much promising result in the present investigation for its economic exploitation except for increased leafiness which is an important characteristic from the forage point of view. Thus hope lies in the selection of new plant types through onward generations of progenies for rangeland forage production.

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A NEW RECORD OF EDIBLE *RUSSULA* FROM INDIA

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RUSSULA LUTEA (Huds. ex Fr.) Fr. an edible fungus is recorded for the first time from India[1]. The specimens have been deposited in the Herbarium, Department of Biosciences, Himachal Pradesh University, Shimla (HPUB) and with Dr M. Locquin, France.

Russula lutea (Huds. ex Fr.) Fr., Epicr. p. 363, 1838; *Hym. Eur.* p. 454, 1874; *Syll. Fung.* **5**: 480, 1887, figure 1A–G.

Pileus 4–7 cm diam., convex when young, becoming applanate at maturity, shallowly depressed in the centre; cuticle peeling easily, glabrous, viscid when wet, deep yellow to golden yellow[2]; margin decurved when young, becoming plane at maturity, slightly striated; flesh 0.4–0.8 cm thick at disc, firm, brittle, unchanging when cut or bruised. Taste mild. Odour pleasant. Lamellae adnexed or free, thin, close, usually equal in length, yellow to orange; edges entire. Stipe 3–5 cm long and 0.8–1.5 cm diam., central, cylindric, equal in diam. throughout or slightly tapering upward, dry, smooth, yellowish white, solid at first hollowing with age. Spore colour in mass ochraceous. Spores 8–10 × 7.5–9 μm, broadly ellipsoid to subglobose, amyloid; ornamentation 0.4–1 μm high, of moderately coarse warts, mostly separate or some confluent forming short ridges; apiculus up to 2 μm long. Basidia 24–52 × 8–13(–15) μm, clavate, tetrasporic; sterigmata 3–6.5 μm long. Pleurocystidia 50–88 × 6–11.5 μm, cylindric to subcylindric, clavate, fusoidclavate or fusiform with subacute to rounded apex; arising in the subhymenium or from the outer portion of trama; filled with hyaline refractive contents or partially empty; abundant. Cheilocystidia similar to pleurocystidia. Subhymenium 20–35 μm thick, pseudoparenchymatous. Hymenophoral trama consisting of hyaline, thin-walled, septate, branched, interwoven hyphae, 1.5–9 μm diam and sphaerocysts up to 48 × 42 μm. Pileus cuticle is made up of hyaline, thin-walled, septate, branched, interwoven, non-gelatinous hyphae, 1.5–5.5 μm diam. Pileus context heteromerous, consisting of hyaline, thin-walled, septate, branched, interwoven hyphae, 2–5.5(–10) μm diam and sphaerocysts up

