

## MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF AN EDIBLE *RUSSULA* MUSHROOM IN NORTHEAST VIETNAM

Chung Nhu Anh<sup>1,2</sup>, Nguyen Minh Chi<sup>3\*</sup>, Trinh Tam Kiet<sup>4</sup>,  
Pham Duy Long<sup>3</sup>, Pham Thi Thu Thuy<sup>3</sup>, Vu Van Loi<sup>3</sup>, Bernard Dell<sup>3,5</sup>

<sup>1</sup>Vietnamese Academy of Forest Sciences

<sup>2</sup>Tay Nguyen University

<sup>3</sup>Forest Protection Research Centre, Vietnamese Academy of Forest Sciences

<sup>4</sup>Institute of Mycology and Biotechnology

<sup>5</sup>Murdoch University, Australia

<https://doi.org/10.55250/jo.vnuf.2023.15.050-059>

### ABSTRACT

Wild mushrooms are extensively gathered by rural communities throughout the uplands of northern Vietnam and nearby countries for food and medicine. These non-wood forest products are important for the livelihood of numerous rural communities. Many of these fungi form symbiotic relationships with the roots of certain species of forest trees, and the fruiting bodies can not be produced in artificial media. In the northeast region of the country, an edible red *Russula* (Nấm chèo or Nấm hồng cô) has been harvested from under wild *Castanopsis*, *Engelhardia* and *Lithocarpus* trees by local people for a long time. However, the identity of this *Russula* is unknown. We collected basidiomes of this edible *Russula* in Cao Bang, Bac Giang and Quang Ninh provinces and described its morphological features. We used ITS rDNA and LSU rDNA sequence analysis to compare with other similar taxa in GenBank. Morphological and molecular analysis identified the taxon as *Russula griseocarnosa*, previously described from southern Yunnan, China. There is strong interest by local governments to commercialize *R. griseocarnosa* in Vietnam. However, over-harvesting could have detrimental effects on the population of this edible species. Therefore, further studies are needed to quantify the ecological requirements and to develop sustainable harvesting protocols of this edible species in Vietnam.

**Keywords:** Fagaceae, rural livelihood, *Russula griseocarnosa*, wild mushroom.

### 1. INTRODUCTION

*Russula* is a large and important genus of ectomycorrhizal fungi and is widely distributed in forests and shrublands from the cool temperate to tropical climate zones [1, 2]. Many species have been reported in South Asia [3], Southeast Asia [4] and China [2, 5, 6] and new species continue to be collected and described [7, 8]. In SE Asia, basidiomes of *Russula* are most commonly observed under host trees in the Pinaceae, Fagaceae and Dipterocarpaceae [9].

*Russula* contains edible, medicinal and poisonous species [4, 10]. The fruiting bodies are all collected from the wild as attempts to cultivate them have been unsuccessful. Because of their flavour when cooked and nutritional

value, rural communities in the uplands of Asia actively collect favoured species for domestic consumption and local trade. Also, *Russula* can be processed into commercial products [5].

In Vietnam, 16 species of *Russula* have been recognized [11-13]. Among these, *R. vinosa* [11], *R. albidula*, *R. rosea*, *R. variata*, *R. virescens* [12], *R. paludosa* and *R. cystidiosa* [13] are reported to be collected for food. In the northeast provinces of the country, an edible *Russula* mushroom with a red pileus, known locally as Nấm chèo or Nấm hồng cô, has been collected by local people for a long time. The taxonomic status of this mushroom is unknown. It is important to correctly identify this *Russula* sp. as some red-capped species contain poisons, some are edible and some are a source of medicines. Therefore, using morphological and

\*Corresponding author: [nguyenminhchi@vafs.gov.vn](mailto:nguyenminhchi@vafs.gov.vn)

molecular traits, this study was undertaken to establish the identity of the edible *Russula* mushroom being collected for food in Cao Bang, Bac Giang and Quang Ninh provinces.

## 2. RESEARCH METHODOLOGY

### Sampling and morphological characterization

In May and June 2022, field surveys were undertaken in Cao Bang, Bac Giang and Quang Ninh provinces (Figure 1) where edible red *Russula* mushrooms are harvested and consumed by local people. The forests in Dong Son and Ky Thuong awards, Ha Long city, Quang Ninh province are primary forests and form part of Dong Son-Ky Thuong Nature Reserve. The remaining forests in Quang Ninh, Bac Giang and Cao Bang provinces are

secondary and community forests managed by local people. Ten sites were chosen with high density of edible *Russula* based on indigenous knowledge of the local people (Table 1). Basidiomes were collected around the base of five host tree species: *Castanopsis tonkinensis*, *C. cerebrina*, *Engelhardia roxburghiana*, *Lithocarpus dealbatus* and *L. ducampii* (Table 1). At each site, 30 basidiomes were selected for observation and measurement *in situ*. Then the basidiomes were harvested, wrapped in tissue paper, stored over ice in a cold container and transported to the laboratory of the Forest Protection Research Centre (FPRC), Vietnamese Academy of Forest Sciences in Hanoi, Vietnam.



