Two new species of *Russula* subsect. *Virescentinae* from southern China

Bin Chen1,2 · Jie Song1 · Junfeng Liang1 · Yangkun Li3

Received: 16 January 2021 / Revised: 31 May 2021 / Accepted: 6 June 2021 © German Mycological Society and Springer-Verlag GmbH Germany, part of Springer Nature 2021

Abstract

Two new species from southern China, *Russula albolutea* and *R. subpunicea*, were described and illustrated. *Russula albolutea* is recognized by a yellowish white pileus with long striations at the margin, a white stipe with a yellowish tinge, globose to broadly ellipsoid basidiospores, hymenial cystidia that are mainly clavate and apically often obtuse and turn mauve in sulfovanillin, and a suprapellis mainly consisting of chains of short inflated cells with attenuated terminal cells. *Russula subpunicea* is characterized by a pinkish to dark pink pileus with striations at the margin, globose to broadly ellipsoid basidiospores with warts and spines sometimes joined to form a reticulum, hymenial cystidia that are mainly clavate, a suprapellis mainly composed of chains of short inflated cells with attenuated terminal cells, and pileocystidia that are mainly clavate and turn reddish in sulfovanillin. In this study, we respectively performed phylogenetic analysis based on the ITS sequence and nrLSU- *RPB2*-mtSSU dataset. By combining detailed morphological features with multigene phylogenetic evidence, we assigned the new taxa to *Russula* subsect. *Virescentinae*.

Keywords Russulaceae · New species · Phylogeny · Taxonomy

Introduction

*Russula* Pers. with eight subgenera is the largest genus of Russulaceae, which likely includes at least 2000 species (Buyck et al. 2018, 2020; Adamčík et al. 2019; Wijayawardene et al. 2020). This genus has a cosmopolitan distribution from Arctic tundra to tropical forests and forms ectomycorrhizae with a diverse range of plants in deciduous, evergreen, broadleaf and coniferous forests, scrubland, and even meadows (Knudsen and Borgen 1982, Buyck et al. 1996, Looney et al. 2018). The genus is mainly characterized by conspicuous basidiomata, colorful brittle pileus, amyloid warty basidiospores, abundant spherocytes in a heteromeric trama, an absence of latex, and hyphae that lack clamp connections (Singer 1986, Romagnesi 1987, Sarnari 1998). Some members of *Russula* are well-known edible fungi and are also commercially traded worldwide (Boa 2004; Wang et al. 2009; Looney et al. 2018; Wang 2020). According to recent statistics on the resource diversity of Chinese macrofungi, there are 78 edible species in China (Wu et al. 2019).

The main features of *Russula* subsect. *Virescentinae* include typically cracked pileus cuticles, a mild taste, white to cream spore prints, and a suprapellis comprising mainly attenuated terminal cells with short inflated subterminal cells (Singer 1986, Sarnari 1998). Recently, 5 *Russula* new species (*R. albidogrisea* J.W. Li & L.H. Qiu; *R. aureoviridis* J.W. Li & L.H. Qiu; *R. prasina* G.J. Li & R.L. Zhao; *R. pseudocrustosa* G.J. Li & Chun Y. Deng; *R. xanthovirens* Y. Song & L.H. Qiu) belonging to the subsect. *Virescentinae* have been successively reported in Asia (Das et al 2017, Song et al 2018, Hyde et al. 2019, Deng et al. 2020), indicating that Asia is a hot spot for the exploration of unknown *Russula* species. We also focused on this subsection and...
found a new member (*R. pallidula* B. Chen & J.F. Liang, Chen et al. 2019). During a survey on the habitat diversity and geographic distribution of Chinese *Russula* subsect. *Virescentinae*, some interesting specimens were found that were different from the known species. Here, two taxa are proposed as new to science based on their morphological features and phylogenetic relations.

