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New record of *Chaetasbolisia erysiphoides* from cold arid soils of Zanskar (Kargil), India

Zanskar is a high altitude semi-desert valley in Ladakh (30°45′–35°50′N and 75°45′–80°31′E) lying on the northern flank of the Great Himalayan range. This mountain range acts as a climatic barrier protecting Zanskar valley from most of the monsoon, resulting in a warm and dry climate during the six months of summer, with a temperature range of 20–27°C, low humidity and scant precipitation. However, winter in this valley is freezing cold as the temperature goes below 0°C (–30°C) owing to heavy snowfall and some parts of it are considered as the coldest inhabited places of the world. The whole of Ladakh region usually remains land-locked and isolated from the rest of the country for about six months (November to May) because of continuous snowfall, snow blizzards and high velocity dust storms. Therefore, the soil usually remains covered by thick snow and its temperature is below zero.

The genus *Chaetasbolisia* Speg., typified by *C. erysiphoides*[1] embodies a rare group of microfungi characterized by superficial, unilocular, dark brown pycnidia with several setae scattered over its body; doliiform to ampulliform conidiogenous cells formed from the inner cells of the pycnidial wall and hyaline aseptate conidia[2]. The genus belongs to the family Didymellaceae in the Pleosporales, Dothideomycetes (ref: Index Fungorum). There are seven species, viz. *C. californiana*, *C. erysiphoides*, *C. falcata*, *C. falcata* var. *minuta*, *C. longiseta*, *C. microglobusa*, *C. raphiae* and *C. sapotae*, described in the genus, but so far no revision has been made[2]. Another species, *Chaetasbolisia indica*, was reported from India[3]. *Chaetasbolisia erysiphoides* initially described[4] as *Chaetophoma erysiphoides* was found to be hypophyllous on leaves of *Photinia loriformis* in China. It was later renamed as *Chaetasbolisia erysiphoides*[5]. The type species was redescribed[6] but not through an examination of the type collection.

In India, the genus was represented so far by only one species, *C. indica*, which was found to be lignicolous and showed differences from the type species *C. erysiphoides* in having much larger conidiomata, small blunt setae and slightly smaller eguttulate conidia[3]. During a mycological survey of cold arid soil of Zanskar valley (India), *Chaetasbolisia erysiphoides*, the type species of the genus was isolated and newly reported as

Table 1. Comparative account of two species of *Chaetasbolisia* reported from India

Species	Morphological characters			
	Conidiomata	Conidiogenous cells	Conidia	Setae
C. erysiphoides	Unilocular, brown, 92–184 µm in diam.	Ampulliform 7.4–9.4 × 1.4–2.5 µm	Oval, hyaline, minutely guttulate, 4.2–5.0 × 2.1 µm	Acute, irregularly verrucose, up to 122 µm long and 3.3–5.1 µm thick
C. indica	Unilocular, brown to blackish, 140–220 µm in diam.	Cylindrical to ampulliform, 4–9 × 2.5–4 µm	Oval, oblong-elliptical, eguttulate, 4–5 × 2 µm	Blunt, smooth, up to 20 µm long and 4–8 µm thick

