 3.89% respectively. The analysis of variance (Table 3) indicate that the model is non-significant and the lack of fit is significant. The concentration of soymeal and CaSO<sub>4</sub> influenced to increase the mycelial growth of Pleurotus. There was a positive correlation (0.220) between soymeal and CFU of Pleurotus, while the CaSO<sub>4</sub> had a negative correlation (-0.133) with CFU. The overall interaction of both substrates had a net positive correlation (0.252) with CFU. The predicted CFU from the model was 1.8 × 10<sup>7</sup> CFU/g. From the optimization results the ideal percentage of soymeal and CaSO<sub>4</sub> were 30.27% and 3.99% respectively. Very little information is available from the submerged fermentation of mushrooms with respect to media optimization. The validation experiment conducted with 30.27% and 3.99% of soymeal and CaSO<sub>4</sub> respectively resulted in a 2 × 10<sup>7</sup> CFU/g of Pleurotus. The percentage of CaSO<sub>4</sub> predicted in the

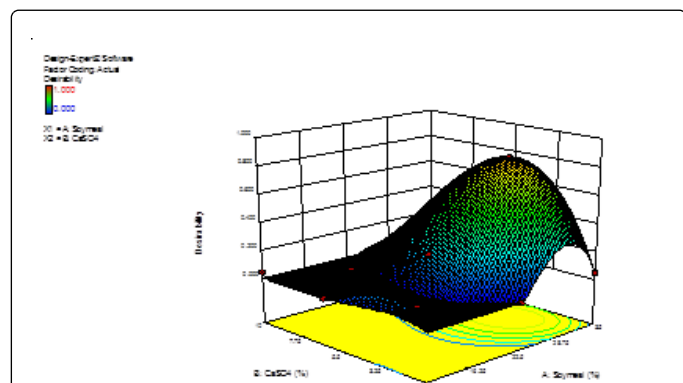
present optimization is in range with the CaSO<sub>4</sub> levels used in solid state fermentation of Pleurotus [36].



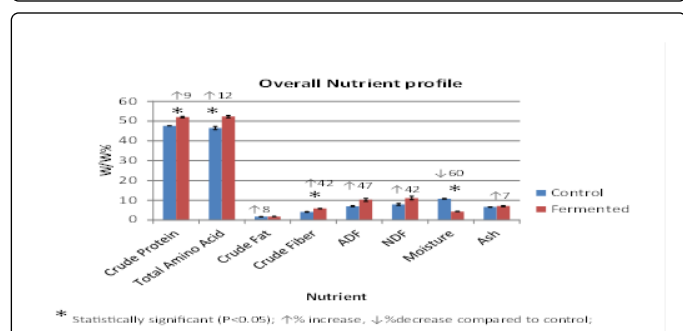
**Figure 1:** Response Surface plot for CFU as influenced by interaction of Soymeal and CaSO<sub>4</sub>.

We predict that increased soymeal concentration increased the nutrient availability for the fungus and it resulted in enhanced mycelial growth. Many scientific studies as reported in the recent review by

Socol et al. [6] that high solid fermentation is ideal for fungi that predominantly grow in mycelial form. High solid SmF is beneficial for production of mushrooms enriched products used in animal feed as it can reduce cost significantly by preventing excessive downstream processing.



**Figure 2:** Desirability RSM plot for CFU as influenced by interaction of Soymeal and CaSO<sub>4</sub>.



**Figure 3:** Nutrition profile of fermented and control soymeal. Means and standard errors provided (values are w/w expressed in %).

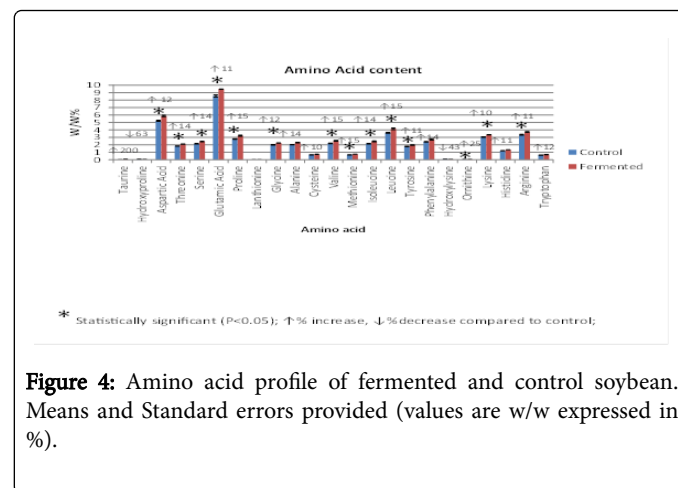
### Nutritional profiling

Figure 3 describes the overall nutritional profile, except for moisture, all other nutrients were enhanced in the fermented sample than the control. The enhancement varied from 7% to 47%. A statistically significant enhancement in fermented sample (compared to control) was seen only for crude protein, crude fiber and total amino acid. Moisture in control was significantly greater (60%) than that in the fermented sample. A similar line of enhancement of crude protein was noticed when soymeal was fermented with *Aspergillus oryzae* [27].

### Amino acid profile of fermented and un-fermented soymeal

Figure 4 describes the nutritional profile of fermented and unfermented soymeal samples. Except for hydroxyproline and hydroxylysine, all other amino acids were enhanced in the fermented sample compared to the control. The enhancement varied from 10% to 200%. The enhancement was not statistically significant for taurine, alanine, cystine, phenylalanine and tryptophan. The amino acid profile for fermented soymeal by *Aspergillus* and combination of *Aspergillus* and *Lactobacillus* had a similar profile compared to Pleurotus

fermented soymeal. A similar enhancement in Threonine, Serine, Proline, Glycine, Alanine, Valine, Methionine, Isoleucine, Leucine, Tyrosine, Phenylalanine, Lysine, Histidine, Arginine and crude protein. Enhanced amino acid and protein content in fermented samples are attributed to microbial growth. It is interesting to note that some of the amino acids like Glutamic acid and lysine have showed at least 11% and 10% increase [37]. It is important note that the fungi did not decrease any essential amino acids during fermentation of soymeal. Similar trends were also reported by Hong et al. [38].



**Figure 4:** Amino acid profile of fermented and control soybean. Means and Standard errors provided (values are w/w expressed in %).

### Conclusion

Fermentation of soymeal with macro-fungus Pleurotus resulted in Fermented Soymeal (FSBM) with positive nutritional attributes. In our study all of the nutrients were enhanced in the fermented sample than the control except for moisture. A statistically significant enhancement in the fermented sample was only seen in crude protein, crude fiber and total amino acid, the enhancement varied from 7% to 47%. All the amino acids were enhanced in the fermented sample compared to the unfermented soymeal. Optimization of media to enhance yield of macro-fungal mycelia by response surface methodology (RSM) provides a blue print for future mushroom submerged fermentation.

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