**Materials and methods**

**Morphological observation**

Fresh basidiomata were photographed under daylight in the field. Specimens were dried at 50–55 °C and deposited in the herbarium of the Research Institute of Tropical Forestry, Chinese Academy of Forestry (RITF). The macromorphological descriptions were based on detailed notes and photographs. The terminology for descriptive terms followed Vellinga (1988). The color designations were taken from Kornerup and Wanscher (1981). The description templates and terminology of the micromorphological features were taken from Adamčík et al. (2019). All experiments were performed on dried specimens using a ZEISS Imager M2 (Carl Zeiss AG; Germany). The basidiospores were observed in Melzer’s reagent and measured from a lateral view excluding ornamentation. Other microscopic features were identified and measured with Congo Red staining after pretreatment in 5% potassium hydroxide (KOH). The coloring of the cystidia contents was observed in a sulfovanillin (SV) solution. The pileipellis was examined with the brilliant cresyl blue test to verify the presence of ortho- or metachromatic reactions (Buyck 1989). The structure and ornamentation of the basidiospores were illustrated using scanning electron microscopy (SEM-JEOL JSM-6510). The statistics of the basidiospore measurements are presented as (Min–)AV-SD–AV–AV+SD(–Max), where Min is the minimum value, Max is the maximum value, AV is the average value, SD is the standard deviation, and Q represents the length/width ratio of the basidiospores.

**DNA extraction, amplification, and sequencing**

Genomic DNA was extracted from dry specimens following an improved CTAB protocol (Zhou and Liang 2011). The following four loci were amplified: 600 base pairs of the ITS region of rDNA using the primers ITS1 and ITS4 (White et al. 1990); 900–1400 base pairs of the nuclear ribosome large subunit (nrLSU) using the primers LR0R and LR5 (Vilgalys and Hester 1990); 700 base pairs of the second largest subunit of RNA polymerase II (*RPB2*) using the primers bRPB2-6f and fRPB2-7cr (Liu and Hall 2004; Matheny 2005); 600 base pairs of the mitochondrial small subunit (mtSSU) with primers MS1 and MS2 (White et al. 1990). The PCR products were subjected to automated DNA sequencing on an ABI 3730 DNA analyzer using an ABI BigDye 3.1 terminator cycle sequencing kit (Shanghai Sangon Biological Engineering Technology and Services Co., Ltd, Shanghai, China). The newly generated sequences were submitted to the GenBank database (Table 1).

**Phylogenetic analyses**

Preliminary multiple sequence alignment was performed using the online version MAFFT 7.475 (http://mafft.cbrc.jp/alignment/server/) with manual evaluations and adjustments in BioEdit v.7.2.0 when necessary to obtain reliable and reasonable results (Hall 1999). The final alignment was submitted to TreeBASE (http://purl.org/phylo/treebase/phylops/study/ TB2:S28210). Species in the subg. *Heterophyllidia* Romagn, with high similarity to our new species were selected for phylogenetic analyses using maximum likelihood (ML) and Bayesian analyses (BA). The ML analysis was determined using RAxML-HPC2 on XSEDE (8.2.12) through the CIPRES Science Gateway (www.phylo.org). The ML analysis was executed by applying the rapid bootstrap algorithm with 1000 replicates to affirm the consistency of the results under the GAMMA model. Bootstrap supports (BS) ≥ 70% were regarded as significant. For BA analyses, GTR model was selected as the best substitution model by MrModeltest (Nylander 2004). The BA was performed using XSEDE (3.2.7a) through the CIPRES Science Gateway (www.phylo.org). The analysis was run with 4 chains for a total of 50,000,000 generations, trees were sampled every 100 generations, and the first 25% of the trees were discarded as the burn-in phase of each analysis. Runs were inspected to ensure the average standard deviation of split frequencies reached below 0.01. The Bayesian posterior probability (PP) values were obtained from the 50% majority-rule consensus trees, and nodes with PP ≥ 95% were considered significantly supported.

**Results**

**Phylogenetic analysis**

The ITS sequence and nrLSU-*RPB2*-mtSSU dataset were respectively analyzed using ML and BA. Both the ML analysis and BA resulted in similar tree topologies, and only the ML tree is shown (Figs. 1 and 2). The posterior probabilities for the BA are also shown along the branches.

