Effects of Radiation on Metabolic activities of Aureobasidium melanogenum based on Biolog FF system

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Abstract

Background

Under the radioactive stress, fungi show extremely strong radiation tolerance and highly diverse genomic structure, as well as abnormal character and nutritional requirements. The genus *Aureobasidium* can tolerate various adversities such as ultraviolet rays, hyperosmotic stress and heavy metal poisoning.

Results

The experiment used ^{60}Co γ radiation, and set four radiation doses of 0 Gy, 2,500 Gy, 5,000 Gy, and 10,000 Gy. Biolog FF technology was used to detect the utilization of carbon source in FF microplate by *Aureobasidium melanogenum* F119, and to analyze the effects of the radiation on carbon metabolic activity of *A. melanogenum* F119. There were significant differences in AWCD (Average well color development) values after explored with different radiation doses. With the increase of radiation dose, the metabolic activity of cells decreased significantly. The utilization of carboxylic acids and amino acids showed a downward trend, while that of carbohydrates showed an upward trend. At the same time, as the radiation dose increased, the utilization of carbon source changed. Among the 95 carbon sources in the Biolog FF microplates, a total of 46 carbon sources were used, and 7 carbon sources increased in average utilization rate with the increase of radiation dose. Among them, the utilization of D-ribose, sucrose, D-arabinose and L-arabinose is the most obvious.

Conclusion

Radiation can obviously reduce the metabolic activity of *A. melanogenum* F119, and the utilization of carbon source will change significantly under high doses of radiation, which may be an effective mechanism for its adaptation to radiation.

Background

Ionizing radiation (IR) can act on biological macromolecules, produce radiochemical effects and damage to organisms, such as ionization, free radicals production, nucleic acid damage, *etc*., [1], which is a deadly environmental stress. However, organisms have produced various survival strategies to deal with radiation during evolution, which can minimize the damage of radiation to the basic metabolic mechanism of organisms and repair them. In the study about microorganisms in the radiation zone, fungi were found to be an important organism enriched in radioactive materials [2–4]. Under radioactive stress, fungi show extremely strong radiation tolerance and highly diverse genomic structure [5], as well as special appearance and nutritional requirements [4], and produce abundant secondary metabolites such as pigments, enzymes and polysaccharides, *etc*.

The genus *Aureobasidium* is a kind of the polymorphic fungi with yeast and mycelium morphology. Its chlamydospores accumulate melanin [6] and can resist various adversities such as ultraviolet rays, hyperosmotic stress and heavy metal poisoning [7, 8]. It can also be used for producing single cell protein, polysaccharide, extracellular polysaccharide, pectinase, pigment, *etc*. [9]. In previous research, our laboratory obtained many strains of genus *Aureobasidium* [10]. These strains not only have high-dose radiation (^{60}Co γ-ray 20 kGy) tolerance, but also have strong resistance to ultraviolet (UV) radiation and multiple heavy metals. Soluble melanin is also produced in large quantities during the growth of these strains, which can effectively improve the survival rate of microorganisms under UV irradiation. Thus demonstrating that it has good protection to UV radiation [11]. However, there were few reports on the changes of growth,

metabolic activity and the underlying stress mechanism and radiation tolerance mechanism of such strains under radiation stress.

Biolog microbial automatic analysis system is a set of microbial carbon source metabolism and identification analysis system. Different identification analysis plates can identify and analyze nearly 2,000 kinds of microorganisms, including bacteria, yeast, filamentous fungi and environmental microbial community diversity [12, 13]. The Biolog FF identification microplates can be used for the identification of filamentous fungi, and also for the analysis of carbon source metabolic diversity of fungal communities in the environment. A black yeast-like fungus F119 was isolated from radiation-contaminated soil samples of Xinjiang. By the colony morphology, mycelial characteristics and phylogenetic tree analysis, it was identified as *A. melanogenum* F119. Different ^{60}Co γ radiation doses were set up for the radiation experiment. Biolog FF technology was used to detect and analyze the carbon source utilization of the strain after radiation. According to average well color development (AWCD) value of a single well, the effect of radiation on the metabolic activity of *A. melanogenum* F119 was analyzed. So as to analyze the radiation adaptation mechanism of *A. melanogenum* F119 and provide theoretical basis for development and application of radiation-resistant fungi.

Results

Identification of Strain F119

The strain F119 can grow at 4 ℃-30 ℃, the optimal culture temperature is 28 ℃, and resistant to 15% NaCl. the initial colonies were all yeast-like, off-white on Czapek Dox Agar at 28 ℃. In the later period, the fungal mycelium was embedded in the culture medium. After 3 days of culture, the colonies turned dark or blackish-brown, and raised (Fig. 1). After 7 days of cultivation, the colony size was 0.2 cm-1.0 cm; the optimal initial growth pH was 6.0. Microscopic observation showed that the vegetative mycelium was transparent, smooth, thin-walled, and had a septum, which was converted into black mycelium in the middle and late stages of culture (Fig. 2). The conidia were transparent to dark brown and they were single cells, smooth, oval, 4.5–10 × 3.0–10 μm.

Comparisons with LSU rDNA D1/D2 domain sequences from GenBank database revealed that strain F119 (557 bp, GenBank accession number JN854147) shared 95.1-99.5% similarity with those of the species of the genus *Aureobasidium*, and the most closely related strains were *A. melanogenum* CBS 105.22^{T} and *A. melanogenum* CBS 621.80^{T}. Based on the analysis of phylogenetic trees, strain F119 merits recognition as a distinct genomic species of the genus *Aureobasidium*.