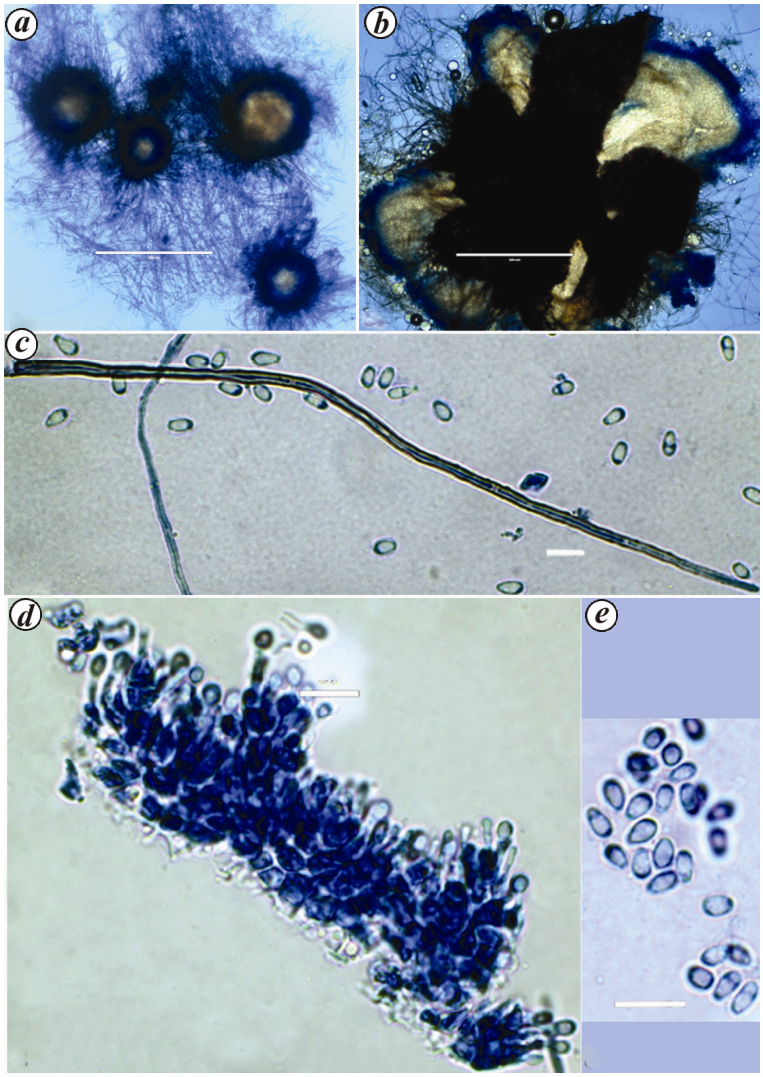

Figure 1. Photomicrographs of *Chaetasbolisia erysiphoides*. ***a***, Perithecia (bar = 200 µm); ***b***, Perithecium exposing the conidiogenous cells and conidia (bar = 200 µm); ***c***, Single rough-walled seta (bar = 10 µm); ***d***, Conidiogenous cells (ampulliform) exposed (bar = 10 µm); ***e***, Hyaline, oval and guttulate conidia (bar = 10 µm); ***a***, ***b*** (bar = 200 µm); ***c***, ***d***, ***e*** (bar = 10 µm).

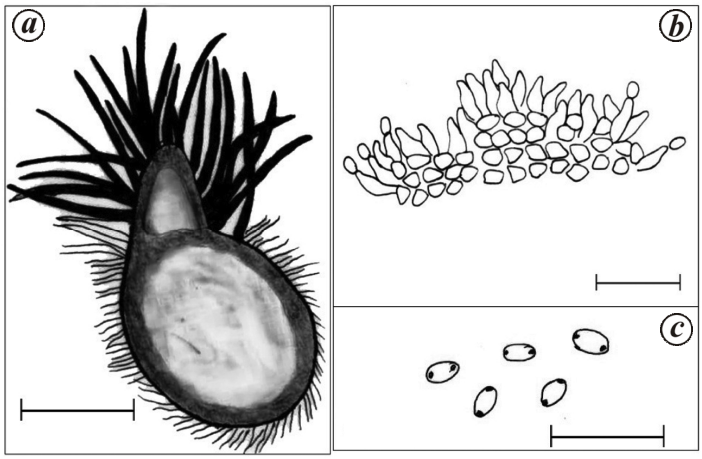

Figure 2. Camera lucida drawings. ***a***, Perithecium; ***b***, Conidiogenous cells; ***c***, Conidia. ***a*** (bar = 42 µm); ***b***, ***c*** (bar = 14 µm).

a psychrotolerant fungal species from India.

Soil samples were collected aseptically from Padum area of Zanskar valley and brought to the laboratory in pre-sterilized polythene bags. Dilution pour plate method using modified Czapek Dox agar (CDA) supplemented with Rose Bengal (0.1 mg/100 ml) and streptomycin sulphate (50 mg/1000 ml) was followed to isolate the soil microfungi. The fungal isolate was identified on the basis of its cultural and morphological characters following a key provided by Sutton[2]. Microscopic line drawings were made with the aid of camera lucida (Erma, Japan) at 400× and 1000× magnifications. Dimensions were determined for perithecia, setae, conidiogenous cells and conidia using an ocular micrometer. Microphotography was done using Sony N50 camera attached to an Olympus CH 20i binocular microscope. The identity of the fungal isolate was also confirmed from National Fungal Culture Collection of India (NFCCI), Agharkar Research Institute, Pune (India).

Chaetasbolisia erysiphoides[1]

Taxonomic description: *Mycelium* – superficial, with branched, septate, brown, 1.4–2.8 µm wide hyphae. *Conidiomata* – pycnidial, superficial, formed throughout the colony within a week of incubation at 28 ± 2°C, separate, light brown with dark margins, globose to subglobose, setiferous, ostiolate, unilocular, thin-walled, 92.3–184.6 × 85.2–170.4 µm. *Setae* – numerous, thick-walled, septate, verrucose, scattered over the pycnidia up to 12 µm long and 3.3–5.1 µm thick. *Conidiogenous cells* – thin-walled, hyaline, enteroblastic, phialidic, discrete and ampulliform, formed from the inner cells of the pycnidial wall, 7.4–9.8 × 1.4–2.5 µm. *Conidia* – solitary, oval, hyaline, aseptate, thin-walled, smooth, guttulate, obtuse at both ends, 4.2–5.0 × 2.1 µm (Figures 1 and 2).