The ITS phylogenetic analysis showed that subsect. *Virescentinae* was a monophyletic group; this was strongly supported by BS (100%) and PP (1). Additionally, the remaining 5 subsections of sect. *Heterophyllidia* were significantly supported as a monophyly. The samples of the two new species,
**Table 1** GenBank accession numbers of sequences used in the multigene phylogenetic analysis. Newly generated sequences are in bold. HT denotes holotype

| Taxon                  | Voucher | Location | nrLSU     | RPB2      | mtSSU      | Reference               |
|------------------------|---------|----------|-----------|-----------|------------|-------------------------|
| R. aff. crustosa       | BB 06.616 | Canada   | KU237461  | KU237747  | KU237305   | Buyck et al. 2018       |
| R. aff. virescens      | BB 09.021 | New Caledonia | KU237582  | KU237868  | KU237430   | Buyck et al. 2018       |
| R. albolutea (HT)      | RITF2653 | China: Hubei | MW397120  | MW411340  | MW403833   | This work               |
| R. albolutea           | RITF4460 | China: Chongqing | MW397121  | MW411341  | MW403834   | This work               |
| R. albolutea           | RITF4461 | China: Yunnan | MW397122  | MW411342  | MW403835   | This work               |
| R. albolutea           | RITF4462 | China: Yunnan | MW397123  | MW411343  | MW403836   | This work               |
| R. cf. vesca           | BB 06.525 | Mexico   | KU237465  | KU237751  | KU237309   | Buyck et al. 2018       |
| R. crustosa            | BPL265  | USA: Tennessee | KT933826  | KT933898  | –          | Looney et al. 2016      |
| R. cyanoxantha         | UE29.09.2002-2 | France | DQ422033  | DQ421970  | –          | Buyck et al. 2008       |
| R. grisea              | UE2005.08.16-01 | Sweden | DQ422030  | DQ421968  | –          | Buyck et al. 2008       |
| R. grisea              | BB 07.184 | Slovakia | KU237509  | KU237795  | KU237355   | Buyck et al. 2018       |
| R. heterophylla        | UE20.08.2004-2 | Sweden | DQ422006  | DQ421951  | –          | Buyck et al. 2008       |
| R. ilicis              | MF 00.300 | Italy    | KU237595  | KU237880  | KU237443   | Buyck et al. 2018       |
| R. ionochlora          | BB 07.338 | Slovakia | KU237508  | KU237794  | KU237354   | Buyck et al. 2018       |
| R. langei              | BB 07.792 | France   | KU237510  | KU237796  | KU237356   | Buyck et al. 2018       |
| R. maguanensis         | HKAS 102277 | China: Yunnan | MH714537  | MH939989  | –          | Wang et al. 2019        |
| R. mariae              | HCCN19111 | South Korea | KF361812  | KF361712  | –          | Park et al. 2013        |
| R. mariae              | BB 07.038 | USA      | KU237538  | KU237824  | KU237384   | Buyck et al. 2018       |
| R. medallata           | BB 07.252 | Slovakia | KU237546  | KU237832  | KU237392   | Buyck et al. 2018       |
| R. mustelina           | FH12226 | Germany | KT933866  | KT933937  | –          | Looney et al. 2016      |
| R. mustelina           | SA 09.88 | Slovakia | KU237596  | KU237881  | KU237444   | Buyck et al. 2018       |
| R. pallidula           | RITF2613 | China: Zhejiang | MH027960  | MH091698  | MW403845   | This work               |
| R. pallidula           | RITF3331 | China: Yunnan | MH027961  | MH091699  | MW403846   | This work               |
| R. phloginea           | RITF4193 | China: Yunnan | MK860704  | –          | MK860708   | Song et al. 2019        |
| R. phloginea           | RITF4194 | China: Yunnan | MK860703  | –          | MK860707   | Song et al. 2019        |
| R. subpallidirosea     | RITF4083 | China: Guangdong | MK860702  | –          | MK860705   | Song et al. 2019        |
| R. subpunicea (HT)     | RITF3715 | China: Guangxi | MW397124  | MW411344  | MW403837   | This work               |
| R. subpunicea          | RITF2648 | China: Zhejiang | MW397125  | MW411345  | MW403838   | This work               |
| R. subpunicea          | RITF1435 | China: Hunan | MW397126  | MW411346  | MW403839   | This work               |
| R. subpunicea          | RITF2615 | China: Hunan | MW397127  | MW411347  | MW403840   | This work               |
| R. substrariata        | HKAS 102278 | China: Yunnan | MH714540  | MH939992  | –          | Wang et al. 2019        |
| R. variata             | BPL241  | USA: Tennessee | KT933818  | KT933899  | –          | Looney et al. 2016      |
| R. vesca               | AT2002091 | Sweden | DQ422018  | DQ421959  | –          | Buyck et al. 2008       |
| R. virolepis           | BB 07.273 | Slovakia | KU237534  | KU237820  | KU237380   | Buyck et al. 2018       |
| R. virolepis           | SFC20121010-06 | South Korea | KF361858  | KF361758  | –          | Park et al. 2013        |
| R. virescens           | HB9989  | Belgium  | DQ422014  | DQ421955  | –          | Buyck et al. 2008       |