Metabolic profiling of A. melanogenum **F119 in the Biolog FF Microplate**

The metabolic abilities of this isolate were tested by using the Biolog FF Microplate which included 95 different carbon sources. The absorbance values at different times (0-144 h) were obtained to study the abundance index of 95 carbon sources metabolized by the strain. It can be seen from Fig. 4, the strain used the most types of carbon source at 72 h. The strain F119 was able to efficiently metabolize 46 carbon sources for growth of the fungus. It included 24 types of carbohydrates: D-arabitol, arbutin, D-cellobiose, D-arabinose, L-arabinose, i-erythritol, D-fructose, gentiobiose, α-D-glucose, maltose, maltotriose, D-mannitol, D-mannose, D-melezitose, β-methyl-D-glucose glycosides, palatinose, D-psicose, D-raffinose, L-rhamnose, D-ribose, stachyose, sucrose, D-trehalose, D-xylose; 6 types of amino acids: L-alanine, L-asparagine, L-aspartic acid, L-glutamic acid; L-proline, L-pyroglutamic acid; 8 types of carboxylic acids: D-galacturonic acid, D-glucuronic acid, fumaric acid, y-hydroxybutyric acid, α-ketoglutaric acid, L-malic acid, quinic acid, succinic acid; 1 type of amines: succinamic acid; 3 types of polymers: Tween 80, dextrin, glycogen; 4 types of miscellaneous: salicin, glycerol, bromosuccinic acid, succinic acid mono-methyl ester (Fig. 5).

Metabolic profiling of A. melanogenum **F119 with exposure to radiation**

In order to explore the utilization capacity of carbon sources from the strain F119, AWCD value was used to measure it [14]. The collected data was analyzed and the average absorbance value was calculated. The results showed: in the control strain, the AWCD value increased with the increase of the cultivation time, tended to be stable at 96–168 h, and eventually reached the maximum at 144 h. The AWCD values of the strain showed the same trend under different radiation doses. Under ^{60}Co γ-ray 2,500 Gy irradiation, the cell metabolic activity was close to the control group, which were respectively 0.2357 and 0.1628; when the radiation dose was greater than 5,000 Gy, the cell metabolic activity dropped rapidly to 0.0782, lower than 50% of the control group; when the radiation dose reached 10,000 Gy, the cell metabolic activity was 0.0162, only about 6% of the control group. It showed that under low dose radiation, the growth and metabolism of the strain were less affected. However, when the radiation dose was greater than 5,000 Gy, the cell growth rate and metabolic activity decreased significantly. When the radiation dose reached 10,000 Gy, the cell growth was almost stagnant and the metabolic activity was extremely low (Fig. 6).

Utilization of carbon sources of A. melanogenum **F119 under different radiation doses**

According to the change of AWCD value and the utilization of carbon sources, this study selected 72 h results to analyze the utilization percentage of six major carbon sources for each sample. It can be seen from Fig. 7 that obvious differences in the utilization percentage of the six major carbon source of strain. With the increase of radiation dose, the utilization percentage of carbohydrates showed an upward trend, while the utilization percentage of carboxylic acids and amino acids showed a downward trend. The utilization percentage of other types of carbon sources was basically the same. But under the radiation of 10,000 Gy, except for carbohydrates, no other carbon sources are used.

doses

Top 10 types of carbon sources that were utilized by the strain under different radiation doses were analyzed. The results were shown in Table 1. A total of 22 carbon sources were involved. Among them, there were 11 kinds of carbohydrates, which accounted for 50% of the total; 2 kinds of amino acids, for 9%; 4 kinds of carboxylic acids, for 18%, only 1 kind of polymer, for 5%, and other 4 kinds of carbon sources were miscellaneous, accounting for 18%.

Table 1
Utilization of top 10 carbon sources by strain under different radiation doses

Radiation Dose(Gy)							
0 Gy		2500 Gy		5000 Gy		10000 Gy	
Carbon source	Absorbance (Ci –R)	Carbon source	Absorbance (Ci –R)	Carbon source	Absorbance (Ci –R)	Carbon source	Absorbance (Ci –R)
L-Malic Acid	0.716	Arbutin	0.608	Arbutin	0.562	D-Ribose	0.188
Fumaric Acid	0.656	Fumaric Acid	0.555	D-Xylose	0.391	Sucrose	0.138
Succinic Acid	0.609	L-Proline	0.537	D-Raffinose	0.242	D-Arabinose	0.126
L-Glutamic Acidine	0.602	L-Malic Acid	0.497	Palatinose	0.239	D-Trehalose	0.126
L-Proline	0.597	Succinic Acid	0.444	D-Melezitose	0.232	Arbutin	0.106
Arbutin	0.576	Salicin	0.402	Dextrin	0.217	D-Xylose	0.105
Palatinose	0.531	D-Xylose	0.389	Bromosuccinic Acid	0.215	L-Arabinose	0.101
Salicin	0.481	Dextrin	0.37	D-Fructose	0.197		
D-Glucuronic Acid	0.476	L-Glutamic Acid	0.367	D-Trehalose	0.195		
D-Xylose	0.468	D-Trehalose	0.336	Succinic Acid Mono-Methyl Ester	0.192		

Change of carbon source utilization by A. melanogenum **F119 under different radiation doses**

The differences among the 10 carbon sources most used by *A. melanogenum* under different radiation doses were compared. It was found that some carbon sources were used under all radiation doses, such as arbutin, D-xylose, D-trehalose. These carbon sources were critical for cellular growth and metabolism. With the increase of radiation intensity, some carbon sources were no longer used by strain in large quantities, such as fumaric acid, L-proline, salicin, L-malic acid, succinic acid, L-glutamic acid. When the radiation dose reached 5,000 Gy and above, the utilization of these carbon source dropped significantly. It was worth noting that D-ribose, sucrose, D-arabinose, and L-arabinose were not used in large quantities at low radiation doses. However, the utilization increased significantly under 10,000 Gy irradiation. This suggested that under high radiation, strain adapted to extreme conditions and began to use these carbon sources to maintain survival.