**Figure 1. Geographical locations where the edible red *Russula* were collected in northeast Vietnam (names of sampling sites are given in Table 1)**

In the laboratory, basidiomes were dissected using a knife and photographed using a Canon G9X camera. Samples of basidiospores, basidia, hymenium, subhymenium and pleuromacrocytidia were mounted in Optika immersion oil and observed under an optical

Olympus BX50 microscope. Tissue samples (10 g) were taken from inside the pileus for molecular work. Finally, 30 specimens were dried at 40°C using a food drier and curated into the FPRC fungal herbarium.

**Table 1. Information on host species and collection sites for the edible red *Russula* in natural forests in Northeast Vietnam**

Sample	Host plant	Number in figure 1	Geographical coordinates	Location (ward, district, province)
BG1	<i>Engelhardia roxburghiana</i> Lindl.	2	21.258953, 106.461720	Nghia Phuong, Luc Nam, Bac Giang
CB2	<i>Engelhardia roxburghiana</i> Lindl.	1	22.766888, 106.499185	Doai Duong, Trung Khanh, Cao Bang
QN7	<i>Engelhardia roxburghiana</i> Lindl.	4	21.420044, 107.306033	Ha Lau, Tien Yen, Quang Ninh
QN8	<i>Lithocarpus ducampii</i> (Hickel & A.Camus) A.Camus	4	21.425544, 107.302358	Ha Lau, Tien Yen, Quang Ninh
QN11	<i>Lithocarpus dealbatus</i> (Hook.f. & Thomson ex Miq) Rehder	5	21.296574, 107.241280	Thanh Son, Ba Che, Quang Ninh
QN19	<i>Engelhardia roxburghiana</i> Lindl.	5	21.301132, 107.246516	Thanh Son, Ba Che, Quang Ninh
QN20	<i>Castanopsis tonkinensis</i> Seemen	6	21.185119, 107.118468	Ky Thuong, Ha Long, Quang Ninh
QN22	<i>Engelhardia roxburghiana</i> Lindl.	6	21.180197, 107.145569	Ky Thuong, Ha Long, Quang Ninh
QN29	<i>Castanopsis cerebrina</i> (Hickel & A.Camus)	3	21.541572, 107.343699	Vo Ngai, Binh Lieu, Quang Ninh
QN50	<i>Engelhardia roxburghiana</i> Lindl.	3	21.510154, 107.347711	Vo Ngai, Binh Lieu, Quang Ninh

**Sequencing and phylogenetic analysis**

DNA was extracted from 10 basidiomes (BG1, CB2, QN7, QN8, QN11, QN19, QN20, QN22, QN29 and QN50) and processed for ITS rDNA and LSU rDNA gene amplification using primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') [14], and primers LROR (5'-ACCCGCTGAACTTAAGC-3') and LR7 (5'-TACTACCACCAAGATCT-3') [15]. Amplifications were carried out in 50-µl-volume reactions containing 20 µl Master Mix (Eppendorf, Germany), 1 µl of each forward and reverse primer, 1 µl of DNA template and 27 µl sterilized water. The PCRs were performed with a C1000 Touch™ thermal cycler (Bio-Rad, USA). The PCR cycling parameters were as follows: initial denaturation for 3 minutes at 94°C, followed

by 30 cycles at 94°C for 30 seconds, 52°C for 30 seconds and 72°C for 1 minute. The amplification was completed at 72°C for 10 minutes and then the PCR product was stored at 10°C. The PCR amplicons were sequenced at 1st BASE (Seri Kembangan, Malaysia). The DNA sequences were compared to the GenBank database via the nucleotide-nucleotide BLAST search interface located at the National Center for Biotechnology Information, Bethesda, USA (Table 2). Relevant sequences were transferred and then processed using BioEdit software [16]. The *Russula* species selected for comparison had basidiome traits (shape, colour, size) similar to the edible *Russula* in this study. Sequences belonging to two different vouchers of some *Russula* species were used to construct the consensus tree in order to cover the two sequences of interest.