*R. albolutea* and *R. subpunicea*, formed a strongly supported clade (BS 100%, PP 1.00) and were clearly distinct from known and sequenced species of the subsect. *Virescentinae*. And *Russula subpunicea* clustered together with unidentified environmental samples of *R.* sp. from Japan.

For multigene phylogenetic analysis, the results were similar to those of the ITS phylogenetic analysis. *Russula albolutea* is the sister taxon, without support, for a clade comprising *R. virescens* (Scheaff.) Fr., *R.* aff. *virescens*, and *R. pallidula*. *Russula subpunicea* clustered together with *R.* aff. *crustosa* Peck with 98% bootstrap support and 1.00 posterior probabilities.

**Taxonomy**

**Russula albolutea** B. Chen & J.F. Liang, sp. nov., Figs. 3a–d, 4, and 5

*Mycobank*: MB836126

**Diagnosis**: Basidiomata small to medium-sized, yellowish white pileus, white stipe with yellowish tinge, subglobose to...
broadly ellipsoid to ellipsoid basidiospores with relatively small ornamentation, hymenial cystidia mainly clavate, apically often obtuse, contents granulose or crystalline, turning mauve in SV, suprapellis mainly composed of chains of short inflated cells with attenuated terminal cells, pileocystidia clavate, apically typically obtuse.

**Holotype:** China, Hubei Province, Shennongjia Forestry District, Hongping Town, 31° 40′ 17.86″ N, 110° 26′ 40.53″
Fig. 2  Phylogenetic tree based on the nrLSU-RPB2-mtSSU dataset. Bootstrap support (BS, when ≥ 70%) and Bayesian posterior probabilities (PP, when ≥ 0.95) were shown. Infrageneric classification of *Russula* follows Buyck et al. (2018)
E; 2560 m asl., in mixed hardwood forests dominated by *Fagus*; 10 August 2016, LYK89 (RITF2653).

**Etymology:** The Latin word “albolutea” refers to the yellowish white pileus.

**Basidiomata:** Small to medium-sized, pileus 50–75 mm in diameter, hemispheric when young, convex with a depressed center when mature; margin incurved, not cracked, striations up to 1/3 of the radius; surface smooth, glabrous, slightly viscous when humid, peeling to 1/3 of the radius; yellowish white (2A2) at the center; margin white (1A1).

**Lamellae:** Adnate, 3–4 mm deep, moderately distant, white (1A1), lamellulae absent or rare, edge entire and concolor.

**Stipe:** 30–40 × 8–15 mm, cylindrical or clavate, curved and slightly inflated at the base, rugulose longitudinally, white with yellowish tinge (2A2), medulla hollow.