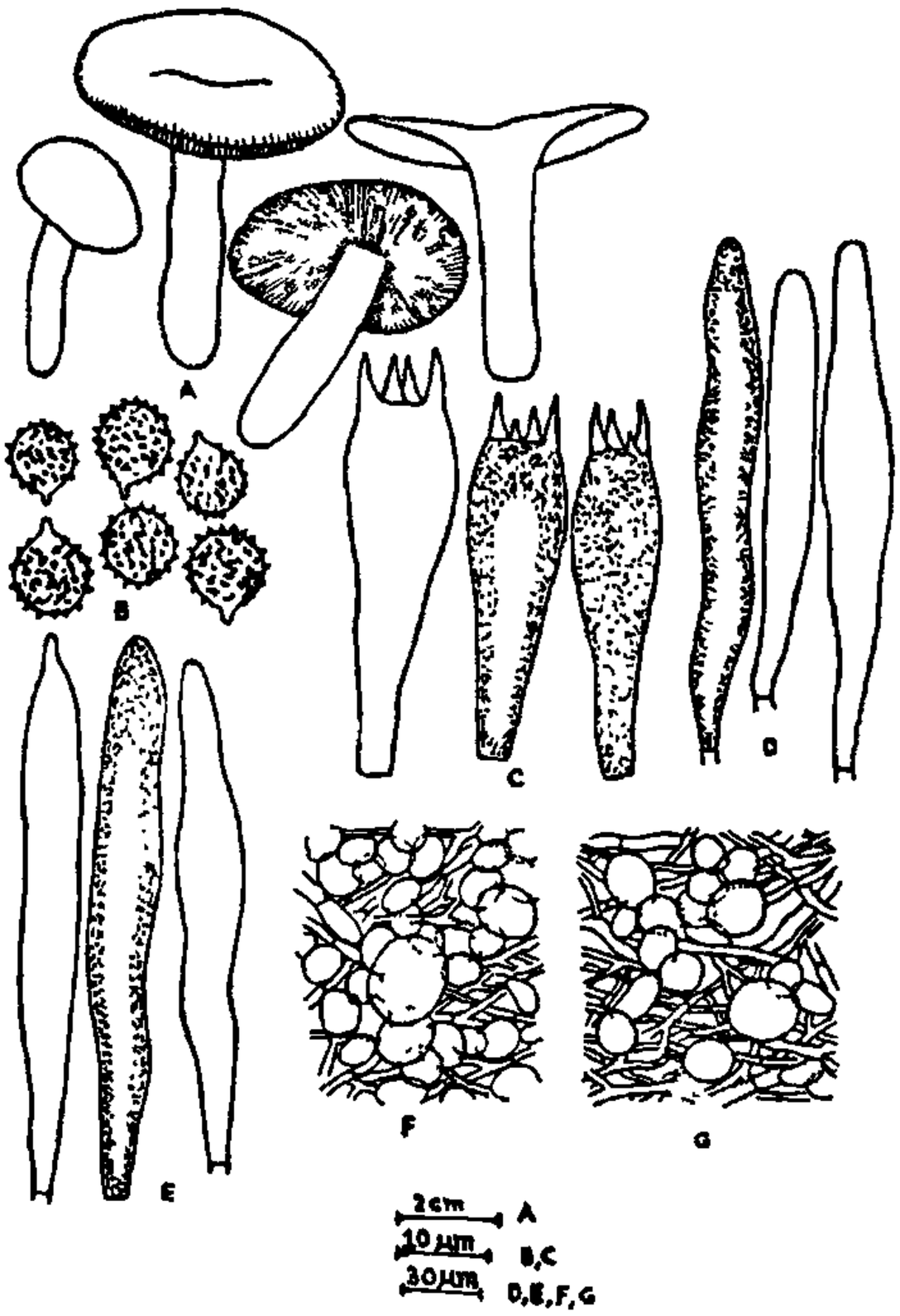

Figure 1A–G. *Russula lutea* (Huds. ex Fr.) Fr. **A.** Basidiocarps with longitudinal section; **B.** Basidiospores; **C.** Basidia; **D.** Cheilocystidia; **E.** Pleurocystidia; **F.** Hymenophoral trama (part), and **G.** Pileus context (part).

to 44 × 40 μm. Stipe cuticle consisting of hyaline, thin-walled, septate, branched, interwoven hyphae, 1.5–4.5(–6) μm diam. Stipe context heteromerous.

Chemical tests (Stipe surface): with 2% aq. phenol—purple; with 10% Ferrous sulphate—salmon; with formalin—negative.

Habit and Habitat: Solitary—scattered, associated with *Cedrus deodara*, *Picea smithiana*, *Pinus wallichiana*, *Quercus incana* and *Rhododendron arboreum*.

Specimens examined: Acc. Nos. Shimla; HPUB 1244, 1284, 1309, 1342, 1357, 1421, 1525.

Remarks: The present species is in conformity with *Russula lutea* (Huds. ex Fr.) Fr. It is reported to be edible by Kibby[3] and Miller[4].

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ABSENCE OF GLYOXALASE-I POLYMORPHISM IN NAIKPODS OF ANDHRA PRADESH, INDIA

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Erythrocyte glyoxalase I (GLO: E.C.4.4.1.5) in humans is polymorphic due to the occurrence of three common phenotypes viz. 1–1, 2–1 and 2–2, determined by two autosomal codominant alleles-GLO^1 and GLO^2, and is known to be located on chromosome 6 between major histocompatibility (HLA) region and phosphoglucomutase-locus-3[1], and it is widely used as a genetic marker in the study of human variation. In recent years several tribal, and caste groups of the Indian subcontinent have been studied for GLO polymorphism and these populations were found to be polymorphic for the two common genes GLO^1 and GLO^2 in varying frequencies[1–10].

In this paper we report the absence of GLO polymorphism, for the first time in an endogamous, proto-Australoid, settled agrarian aboriginal Naikpod tribal group inhibiting the north-western parts of Andhra Pradesh. Naikpods were previously investigated for various genetic markers[11–13] but no data are available for GLO in this population.

A total of 353 blood samples were collected from unrelated Naikpod individuals living in the villages of Armur taluk of Nizamabad district, Chinnoor and Luxettipet taluks of Adilabad district of Andhra Pradesh. Hemolysates were prepared and subjected to starch gel electrophoresis for the identification of GLO phenotypes[14]. A known GLO 2–1 phenotype sample was included as reference in each electrophoretic run.

All the 353 samples are found to be homozygous for the GLO^2 gene. Absence of GLO^1 gene in Naikpods is unexpected considering the polymorphic nature of GLO in all the population groups studied earlier[1–10]. The frequency of GLO^1 varies from 14.7% in Brahmins of Delhi[2] to about 37% in Narikoravas (a nomadic tribe of South India)[5]. In other Indian populations its frequency was reported[9] between 15 and 33%.

Absence of GLO^1 gene was reported earlier in the aboriginal populations of Australia and Papua New Guinea[2]. In general, the frequencies of GLO^1 gene among Indian populations are lower than in Caucasian populations where its frequency is reported[1,9] to be above 40%. Although Indian populations are genetically more heterogeneous in view of their endogamous marriage pattern due to social, cultural, historical, geographical and religious barriers, the absence of GLO^1 gene in Naikpods is a significant finding and at the moment we are not in a position to offer any explanation.

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