In addition, 95 carbon sources of 3 treatment groups and control group were counted. the utilization of 7 carbon sources increased significantly with radiation intensity increased, all of which were carbohydrates: D-arabinose, L-arabinose, D-ribose, sucrose, D-trehalose, D-xylose, arbutin. The utilization of these carbon sources increased significantly when the radiation intensity increased, which may indicate that the cells use these substances to participate in the maintenance of growth metabolism and stress response under extreme conditions.

Discussion

After more than 20 years of systematic excavation by scholars, about 2,000 strains of fungi were isolated in the nuclear leakage contaminated area of the Chernobyl nuclear power plant, involving 200 species of 98 genera [15, 16]. Some fungi show preferential absorption and accumulation of radionuclides. Salama *et al* found that 10-50Gy low-dose X-ray and γ-ray can promote fungal spore germination and hypha growth [17], and 80%-90% of various fungal spores could germinate after being irradiated with a radiation dose of 300 Gy. Tugaĭ *et al* [18] pointed out that the fungus appeared radiotropism and radiostimulation under radioactive environment. Our lab has obtained more than 1,000 strains of radiation-tolerant microorganisms from radiation-contaminated soil samples of Xinjiang, including bacteria, actinomycetes, fungi, *etc*. Among them, more than 100 strains of yeast and filamentous fungi have been classified and identified as belonging to 15 genera [8], and many genera have no previous reports related to characteristics of radiation tolerance.

In recent decades, melanin has been reported many times in researches of fungal radiation metabolites. Paleontological studies have found that many fungal fossils have blackened in the sediments of the early Cretaceous, and the extinction of many animals and plants during the same period was basically attributed to suffering from cosmic radiation [19, 20]. Melanin can enhance the survival of microorganisms in various extreme environments, including high altitude, Arctic and Antarctic regions [21]. Melanized fungi in environments exposed to high levels of ionizing radiation has been reported for several decades, for example from a nuclear weapons test site in Nevada [22], and from a forest experimentally exposed to chronic irradiation at the Brookhaven National Laboratory [23]. Melanized fungi are found at high abundance in the soils contaminated with radioactive isotopes in and around the Chernobyl nuclear power plant [4]. Dramatic examples of such radiation protection were provided by the reports that melanized microorganisms were colonizing the highly radioactive environment inside the damaged nuclear reactor in Chernobyl [6] and cooling pool water in nuclear reactors [7]. In the Helix Valley of Israel, the content of melanin in spores of *Aspergillus niger* from the south-facing slope with strong UV radiation was three times than that of the shady north-facing slope (Sunshine of the south-facing slope was 2 ~ 8 times that of the north-facing slope) [24]. Studies have found that some melanin-producing fungi were not only resistant to radiation, it could also be stimulated and proliferated by chronic sublethal radiation conditions [25]. These phenomena indicated that melanin has the function of protecting fungi from radiation damage, so that it could become a dominant population in the radiation environment.

The genus *Aureobasidium* is a polymorphic fungus with yeast and mycelium morphology. Its chlamydospores accumulate melanin and can resist various environmental stresses such as UV, hyperosmotic stress and heavy metal toxicity [8–10]. Therefore, it is an ideal material for studying environmental adaptation mechanism. Our lab found that the strain F119 can produce a large amount of soluble melanin, and the maximum fermentation yield could reach more than 1.0 g/L [11]. The melanin can effectively improve the survival rate of the strain under ultraviolet irradiation through the research about its UV protection characteristics of *Escherichia. coli* and *Bacillus. thuringiensis*. It is proved that it has a good protective effect of absorbing ultraviolet radiation [8]. And its radiation protection effect needs to be further verified. At present, most research on the genus *Aureobasidium* mainly focuses on the production of pullulan [26–29], as well as related to the production of single cell proteins, cell wall polysaccharides, extracellular polysaccharides, pectinase, pigments, *etc*.[30]. Still, the radiation resistance mechanism of this strain has not been reported.

In addition to detecting the carbon source utilization of various filamentous fungi and identifying fungal species, the Biolog FF microplate can also analyze the characteristics and metabolism of fungal communities in the environment [31]. In this experiment, the growth and metabolism of the strain were less affected under low dose radiation, but when the radiation dose was over 5,000 Gy, the cell metabolic activity was significantly lower than that of the control group, suggesting that the cell growth rate and the activity of metabolism started to drop sharply under high dose radiation. When cells grew 96 hours into stable phase, the AWCD value was about 1/2 of the control group under 5,000 Gy; when

the radiation dose reached 10,000 Gy, the AWCD value was less than 1/10 of the control group, and the cell growth was almost stagnation, metabolic activity was extremely low. According to Zhang *et al* [8], the growth curve of this strain after radiation showed that the cell survival rate has the same downward trend as this experiment when the radiation dose is over 5,000 Gy, indicating that the reduction in the number of cell survival will lead to a decrease in the metabolic activity of the cell population.