**Context:** 2–3 mm thick in half of the pileus radius, white (1A1), without color change when bruised, taste mild to slightly bitter, odor indistinct.  

**Spore print:** White.

**Basidiospores:** 5.8–6.6–8.2 × 5–6–6.8–7.2 μm, Q = 1.00–1.11–1.22(1.38), globose to broadly ellipsoid; ornamentation of relatively small, moderately distant [4–6(–8) in a 3 μm diameter circle] amyloid warts, 0.3–0.5 μm high, subreticulate, rarely isolated, fused in long branched chains [1–2(–3) in the circle], occasionally connected by line connections [0–1(–2) in the circle]; suprahilar spot large, imamyloid.  

**Basidia:** 28(28.5)–32.8–39(43) × (7)8.3–10–11.6(14) μm, mostly 4-spored, some 2- and 3-spored, clavate or fusiform; basidiola clavate or subcylindrical, ca. 5–11 μm wide.  

**Hymenial cystidia on lamellae sides:** Dispersed to moderately numerous, ca. 600–800/mm², (38)41–50.6–63(68) × 5–8.1–12 μm, clavate, fusiform or subcylindrical, apically always obtuse, occasionally mucronate, thin-walled; contents abundant granulose or crystalline, turning mauve in SV.  

**Hymenial cystidia on lamellae edges:** Dispersed, often smaller in size, 27(27.5)–40–63(66) × (6)6.5–8.1–9.8 μm, clavate or cylindrical, apically often obtuse or mucronate, sometimes with 2–4-μm-long appendage, thin-walled; contents granulose or crystalline, mainly in the middle and upper part, turning mauve in SV.  

**Marginal cells:** (14)14.7–20–26.2(26.7) × (4.4)5.3–7.2–9.8 μm, clavate or subcylindrical, sometimes flexuous.  

**Pileipellis:** Orthochromatic in cresyl blue, sharply delimited from the underlying context, 160–220 μm deep, two-layered. Suprapellis 120–160 μm deep, mainly composed of chains of short inflated cells with attenuated terminal cells. Hyphal terminations near the pileus margin occasionally branched, sometimes flexuous, thin-walled; terminal cells...
(10.4)10.8–18.8–34(42) × (3.6)4–5.2–6.8(7.1) μm, mainly subcylindrical or clavate, apically obtuse; subterminal cells often wider, ca. 5–8 μm wide, always unbranched. Hyphal terminations near the pileus center similar to those near the pileus margin; terminal cells (11.4)12.5–21.7–28(40) × 3.7–4.8–6.4(7.3) μm, mainly subcylindrical, occasionally ellipsoid, apically obtuse; subterminal cells often wider, ca. 5–7 μm wide, always unbranched. Hyphal terminations near the pileus center similar to those near the pileus margin; terminal cells (11.4)12.5–21.7–28(40) × 3.7–4.8–6.4(7.3) μm, mainly subcylindrical, occasionally ellipsoid, apically obtuse; subterminal cells often wider, ca. 5–7 μm wide, always unbranched. Pileocystidia near the pileus center always one-celled, (35)39–49–60(85) × (3.6)4–5.4–8.1(9.6) μm, cylindrical, clavate or fusiform, occasionally curved at the middle part, apically usually obtuse, sometimes constricted; contents abundant, granulose or crystalline, turning reddish in SV. Pileocystidia near the pileus center often smaller, always one-celled, (28)32–43–54(58) × 4.2–5.1–6.1(6.3) μm, thin-walled, clavate or cylindrical, apically typically obtuse or occasionally mucronate, contents granulose or occasionally crystalline, turning reddish in SV. Subpellis 50–70 μm deep, composed of horizontally oriented, relatively dense, intricate, 2–6-μm-wide hyphae. Cystidioid hyphae: In subpellis and context with heteromorphous-granulose contents, oleiferous hyphae in context with granulose or crystalline contents.