Table 2. GenBank accession numbers of *Russula* voucher in this study

Species	Voucher	GenBank accession		Reference
		ITS rDNA	LSU rDNA	
<i>R. griseocarnosa</i>	BG1	-	-	This study
<i>R. griseocarnosa</i>	CB2	-	-	This study
<i>R. griseocarnosa</i>	QN7	-	-	This study
<i>R. griseocarnosa</i>	QN8	-	-	This study
<i>R. griseocarnosa</i>	QN11	-	-	This study
<i>R. griseocarnosa</i>	QN19	-	-	This study
<i>R. griseocarnosa</i>	QN20	-	-	This study
<i>R. griseocarnosa</i>	QN22	-	-	This study
<i>R. griseocarnosa</i>	QN29	-	-	This study
<i>R. griseocarnosa</i>	QN50	-	-	This study
<i>R. griseocarnosa</i>	KUN F51713	EF627041	EF627044	[8]
<i>R. griseocarnosa</i>	E138	JAGKRU010000012	JAGKRU010000067	[17]
<i>R. decolorans</i>	FH12196	KT933992	-	[18]
<i>R. decolorans</i>	549/BB 07.322	-	KU237541	-
<i>R. amethystina</i>	929IF52	AY061653	-	[19]
<i>R. amethystina</i>	hue215, TUB	-	AY606971	[20]
<i>R. vinosa</i>	500RUF26	AY061724	-	[19]
<i>R. vinosa</i>	KUN F52026	-	EF627045	[8]
<i>R. integra</i>	FH12172	KT933984	-	[18]
<i>R. integra</i>	518/BB 07.198	-	KU237513	-
<i>R. xerampelina</i>	2-684RUS28	AY061734	-	[19]
<i>R. xerampelina</i>	OSA-MY-1762	-	AB154752	[21]
<i>R. laeta</i>	R70	MG679812	-	[22]
<i>R. laeta</i>	519/BB 07.267	-	KU237514	-
<i>R. badia</i>	R75	MG679813	-	[22]
<i>R. badia</i>	587/BB 07.324	-	KU237571	-
<i>R. minutula</i>	BPL574	KY509454	-	[23]
<i>R. minutula</i>	539/BB 08.636	-	KU237531	-
<i>R. azurea</i>	3515	JF908662	-	[24]
<i>R. azurea</i>	537/08.668	-	JN940591	-
<i>R. lilacea</i>	BPL645	KY509453	-	[23]
<i>R. lilacea</i>	435/07.213	-	JN940592	-
<i>R. laricina</i>	1112IS75	AY061685	-	[19]
<i>R. laricina</i>	575/08.681	-	JN940593	-
<i>R. nauseosa</i>	FH12173	KT933985	-	[18]
<i>R. nauseosa</i>	588/BB 07.285	-	KU237572	-
<i>R. zvarae</i>	FH12175	KT933986	-	[18]
<i>R. zvarae</i>	538/08.639	-	JN940603	-
<i>Albatrellus ovinus</i>	Dai15171	MW534158	MW534173	[25]

Phylogenetic analyses were performed using the ITS and LSU sequences. The evolutionary history was inferred by using the Maximum Likelihood method based on the Kimura 2-parameter model [26]. Consensus trees with the highest log likelihoods (1158.71) were created. Evolutionary analyses were conducted in MEGA7 [27]. *Albatrellus ovinus* was used as the outgroup taxon to root the tree.

### 3. RESULTS

#### Morphology

Pileus dark pink to red (Figure 2a, b), bell-shaped when young (Figure 2a, c), later hemispherical (Figure 2d), and finally flat (Figure 2b) or slightly sunken in the centre when mature (Figure 2f). Pileus edge flat (Figure 2e, g), margin does not striate when young, shortly and very obscurely striate. Pileus surface smooth, glossy, and hairless;



when the weather is humid, it can be slightly slimy/sticky, easy to separate from the basidiomata flesh. Mature pileus (8.0-) 10.6 (-