At present, studies on the anti-radiation effects of microorganisms represented by *Deinococcus radiodurans*, showed that under the damage of radiation, cells will initiate a stress mechanism and repair themselves, including the removal of free radicals by antioxidant enzymes, DNA and protein repair, *etc*. [32]. In this experiment, radiation caused an increase in the utilization of carbohydrates and amines. Amines exist in all biological cells and change accordingly as the cells proliferate and differentiate. A large number of studies have shown that amines can regulate DNA conformation and participate in RNA and protein synthesis through direct interaction with DNA [33]. Carbohydrates are the main components and main energy-supplying substances of cells, and have important functions to regulate cell activities. The most useful way to use carbon sources is sugar, they might play a key role in survival of cells. The tricarboxylic acid cycle (TCA) is the ultimate metabolic pathway of glucose, lipids and amino acids. Wang *et al* [34] examined metabolic activities of five botryticides against *Botrytis cinerea* using the Biolog FF Microplate. They found the substances metabolized in the TCA were inhibited with increasing concentration of boscalid, including bromosuccinic acid, fumaric acid, α-ketoglutaric acid, D-malic acid, L-malic acid, quinic acid, succinamic acid, succinic acid, L-alaninamide, L-alanine, L-aspartic acid, L-glutamic acid, L-phenylalanine, L-proline, L-pyroglutamic acid, L-serine, L-threonine and putrescine. However, when TCA is suppressed, the pentose phosphate pathway (PPP) can be used to metabolize carbohydrates. Some carbon substrates in PPP could be still used and their metabolism was not inhibited, including D-arabinose, L-arabinose, D-ribose, and D-xylose. In our study, D-ribose, sucrose, D-arabinose, L-arabinose, the utilization showed a clear advantage under high dose radiation. Another 17 carbon sources showed the same trend, including D-arabinose, L-arabinose, D-xylose, *etc*. It also proved that TCA is not the only way of glucose metabolism. When TCA is inhibited, PPP can be used to metabolize carbohydrates. This result can serve as a reference for studying the growth and metabolism of *A. melanogenum* under high radiation conditions.

Conclusions

In this study, the Biolog FF technology was used to study the carbon metabolism characteristics of *A. melanogenum* under different radiation doses. The results showed that the AWCD values of strain under different radiation doses were significantly different. With the increased of radiation dose, the metabolic activity of cells decreased significantly. Meanwhile, the utilization of carbohydrate increased, but the utilization of carboxylic acids, amino acids and other carbon sources decreased. Among them, D-ribose, sucrose, D-arabinose, and L-arabinose had low utilization rates at low radiation doses, but their utilization rates increased significantly under high doses. A total of 17 carbon sources showed similar trends among the 95 carbon sources. This result indicated that radiation can significantly reduce the metabolic activity of the strain, and the utilization type of carbon source will change significantly under high-dose radiation. This may be an effective mechanism for the strain to respond to radiation stress and adaption. This study provided a useful reference for further exploring the stress mechanism and metabolic change of *A. melanogenum* under radiation condition.

Methods

Strain screening

The strain F119 was isolated from 5 cm-20 cm below the surface of the soil from a radiation-contaminated environment in Xinjiang. Put 1.0 g soil sample in a 15 mm × 150 mm sterile test tube, placed it under ^{60}Co γ-ray radiation for 10 kGy

dose irradiation treatment, and then added to the test tube with 5 mL of Czapek Dox medium ($NaNO_3$ 2 g L^{-1}, K_2HPO_4 1 g L^{-1}, KCl 0.5 g L^{-1}, $MgSO_4$ 0.5 g L^{-1}, $FeSO_4$ 0.01 g L^{-1}, sucrose 30 g L^{-1}), enriched by shaking at 28 ℃ for 3 days. Took 1 mL of the above enriched solution into a test tube containing 9 mL of physiological saline, and successively diluted, then applied 0.2 mL of the diluted solution to the Czapek Dox Agar and incubated at 28 ℃ for 7 days under constant temperature to observe the colony. Observed the growth of the colony, picked a single colony for purification.

PCR amplification of LSU rDNA D1 / D2 region

Fresh strain was inoculated in Malt Extract Broth (Malt powder 30 g L^{-1}, soy peptone 3 g L^{-1}), cultured at a constant temperature of 28 ℃ for 4 days, centrifuged to collect cells, and washed with Tris-EDTA buffer solution for three times. After the cells were ground with liquid nitrogen, the DNA was extracted according to the method of Gerrits *et al*. [35]. The DNA was washed with 70% ethanol and then dried naturally. 50 μL of sterile double-distilled water was added, dissolved at 4 ℃ for 2 h, and stored at -20℃ for future use. PCR amplification of the LSU rDNA D1/D2 region used fungal universal primers, NL1: 5'-GCATATCGGTAAGCGGAGGAAAAG-3', NL4: 5'-GGTCCGTGTTTCAAGACGG-3'. A 50 μl reaction mixture was prepared, which contained approximately 50 ng of genomic DNA, 10 × polymerase chain reaction (PCR) buffer, 20 pmol concentration of each PCR primer, 2.5 mM concentration of dNTPs, and 2.5U of Taq DNA polymerase. After 5 min denaturation at 95 ℃, the reaction mixture was run through 35 cycles of denaturation for 1 min at 95 ℃, annealing for 1 min at 52 ℃, and extension for 2 min at 72 ℃, followed by a final extension for 10 min at 72 ℃[7]. The PCR product was electrophoresed on 1% agarose gel to determine the size of the PCR product, then it was recovered by Gel Recovery Kit (Shanghai Huashun Biotechnology Co., Ltd.), dissolved in deionized water, and sent to Beijing Dingguo Changsheng Biotechnology Co., Ltd. for sequencing.