Additional specimens examined China, Chongqing City, Shizhu County, Huangshui Town, Dafengbao Nature Reserve Communities, 30° 14′ 33.12″ N, 108° 23′ 31.10″ E, 1557 m asl., 28 July 2016, LHJ160728-04 (RITF4460); Yunnan Province, Yuxi City, Huaning County, 24° 12′ 48.36″ N, 102° 56′ 44.72″ E, 1600 m asl., August 2016, LHJ-3735 (RITF4461); Yunnan Province, Menghai County, Mengzhe Town, Mannong Village, 21° 54′ 17.80″ N, 100° 17′ 23.32″ E, 1242 m asl., 10 August 2016, MH2016-83 (RITF4462).

Notes: Both morphology and phylogeny place *R. albo-lutea* clearly in subsect. *Virescentinae*. Given the pileus coloration, the present species resembles four taxa (*Russula pseudocrustosa*, *R. pallidula*, *R. indoalba* A. Ghosh et al., and *R. albidogrisea*) of this subsection. However, *R. pseudocrustosa*, originally described from China, possesses a cracked pileus with a radically disrupted cuticle and typically larger hymenial cystidia (67–88 × 8–12 μm, Deng et al. 2020). The Chinese species *R. pallidula* can be distinguished by the typically smaller basidiomata (40–55 μm) and pale turtle green to pale olive-buff pileus with minute white to cream scales at the margin (Chen et al. 2019). *Russula indoalba* (originally reported from India) is distinct in its wavy to interrupted pileus margin, adnexed to almost free lamellae, yellowish-cream spore print, larger basidia (45–60 × 9–13 μm), and hymenial cystidia on the lamellae sides (47–90 × 8–16 μm, Hyde et al. 2016). *Russula albidogrisea*, originally reported from China, has larger basidia (41–48 × 9–11 μm) and smaller hymenial cystidia on the lamellar sides (35–50 × 5–11 μm, Das et al. 2017). In the field, *Russula albolutea* may be confused with Indian species *R. natarajanii* K. Das, J.R. Sharma & Atri which often has the larger basidiomata (60–105 μm), a tuberculate pileus margin, longer hymenial cystidia on the lamellar sides (60–90 × 6–10.5 μm) and absence of hymenial cystidia on the lamellar edges (Das et al. 2006).

*Russula subpunicea* B. Chen & J. F. Liang, sp. nov., Figs. 3a–k, 6, and 7

MycoBank: MB836124

**Diagnosis:** Basidiomata small to medium-sized; yellowish white to pinkish to dark pink pileus; adnate to subfree lamellae; spore print white; subglobose to broadly ellipsoid to ellipsoid basidiospores with relatively small amyloid warts or spines; hymenial cystidia mainly clavate; subcylindrical, lageniform, or clavate marginal cells; terminal cells of hyphal terminations in pileipellis lageniform or clavate;

![Fig. 5 Russula albolutea (RITF 2653, holotype). a Pileipellis and pileocystidia near the pileus margin. b Pileipellis and pileocystidia near the pileus center. Scale bar = 10 μm](image-url)
suprapellis mainly composed of chains of short inflated cells with attenuated terminal cells; and pileocystidia mainly clavate.

**Holotype:** China, Guangxi Zhuang Autonomous Region, Pingxiang City, Fubo Forest Farm, 22° 01′ 42.11″ N, 106° 50′ 1.07″ E; 641 m asl., in mixed forests of Castanopsis hystrix and Betula alnoides, 19 August 2016, JXM189 (RITF3715).