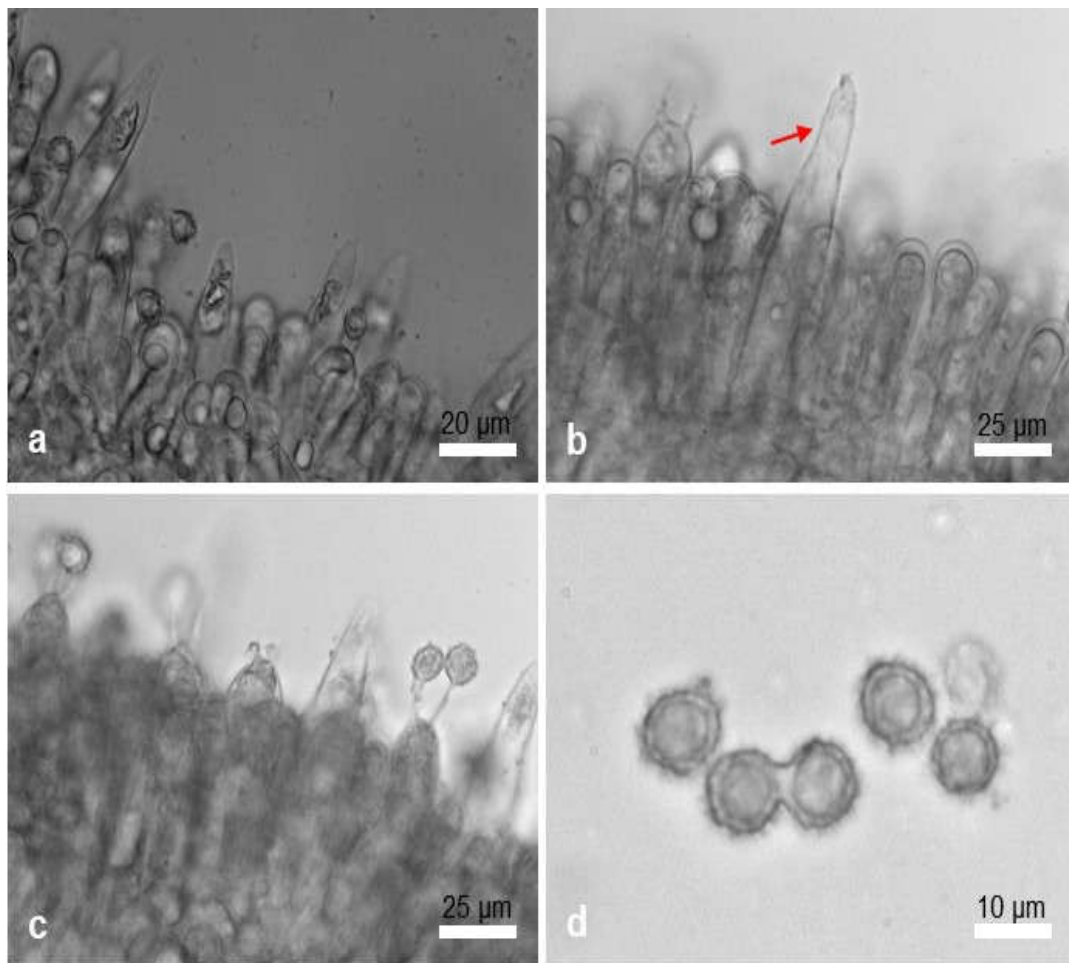
13.2) cm in diameter, (1.5) 1.8 (-2.1) cm in thickness. Gills and internal basidiomata pulp white (Figure 2e, g).



**Figure 2. Appearance of the basidiomes of the edible red *Russula*: a. basidiome cluster; b. top of pileus; c, d. young basidiomes; e. dissected basidiome; f. pileus of mature basidiome; g. gill arrangement**

Stipes white, slightly pinkish, cylindrical (Figure 2d), slightly bigger towards the base then tapering (Figure 2a, c), (5.1-) 5.6 (-6.2)

cm in length, (1.8-) 2.2 (2.5) cm in diameter, firm when young, but soft, spongy, dense, and interior grayish-white when old (Figure 2e).



**Figure 3. Microscopic characteristics of the edible red *Russula*: a. pileipellis; b. hymenium and subhymenium with one pleuromacrocytidium (red arrow); c. basidia and attached basidiospores; d. basidiospores**

Pileipellis an ixotrichoderm (155-) 180.1 (-245)  $\mu\text{m}$  thick, composed of (4.1-) 5.5 (-7.2)  $\mu\text{m}$  thick (Figure 3a). Terminal cells (1890-) 1950 (-2010)  $\mu\text{m}$  long, inflating up to (8.0-) 9.1 (-10.1)  $\mu\text{m}$  thick. Pleuromacrocytidia (90-) 116.3 (-142)  $\times$  (12.2-) 15.3 (-18.3)  $\mu\text{m}$ , abundant, emergent, projecting (29-) 40.5 (-51)  $\mu\text{m}$  beyond the hymenium (Figure 3b), fusiform, mostly with acute apex, some thick-walled in centre, wall (1.1-) 1.3 (-1.5)  $\mu\text{m}$  thick. Basidia (35-) 43.5 (-52)  $\times$  (9-) 10.5 (-12)  $\mu\text{m}$ , 4-spored, clavate (Figure 3c). Basidiospores (8.5-) 9.4 (-10.2)  $\times$  (7.5-) 7.7 (-8.1)  $\mu\text{m}$ , subglobose to ellipsoid, ornamented with large conical spines, sometimes enlarged and connected at the base.