Chaetasbolisia erysiphoides is reported for the first time from the cold arid region (Zanskar) of Kargil district (Jammu and Kashmir), India. The species is morphologically different from *C. indica*, the only species in the genus earlier described from India, from tropical moist and mixed forests of Shahdol division of Madhya Pradesh[3]. The two species are compared (Table 1).

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Fall armyworm in Africa: which 'race' is in the race, and why does it matter?

Fall armyworm (*Spodoptera frugiperda*) has already invaded almost half of Africa since its first observation in the continent in January 2016 (refs 1, 2). At its current rate of invasion, the pest may conquer Africa before the end of 2017. Although this polyphagous pest feeds on more than 80 plant species, it is considered to be a 'pest of grasses'[3], because of its overwhelming preference for Poaceae (or Gramineae). In Africa, maize is the primary host plant of fall armyworm. However, based on feeding preferences, two different races or strains of *S. frugiperda* – a maize strain and a rice strain – have been reported in its native range of the tropical Americas[4]. These two strains occur in Africa as well. For instance, fall armyworm in Nigeria was found to be the rice strain, whereas the population in Sao Tome and Principe was found to be the maize strain[2], despite the fact that both populations severely damaged the maize crop. Understanding the genetic and physiological differences or similarities between these strains is important for the use of pheromone-based monitoring, which has been suggested as a tool for fall armyworm surveillance programmes[1]. Such knowledge also would be useful for the selection of appropriate biocontrol agents and chemical pesticides.

Although *S. frugiperda* has spread to at least 21 countries in Africa[1], the strain that occurs in these countries is unknown, except for Nigeria, and Sao Tome and Principe. As no specific strains from East Africa have been reported, we obtained a *S. frugiperda* population from Arusha, Tanzania (lat. 3°22.646′S, long. 36°48.401′E and altitude 1232 m amsl) feeding on maize, and confirmed it as the rice strain based on a partial *cytochrome c oxidase I* (*coxI*) gene sequence at the World Vegetable Center headquarters in Taiwan. The *S. frugiperda* population in Tanzania GenBank accession numbers: MF278657 to MF278659) is genetically identical to the population in Nigeria. The phylogenetic analysis clearly differentiated the maize (Sao Tome and Principe population) and rice (Nigeria and Tanzania populations) strains into two distinct clades (Figure 1). Based on a pair-wise population comparison, the genetic distance (F_{ST}) between the rice and maize strains was 1 (maximum genetic diversity between the two populations), although the level of significance was found only at $P < 0.10$. However, the use of nuclear regions or genes for population comparison can shed additional light on how far these strains are genetically dissimilar, because the above results and an earlier study in Africa[2] are based on the maternally inherited mitochondrial *coxI* gene that is sometimes disputed in DNA barcoding.

The female moths of *S. frugiperda* were reported to produce Z9–14 : Ac and Z11–16 : Ac as the major pheromone compounds, as well as a number of other compounds such as Z9–12 : Ac and Z7–12 : Ac in low amounts[5–7]. However, two independent studies have shown that the pheromone composition of the two strains differed significantly[8,9]. Maize strain females originating from Florida, USA produced significantly more Z11–16 : Ac than rice strain females[8]. However, maize strain females collected from Louisiana, USA had a higher proportion of Z9–14 : Ac and lower proportions of Z7–12 : Ac and Z11–16 : Ac than their rice strain counterparts[9]. Thus, the same strain produces different proportions of pheromone components in different geographical locations. These variations could contribute to variations in male responses under field conditions. Sex pheromone lures containing three components (Z9–14 : Ac, Z11–16 : Ac and Z7–12 : Ac) attracted almost 60% of maize strain males[10]; hence this commercial lure was biased to attract maize strain males, leading to an underestimation of rice strain populations. A subsequent study that used two different four-component blends resembling the maize- and rice-strain female blend found that both strains showed geographic variations rather than strain-specific differences in their response to pheromone lures[11].

Are these strains reproductively isolated? This is partly answered by the fact that the two strains differ in the timing of their mating activity – the maize strain mates soon after the onset of scotophase, while the rice strain mates at the end of the scotophase[12,13]. Although some evidence is available for naturally occurring hybridization in the field[14], a recent study tracked the basis of allochronic differentiation in mating time, which acts as a premating isolation barrier between the strains of *S. frugiperda*[15]. The study identified a major quantitative trait chromosome underlying differentiation in circadian timing of mating activity and showed strain-specific polymorphisms as well as differential expression of the clock gene *vrille* between the strains. Thus, it