**Etymology:** The Latin word “subpunicea” refers to the pinkish pileus.

**Basidiomata:** Small to medium-sized; pileus 12–87 mm in diameter; initially hemispheric when young, applanate to convex, convex with a depressed center after mature; margin incurved, cracked, and striations up to 1/4 of the radius; surface smooth, glabrous, slightly viscous when humid, peeling to 1/4 of the radius; yellowish white (2A2) with odor pinkish (11A2) tinge when young, odor pinkish (11A2) or grayish orange (6B4) after maturation, shallower at the margin. **Lamellae:** Adnate to subfree, 2–4 mm deep, dense, white (1A1) to cream, lamellulae absent, edge entire and concolor. **Stipe:** 25–40 × 7–15 mm, cylindrical, slightly attenuated at the base, white (1A1) to dirty white, and medulla initially stuffed becoming hollow. **Context:** 2–3 mm thick in half of the pileus radius, white (1A1), unchanging when bruised, taste slightly bitter, odor indistinct. **Spore print:** White (1A1).

**Basidiospores:** (4.9)5.3–6.3–7.4 × (4.3)4.6–5.3–6.0(7.1) μm, Q = (1.00) 1.02–1.14–1.26 (1.36), globose to broadly ellipsoid; ornamentation of relatively small, moderately distant to dense [3–5(–6) in a 3 μm diameter circle] amyloid warts or spines, 0.4–0.8 μm high, occasionally reticulate, fused in short- or long-branched chains [1–2(–3) in the circle],

---

**Fig. 6** Rusula subpunicea (RITF 3715, holotype). a Basidia. b Basidiola. c Marginal cells. d Hymenial cystidia on lamellae sides. e Hymenial cystidia on lamellae edges. Scale bar = 10 μm
frequently connected by line connections [0–1(–2) in the circle]; suprahilar spot large, amyloid. **Basidia:** 30–34.3–39(40) \times (5).6–8–10.7(12.8) μm, mostly 4-spored, some 2- and 3-spored, clavate; basidiola clavate or subcylindrical, ca. 5–9 μm wide. **Hymenial cystidia on lamellae sides:** Moderately numerous, ca. 1200–1500/mm², 44–75.5–105(114) \times (5.8)6.2–8.4–10 (10.4) μm, clavate or subcylindrical, apically mainly obtuse, often with 2–6-μm-long appendage, thin-walled; contents heteromorphous or granulose, mainly in the middle and upper part, turning tawny in SV. **Hymenial cystidia on lamellae edges:** Sometimes shorter, 51–70.6–93(95) \times 6–8.9(10.9) μm, clavate or cylindrical, apically mainly obtuse, sometimes with 2–5-μm-long appendage thin-walled; contents heteromorphous-cry stalline, almost without color change in SV. **Marginal cells:** (9.5–)12.5–16.8–23.5(25.3) \times (3.7)4.4–5.8–7.2(7.5) μm, subcylindrical, lageniform, or clavate, sometimes flexuous. **Pileipellis:** Orthochromatic in cresyl blue, sharply delimited from the underlying context, 120–180 μm deep, two-layered. Suprapellis 50–70 μm deep, composed of chains of short inflated cells with attenuated terminal cells. Hyphal terminations near the pileus margin typically branched, occasionally flexuous, thin-walled; terminal cells (10)11–19.5–34(42) \times (2.3)2.6–4.6–7.2(8) μm, mainly attenuated or narrowly lageniform, occasionally clavate or cylindrical, apically constricted or obtuse; subterminal cells frequently shorter, ca. 3–8 μm wide, typically unbranched. Hyphal terminations near the pileus center similar to those near the pileus margin; terminal cells (9.2)9.5–16.6–20.5(23) \times 2.8–4.6–6 μm, cylindrical, clavate, lageniform, apically obtuse or occasionally constricted; subterminal cells often shorter, rarely branched, ca. 4–9 μm wide. Pileocystidia near the pileus margin always one-celled, (30)35–45–55 × 4.2–5.4–6.5(–7) μm, mainly clavate, occasionally fusiform, apically typically obtuse, sometimes with ellipsoid 2–5-μm-long appendage, thin-walled; contents granulose or crystalline, turning reddish in SV. Pileocystidia near the pileus center similar in size, always one-celled, 26–36.7–56.7(61) \times (4)4.5–6–7.3(9) μm, thin-walled, mainly clavate, occasionally fusiform, apically often obtuse or occasionally mucronate, occasionally with 2–5-μm-long appendage, contents granulose, turning reddish in SV. Subpellis 80–120 μm deep, composed of horizontally oriented, relatively dense, intricate, 2–6-μm-wide hyphae. **Cystidioid hyphae:** In subpellis and context with granulose contents, oleiferous hyphae in context with granulose or crystalline contents.