Spines (1.3-) 3.7 (-2.2)  $\mu\text{m}$  long, strongly but often partially amyloid (Figure 3d).

#### Sequence analysis

The ITS rDNA and LSU rDNA gene sequences of ten samples in this study were compared with reference sequences obtained from the National Center for Biotechnology (NCBI) GenBank for *Russula amethystina*, *R. azurea*, *R. badia*, *R. decolorans*, *R. integra*, *R. laeta*, *R. laricina*, *R. lilacea*, *R. minutula*, *R. nauseosa*, *R. griseocarnosa*, *R. vinosa*, *R. xerampelina*, *R. zvarae* (Table 2). The results indicated that all ten samples had 99.8% homology with *Russula griseocarnosa* (Figure 4). Bootstrap values were equal to or greater than 50% derived from 1,000 iterations.

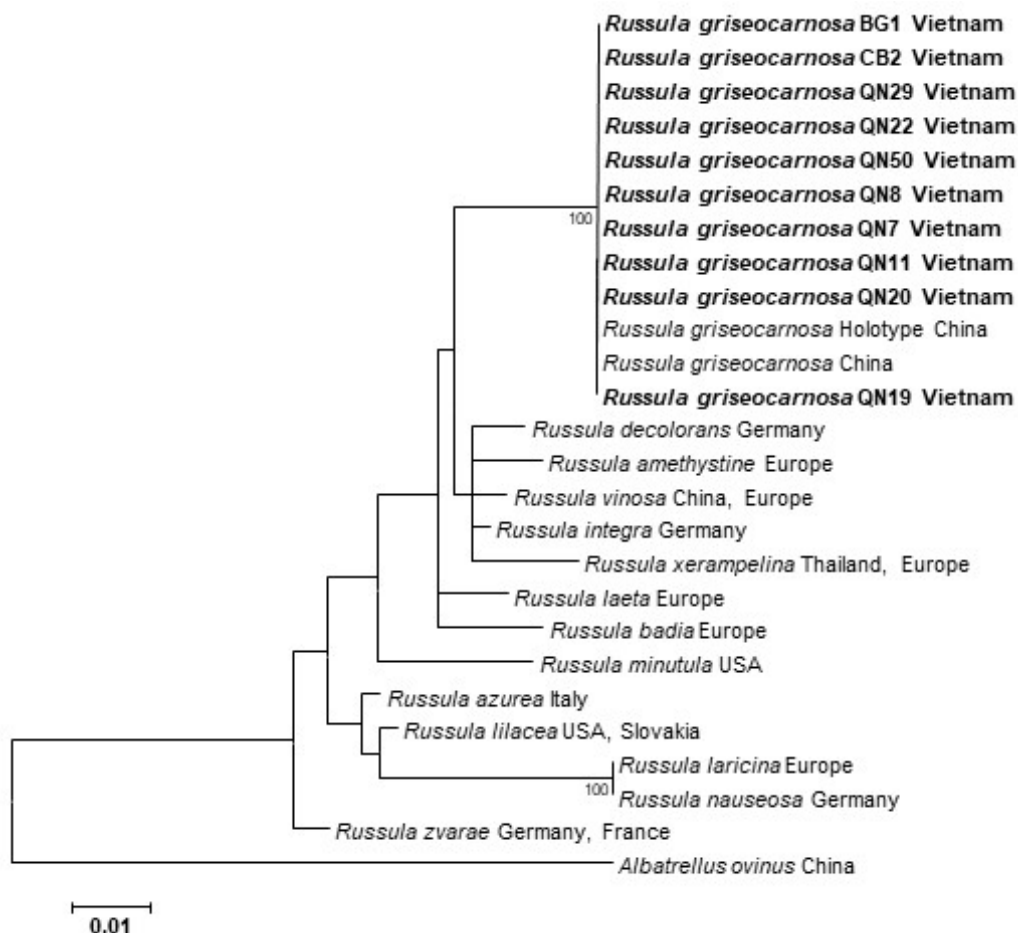


Figure 4. Consensus tree of the concatenated sequences of ITS rDNA and LSU rDNA from different species of the genus *Russula*. EF627041 and EF627044 are the GenBank numbers of *R. griseocarnosa* holotype. The Maximum Likelihood method was used to construct the tree. The bar represents an expected sequence variation of 1.0%. *Albatrellus ovinus* was used as the outgroup taxon to root the tree.