Phylogenetic tree construction and analysis

The LSU rDNA D1/D2 domain sequence obtained from the strain F119 was BLAST compared with the known sequences in the GenBank database using BLAST (http://www.ncbi.nlm.nih.gov/BLAST/) to determine the species with the closest relationship. Obtained the sequence of related species from the database, and combined it with the sequences of type strains from the database of the Fungal Biodiversity Research Center (http://www.cbs.knaw.nl/databases/). The phylogenetic trees were reconstructed from the alignment of the sequence of F119 and those of closely related species of the genus *Aureobasidium* using the neighbour-joining method [36] in the program MEGA version 7.0 [37]. Kimura's two parameter model was used to calculate Evolutionary distance matrices of the neighbour-joining method [38]. Bootstrap analysis (1,000 resamplings) was used to evaluate the topology of phylogenetic trees [39].

Strain growth and radiation test

The strain F119 were inoculated in Malt Extract Broth. After shaking cultured at 30 ℃ for 3 d, the cells were collected by centrifugation at 5,000 r/min, and were washed 3 times with 1 × PBS (phosphate buffered solution, pH 7.2). Determine the OD of the cells using an ultraviolet spectrophotometer (UV-2550, Shimadzu Instruments (Shanghai) Co., Ltd., Japan) at 600 nm. Adjust it to an OD of 1 using 1 × PBS. Took 5 mL of the above suspension into a 15 mm × 150 mm sterile test tube and sent it to the Radiation Center of Xinjiang Institute of Geography and Ecology, Chinese Academy of Sciences, and irradiated at doses of 0 Gy (as control), 2,500 Gy, 5,000 Gy and 10,000 Gy at ^{60}Co γ-ray (dose rate 100 Gy/min). After the radiation was completed, immediately took them back to the laboratory for processing with an ice box.

Biolog FF microplates culture and data analyses

Filamentous Fungi Inoculating Fluid (FF-IF, catalog # 72106) (containing 2.5 g L^{-1}phytagel and 0.3 g L^{-1} tween 40) and FF Microplate test panels (catalog # 1006) containing 95 different carbon sources were purchased from Biolog Inc. (Hayward, CA, USA) and stored at 4 ℃ until needed. Added the irradiated sample solution to the FF-IF inoculum drop by drop, mixed well and controled the concentration within 75% ± 2%. Pour the inoculum into a sterile empty plate or V-

groove, add 100 µl of suspension to each well of the Biolog FF microplate, controled the humidity, and incubated at 30 °C with constant temperature. The color development was read as absorbance every 24 h with Microstation (Biolog Inc.) at a wavelength of 590 nm. AWCD value was used to represent the average microbial metabolic activity. AWCD value was calculated with the following formula: $AWCD=\sum(C-R)\ n$, where C is color production, R is the absorbance of the control (water) and n is the number of substrates (n = 95) [40].

In the experiment, 95 carbon sources in Biolog FF microplate wells were classified into six types of carbon sources to analyze the utilization of different types of carbon sources by samples. They are 44 carbohydrates, 13 amino acids, 17 carboxylic acids, 6 amines, 5 polymers and 10 miscellaneous [17].

Statistical analysis

Data analysis and graph drawing was carried out using the Biolog identification system (Biolog, USA), Microsoft Excel and GraphPad Prism Software version 7.0 (GraphPad Software, USA). All the experiments were done in triplicate. Analysis of the variants was carried out on all data at $p < 0.05$.

Abbreviations

AWCD: Average well color development; IR:Ionizing radiation; UV:Ultraviolet; *A. melanogenum*:*Aureobasidium melanogenum*; TCA:Tricarboxylic acid cycle; PPP:Pentose phosphate pathway; PCR:Polymerase chain reaction; OD:Optical density; PBS:Phosphate buffer saline

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Availability of data and materials

All data generated or analyzed during this study are included in this published article and its supplementary information files.

Competing interests

The authors declare that there are no competing interests.

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Authors' contributions

Z.J. and Z.Z.D. designed, wrote and revised the paper. T.Q.Y. did the radiation experiment. G. M.Y. identified the strain. W.W amplified gene and constructed the phylogenetic tree. Z.L.J. performed Biolog FF microplates culture and data analyses. All authors approved the final manuscript.