**Additional specimens examined:** China, Zhejiang Province, Lishui City, Baiyunshan Ecology Forest Farm, 28° 28′ 50.14″ N, 119° 55′ 0.46″ E, 141 m asl., 20 August 2015, JXM33 (RITF2648); Hunan Province, Yongzhou City, Dongan County, Shunhuang Mountain National Forest Park, 26° 23′ 54.40″ N, 111° 02′ 54.97″ E, 457 m asl., 5 July 2012, yuan37 (RITF1435); ibid., 13 July 2015, LYK49 (RITF2615).

Notes: The combination of morphological features and phylogenetic analysis place *R. subpunicea* in subsect. *Virescentinae*. Phylogenetically, our new species *R. subpunicea* is clustered with an unidentified environmental sample of “*R. sp.*” from Japan, which share 97% query coverage and 99.82% identity on ITS sequence region with the new species. However, there are no details available except the sequence information in GenBank.

Morphologically, *R. subpunicea* may be confused in the field with three recently reported new species: *R. maguanensis* J. Wang et al., *R. substriata* J. Wang et al., and *R. orientipurpurea* Wisitr., H. Lee & Y.W. Lim from Asia. However, the Chinese...
species *R. maguansensis* has a sticky tuberculate-striate pileus, a finely to coarsely cracked pileus cuticle, larger basidiospores 

\[(7.5) 8.0–8.5–9.5 \times (6.5) 7.0–7.4–8.0(8.5) \mu m\]

with isolated warts, shorter hymenial cystidia on the lamellae edges (32–52 \(\times 7–12\)), and a thicker pileipellis (500–800 \(\mu m\), Wang et al. 2019). *Russula substrita*, originally also reported from China, possesses a sticky tuberculate-pileate pileus, a finely to coarsely cracked pileus cuticle, larger basidiospores \(8.0–9.0–10.0(11.0) \times (6.5) 7.0–7.5–8.0(9.0) \mu m\) with isolated warts, shorter hymenial cystidia on the lamellae edges (23–45 \(\times 6–11 \mu m\), and typically one-layered and locally two-layered pileipellis (220–400 \(\mu m\), Wang et al. 2019). *Russula orientipurpurea* (originally reported from South Korea) has a pruinose pileus surface, absence of hymenial cystidia on the lamellae edges and pileocystidia, longer marginal cells \([28.5] 48–67.8–88 \(\times 121\) \(\mu m\)] with isolated warts, shorter hymenial cystidia on the lamellae edges \((23–45 \times 6–11 \mu m\), and typically one-layered and locally two-layered pileipellis (220–400 \(\mu m\), Wang et al. 2019).
DL, Fan XL, Dissanayake LS, Erdoğdu M (2020) Outline of Fungi and fungus-like taxa. Mycosphere 11(1060):1456. https://doi.org/10.5943/mycosphere/11/1/8
Wisitrassameewong K, Park MS, Lee H, Ghosh A, Das K, Buyck B, Looney BP, Caboň M, Adamčík S, Kim C, Kim CS, Lim YW (2020) Taxonomic revision of Russula subsection Amoninae from South Korea. MycoKeys 75:1–29. https://doi.org/10.3897/mycokeys.75.53673
Wu F, Zhou LW, Yang ZL, Bau T, Li TH, Dai YC (2019) Resource diversity of Chinese macrofungi: edible, medicinal and poisonous species. Fungal Divers 98:1–76. https://doi.org/10.1007/s13225-019-00432-7
Zhou LL, Liang JF (2011) An improved protocol for extraction of DNA from macrofungi. Guangdong Forest Science Technology 27:13–16

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.