#### 4. DISCUSSION

*Russula griseocarnosa* X.H. Wang, Zhu L. Yang & Knudsen is identified as the main species of red *Russula* being collected for food in northeast Vietnam. Mushroom collectors report on high population densities of this species in natural and secondary forests. Now the authorities in these provinces, especially Quang Ninh, are formulating plans to commercialize speciality mushrooms including ectomycorrhizal fungi from the wild [28]. The true identity of the red *Russula* will allow scaling up of the marketing brand of *R. griseocarnosa* in Vietnam and give confidence of its edibility to consumers.

The morphological characteristics of *R. griseocarnosa* in this study (shape, colour, size

of basidiomes; and microscope examination of basidiospores, basidia, hymenium, subhymenium and pleuromacrocytidia) are highly similar to those described for the type collection of *R. griseocarnosa* collected in Xishuangbanna Nature Reserve in Yunnan Province [8]. There, *R. griseocarnosa* was associated with members of the Fagaceae. This kind of evergreen forest is contiguous with the upland forests of northern Vietnam. Therefore, it is likely that *R. griseocarnosa* has a wider geographical range across northern Vietnam than reported in this study.

The shape, colour and size of basidiomes of *R. griseocarnosa* are similar to *R. rosea* [11, 13], which is widely distributed in Quang Nam province [13]. However, the basidiospores,

basidia, hymenium, subhymenium and pleuromacrocystidia differ from *R. rosea*. Further taxonomic work is required to establish the status of *R. rosea* as this is a European species and is unlikely to occur in SE Asia.

Molecular methods are considered to be essential to identify cryptic species within the large *Russula* genus [7, 8, 29-32]. The ITS rDNA and LSU rDNA gene sequences were used to identify *R. griseocarnosa* sp. nov. in China [8]. Previously *R. vinosa*, a European species, had been used for this taxon. Based on these gene sequences, the basidiomes analysed in this study all showed high homology with the holotype of *R. griseocarnosa*.

*Russula griseocarnosa* is preferred widely by rural people in northeast Vietnam as a specialty food. Prices for fresh and dried basidiomes are estimated to reach 8-10 US\$/kg and 50-70 US\$/kg, respectively [28]. To support sustainable harvesting, further research should investigate options for forest management, and whether the edible red *Russula* can be cultivated in association with suitable host trees in home gardens.

## 5. CONCLUSION

Based on morphology and sequence analysis of ITS rDNA and LSU rDNA, the edible red *Russula* (Nám chèo) in Cao Bang, Bac Giang and Quang Ninh provinces is *Russula griseocarnosa*, which is previously described from Yunnan, China.

**Acknowledgments** This work was supported by the Quang Ninh government under decree number 19/2021/HĐ-KHCN-BTG dated 19/10/2021.

## REFERENCES

[1]. Michael Kuo (2009). The genus *Russula*. Retrieved from the Mushroomexpert.com Web site: <http://www.mushroomexpert.com/russula>.

[2]. Pengfei Wang, Ying Zhang, Fei Mi, Xiaozhao Tang, Xiaoxia He, Yang Cao, Chunli Liu, Dan Yang, Jianyong Dong & Keqing Zhang (2015). Recent advances in population genetics of ectomycorrhizal mushrooms *Russula* spp. *Mycology*. 6(2): 110-120.

[3]. RK Verma, Vimal Pandro & Abhishek Pyasi (2018). Diversity and distribution of *Russula* in India with reference to central Indian species. *International Journal of Current Microbiology Applied Science*. 7(10): 3078-3103.

[4]. Tharnrat Kaewgrajang, Sirapitcha Kaewjunsri, Nicharee Jannual & Mingkwan Nipitwattanaphon (2020). Morphology and molecular identification of some *Lactarius* and *Russula* species. *Genomics Genetics*. 13(2&3): 44-58.

[5]. Wei Shiyang, Mo Tianyan, Liu Bin, Huang Fuchang & Yao Xiaohua (1998). Studies on *Russula* and its ecological environment in the Mount Liuwanshan *Castanopsis hystrix* woodland of Pubei County in Guangxi. *Journal of Guangxi Agricultural University*. 17(1): 25-32.

[6]. Fang Wu, Li Wei Zhou, Zhu Liang Yang, Tolgor Bau, Tai Hui Li & Yu Cheng Dai (2019). Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. *Fungal Diversity*. 98(1): 1-76.

[7]. Bin Chen, Junfeng Liang, Xumeng Jiang & Jie Song (2022). Morphological characters and molecular phylogeny reveal three new species of subgenus *Russula* from China. *Life*. 12(4): 480.

[8]. Xiang Hua Wang, Zhu Liang Yang, Yan Chun Li, Henning Knudsen & Pei Gui Liu (2009). *Russula griseocarnosa* sp. nov. (Russulaceae, Russulales), a commercially important edible mushroom in tropical China: mycorrhiza, phylogenetic position, and taxonomy. *Nova Hedwigia*. 88(1/2): 269-282.