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Figures

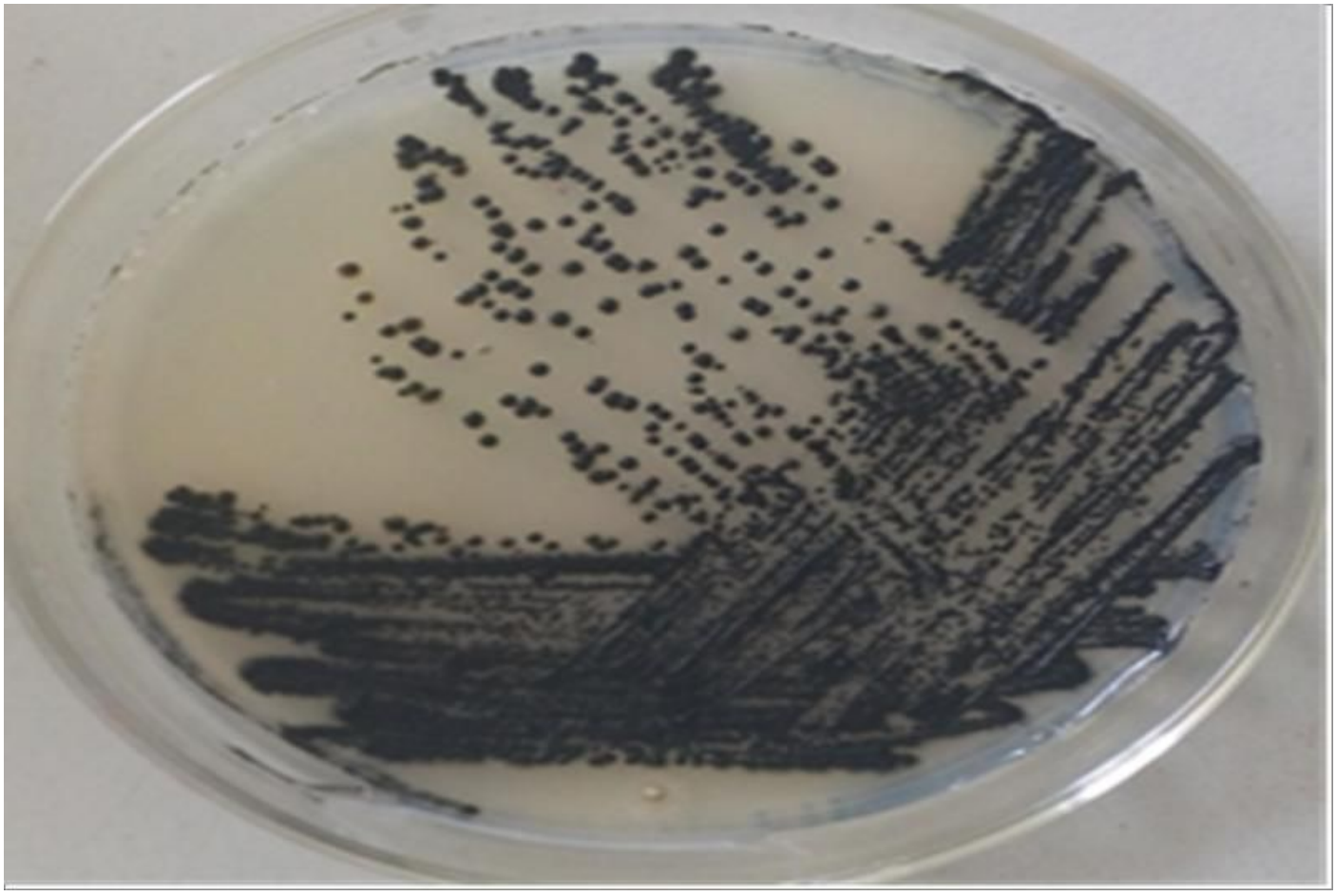

Figure 1

Colony morphology of the strain which was cultured on Czapek Dox Agar at 28 ℃for 3 days

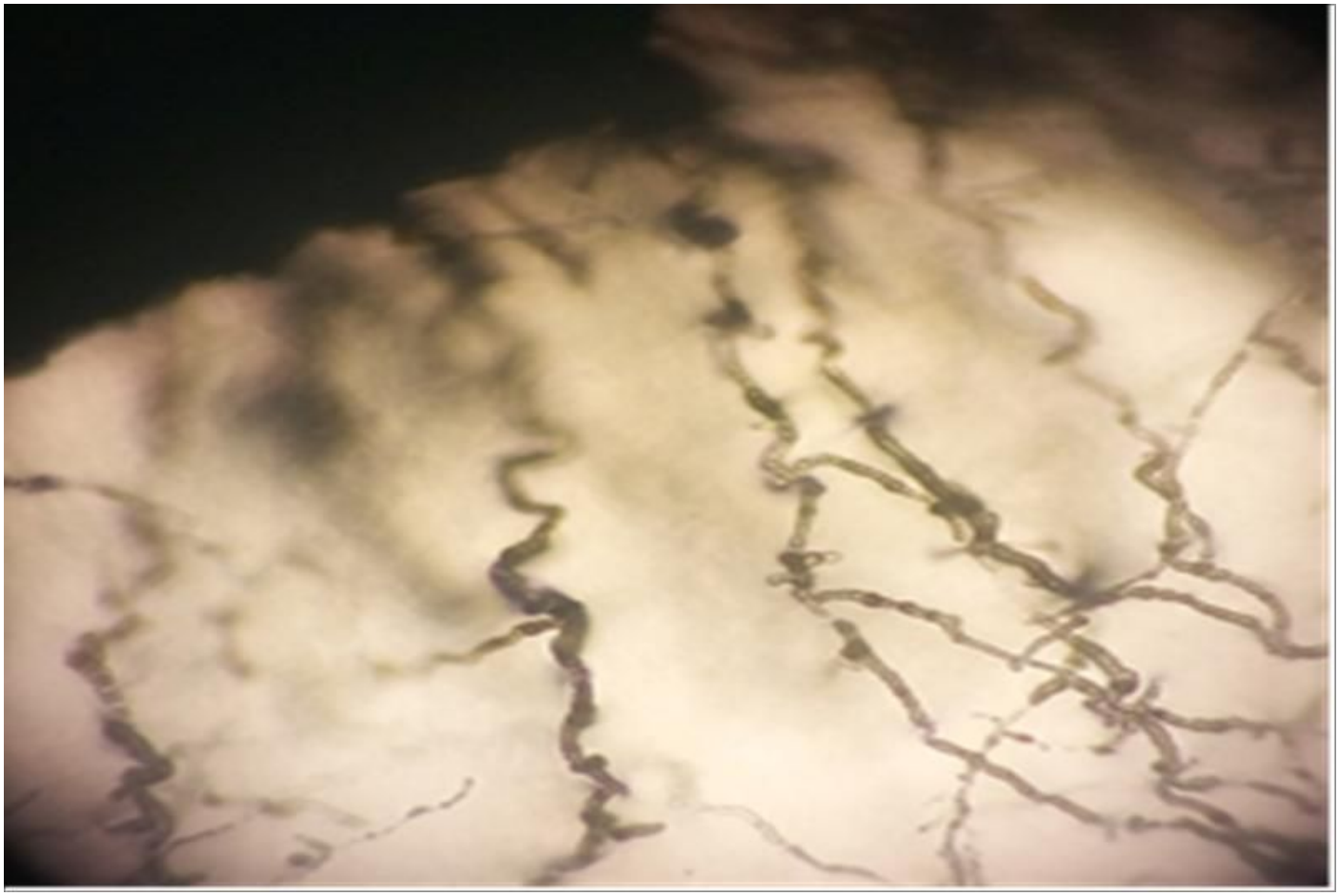

Figure 2

Mycelial characteristics of the strain which was cultured on Czapek Dox Agar at 28 °Cfor 7 days and observed using Olympus BX43 (40×)

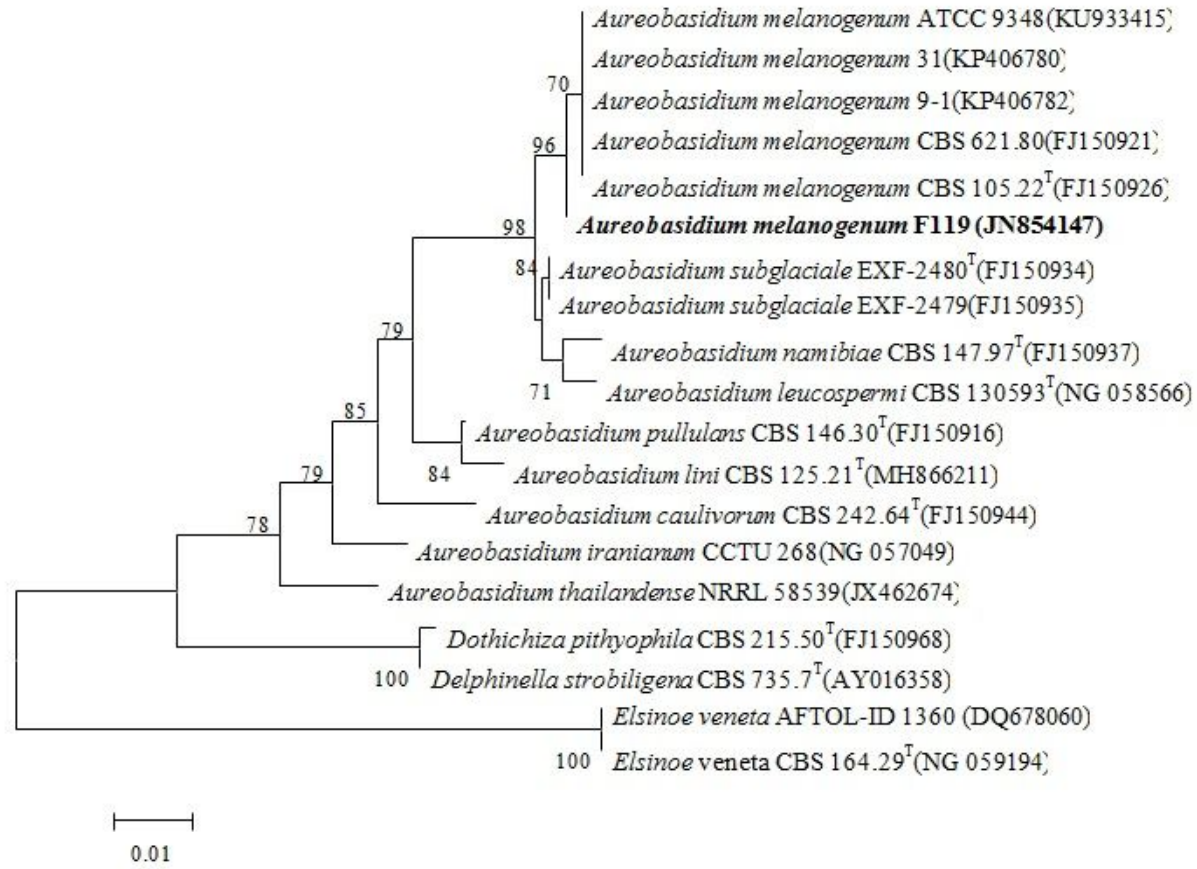

Figure 3

Neighbour-joining phylogenetic tree based on LSU rDNA D1/D2 domain sequences showing the relationships of strain F119 and its closely related species within the genus Aureobasidium. Bootstrap values (≥70%) based on 1,000 replications are shown at branch nodes. Bar 0.01 substitutions per nucleotide position.

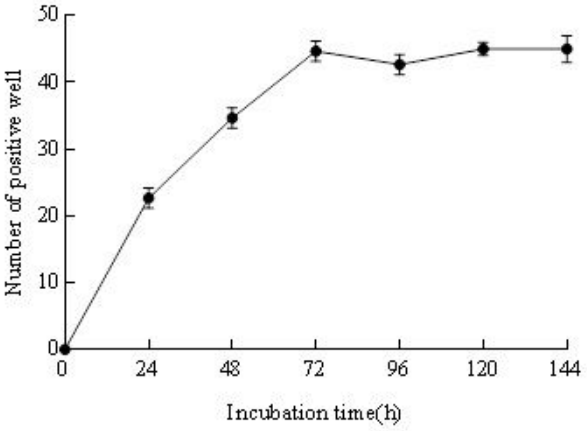

Figure 4

Utilization of sole carbon sources by strain on the basis number of positive wells