[9]. B Dell, R Sanmee, P Lumyong & S Lumyong (2005). Ectomycorrhizal fungi in dry and wet dipterocarp forests in northern Thailand-diversity and use as food. Proceedings of the 8th round table conference on dipterocarps. Ho Chi Minh city.

[10]. Blessing C Ijioma, Ngozi C Ihediohanma, Ngozi C Onuegbu & Damaris C Okafor (2015). Nutritional composition and some anti-nutritional factors of three edible mushroom species in South Eastern Nigeria. *European Journal of Food Science Technology*. 3(2): 57-63.

[11]. Trinh Tam Kiet (2012). Macro fungi of Vietnam. Science and Technology Publishing House, Hanoi. 220.

[12]. Nguyen Phuong Dai Nguyen (2017). On the occurrence of *Russula* genus in Chu Yang Sin national park, Dak Kak province. The 7th National Scientific Conference on Ecology and Biological Resources. Hanoi.

[13]. Tran Thi Phu & Trinh Tam Kiet (2019). New records of macrofungi from Ngoc Linh Mountain, Quang Nam province, Vietnam. *Journal of Biology*. 41(1): 27-33.



- [14]. Thomas J White, Thomas Bruns, S Lee & J W Taylor (1990). Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: PCR protocols: a guide to methods and applications. M A Innis, D H Gelfand, J J Sninsky & T J White (eds.). San Diego, CA: Academic Press, New York, USA. 315-322.
- [15]. Rytas Vilgalys & Mark Hester (1990). Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. *Journal of Bacteriology*. 172(8): 4238-4246.
- [16]. Tom A Hall (1999). BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic acids symposium series*. [London]: Information Retrieval Ltd., c1979-c2000. 95-98.
- [17]. Yuanchao Liu, Huiping Hu, Manjun Cai, Xiaowei Liang, Xiaoxian Wu, Ao Wang, Xiaoguang Chen, Xiangmin Li, Chun Xiao, Longhua Huang, Yizhen Xie & Qingping wu (2022). Whole genome sequencing of an edible and medicinal mushroom, *Russula griseocarnosa*, and its association with mycorrhizal characteristics. *Gene*. 808: 145996.
- [18]. Brian P Looney, Martin Ryberg, Felix Hampe, Marisol Sánchez-García & P Brandon Matheny (2016). Into and out of the tropics: global diversification patterns in a hyperdiverse clade of ectomycorrhizal fungi. *Molecular Ecology*. 25(2): 630-647.
- [19]. Steven L Miller & Bart Buyck (2002). Molecular phylogeny of the genus *Russula* in Europe with a comparison of modern infrageneric classifications. *Mycological Research*. 106(3): 259-276.
- [20]. Ursula Eberhardt & Annemieke Verbeken (2004). Sequestrate *Lactarius* species from tropical Africa: *L. angiocarpus* sp. nov. and *L. dolichocaulis* comb. nov. *Mycological Research*. 108(9): 1042-1052.
- [21]. Yoshito Shimono, Manami Kato & Susumu Takamatsu (2004). Molecular phylogeny of Russulaceae (Basidiomycetes; Russulales) inferred from the nucleotide sequences of nuclear large subunit rDNA. *Mycoscience*. 45(5): 303-316.
- [22]. Tereza Leonhardt, Jan Borovička, Jan Sáčký, Jiří Šantrůček, Jan Kameník & Pavel Kotrba (2019). Zn overaccumulating *Russula* species clade together and use the same mechanism for the detoxification of excess Zn. *Chemosphere*. 225: 618-626.
- [23]. Brian P Looney, Slavomír Adamčík & P Brandon Matheny (2020). Coalescent-based delimitation and species-tree estimations reveal Appalachian origin and Neogene diversification in *Russula* subsection *Roseinae*. *Molecular Phylogenetics and Evolution*. 147: 106787.
- [24]. Todd W. Osmundson, Vincent A. Robert, Conrad L. Schoch, Lydia J. Baker, Amy Smith, Giovanni Robich, Luca Mizzan & Matteo M. Garbelotto (2013). Filling gaps in biodiversity knowledge for macrofungi: contributions and assessment of an herbarium collection DNA barcode sequencing project. *Plos One*. 8(4): e62419.
- [25]. Hong Min Zhou, Ying Da Wu & Yu Cheng Dai (2021). A new species of *Albatrellus sensu stricto* (Albatrellaceae, Russiales) from China. *Phytotaxa*. 510(1): 43–52.
- [26]. Motoo Kimura (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution*. 16(2): 111-120.
- [27]. Sudhir Kumar, Glen Stecher & Koichiro Tamura (2016). MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*. 33(7): 1870-1874.
- [28]. Quang Ninh (2020). Decision No. 4618/QĐ-UBND dated December 15, 2020 of the People's Committee of Quang Ninh province approving the framework project for conservation of genetic resources in Quang Ninh province in the 2021-2025 period.
- [29]. Myung Soo Park, Jonathan J Fong, Hyun Lee, Seung Yoon Oh, Paul Eunil Jung, Young Ju Min, Soon Ja Seok & Young Woon Lim (2013). Delimitation of *Russula* subgenus *Amoenula* in Korea using three molecular markers. *Mycobiology*. 41(4): 191-201.
- [30]. Slavomír Adamčík, Miroslav Caboň, Ursula Eberhardt, Malka Saba, Felix Hampe, Marek Slovak, Jesko Kleine, Helga Marxmueller, Soňa Jančovičová & Donald H Pfister (2016). A molecular analysis reveals hidden species diversity within the current concept of *Russula maculata* (Russulaceae, Basidiomycota). *Phytotaxa*. 270(2): 71-88.
- [31]. Hyun Lee, Myung Soo Park, Paul Eunil Jung, John A Eimes, Soon Ja Seok & Young Woon Lim (2017). Re-evaluation of the taxonomy and diversity of *Russula* section *Foetentinae* (Russulales, Basidiomycota) in Korea. *Mycoscience*. 58(5): 351-360.
- [32]. Sacha Melera, Carlo Ostellari, Neria Roemer, Peter G Avis, Mauro Tonolla, François Barja & Barbara Narduzzi-Wicht (2017). Analysis of morphological, ecological and molecular characters of *Russula pectinatoides* Peck and *Russula praetervisa* Sarnari, with a description of the new taxon *Russula recondita* Melera & Ostellari. *Mycological Progress*. 16: 117-134.

## ĐỊNH DANH LOÀI NẤM CHỆO THU THẬP TẠI VÙNG ĐÔNG BẮC VIỆT NAM

Chung Như Anh<sup>1,2</sup>, Nguyễn Minh Chí<sup>3\*</sup>, Trịnh Tam Kiệt<sup>4</sup>,  
Phạm Duy Long<sup>3</sup>, Phạm Thị Thu Thủy<sup>3</sup>, Vũ Văn Lợi<sup>3</sup>, Bernard Dell<sup>3,5</sup>

<sup>1</sup>Viện Khoa học Lâm nghiệp Việt Nam

<sup>2</sup>Trường Đại học Tây Nguyên

<sup>3</sup>Trung tâm Nghiên cứu Bảo vệ rừng, Viện Khoa học Lâm nghiệp Việt Nam

<sup>4</sup>Viện Nấm và Công nghệ sinh học

<sup>5</sup>Đại học Murdoch, Australia

### TÓM TẮT

Các loài nấm hoang dã được người dân miền núi phía Bắc Việt Nam và các quốc gia lân cận thu hái làm thực phẩm và dược liệu. Những lâm sản ngoài gỗ này có vai trò quan trọng đối với sinh kế của người dân. Nhiều loài nấm không thể hình thành thể quả trên môi trường nhân tạo mà phải cộng sinh với hệ rễ của cây rừng. Một loài nấm ăn được thuộc chi *Russula* với tên gọi phổ thông là Nấm chèo hoặc Nấm hồng cô thường được người dân ở vùng Đông Bắc sử dụng làm thực phẩm nhưng chưa được giám định loài. Nghiên cứu này đã thu thập Nấm chèo ở tỉnh Cao Bằng, Bắc Giang và Quảng Ninh để mô tả đặc điểm hình thái. Đồng thời giải trình tự hai gen ITS rDNA & LSU rDNA và so sánh với các trình tự tham chiếu trong ngân hàng gen. Kết quả nghiên cứu đặc điểm hình thái và giải trình tự gen cho thấy loài Nấm chèo có tên khoa học là *Russula griseocarnosa*. Đặc điểm hình thái của Nấm chèo tương đồng với loài *R. griseocarnosa* ở Trung Quốc. Nhiều địa phương ở Việt Nam đang đẩy mạnh thương mại hóa loài Nấm chèo. Tuy nhiên, việc khai thác quá mức đã làm suy giảm mật độ quần thể. Các nghiên cứu tiếp theo cần làm rõ đặc điểm sinh thái và kỹ thuật thu hái Nấm chèo.

**Từ khóa:** nấm ăn, Nấm chèo, nấm cộng sinh, *Russula griseocarnosa*.

Received : 13/01/2023

Revised : 17/02/2023

Accepted : 02/3/2023