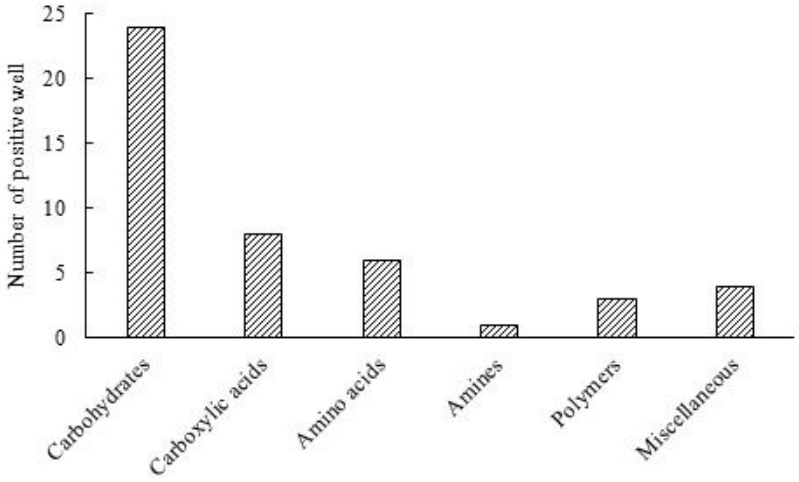

Figure 5

Types of carbon sources used by strain on the basis number of positive wells

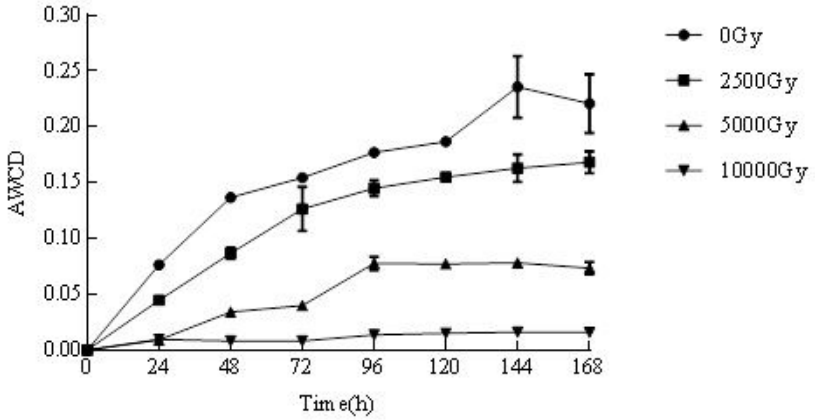

Figure 6

Utilization of sole carbon sources by strain on the basis average well colour development (AWCD) under different radiation doses

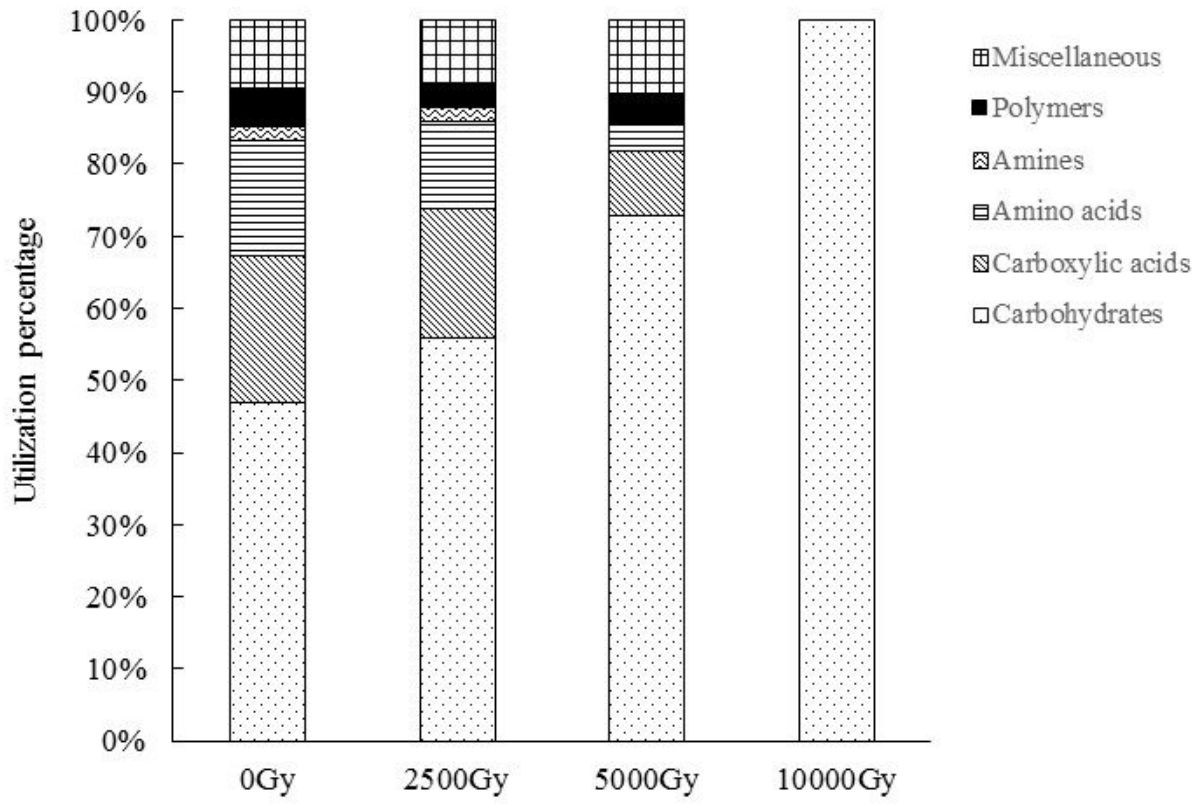

Figure 7

The utilization percentage of six major carbon source of strain under different radiation doses