5 mm to 2.0 cm. The average length is around 1.5 cm while the width varies between 3 mm and 5 mm.

Since these markings are made by a marine worm, their presence along with the sedimentary structures indicate shallow water shelf conditions of deposition of the rocks of Shillong Group.

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THE URANI-FEROUS BIOTITE-SERICITE SCHIST OF KASTURI GATTU HILLOCK, NORTH-EAST OF SOMASILA, NELLORE DISTRICT, ANDHRA PRADESH

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SOMASILA is a village about 90 km, West of Nellore, situated on the Madras–Vijayawada railway line. Somasila is located on the northern bank of North Pennar River, just at the point where the river, flowing east, emerges from the Velikonda Range of hills in the Eastern Ghats (in the South-Western corner of Toposheet No. 57 N/6).

The hillock of Kasturi Gattu is approximately 70 m high (from the ground level) and is located about 5 km NNE of Somasila, and about 2 km north of the village of Khambampadu. There are a number of quarries on this hillock, where the fairly hard rock is quarried and used in the construction of the Somasila dam, now being built across the River Pennar.

The base of Kasturi Gattu hillock on the western side, is composed of lower Proterozoic amphibole–biotite–quartz rock, quartz–biotite–muscovite–chlorite schist, Quartz–Chlorite schist etc.

In the northern part of Kasturi Gattu hillock, dark coloured biotite–chlorite schist is present, and as one proceeds to the south, the schist is silicified and feldspathised, partly obliterating the schistosity. It is observed that bands of silicified and feldspathised schist are separated by non-silicified biotite-schist bands. Four bands of the silicified schist were observed in the quarries, in the southern part of Kasturi Gattu hillock.

The unsilicified biotite-chlorite schist in the northern part of the hillock, is not radioactive, but the silicified and feldspathised schist seen further to the south, is weakly to moderately radioactive assaying 0.01 to 0.02% U_3O_8.

The schist, traversed by a Joint/fracture plane trending N30° East, shows higher radioactivity, and assays upto 0.10% U_3O_8. In all these radioactive schistose rocks, the contents of ThO_2 is less than 0.01%.

The lowest lithological member of the Middle Proterozoic formation–the regolith, represented by quartz-sericite phyllite is moderately radioactive and contains upto 0.012% U_3O_8, with practically no thorium. This unit is overlain by a moderately radioactive oligomict quartz-Pebble conglomerate, assaying upto 0.013% U_3O_8 and 0.06% ThO_2. The top most bed is a white quartzite, which is a marker horizon and can be traced for one kilometer, in a NW-SE direction.

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SISTER CHROMATID EXCHANGES IN VIRUS-INFECTED CHINESE HAMSTER OVARY CELLS

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MONITORING the frequency of sister chromatid exchanges (SCEs) has become a sensitive indicator of subtle alterations in the genetic material. It is known that SCE frequencies can be elevated by a host of chemical and physical agents; however, relatively few reports have been published on SCEs induced by viruses. Here we report the results of studies on SCEs in Chinese Hamster Ovary (CHO) cells experimentally infected with 4 DNA viruses belonging to 3 groups, *viz* Poxvirus (Vaccinia), Herpesvirus (Herpes Simplex

types 1 and 2, HSV-1 and HSV-2) and Papovavirus (Simian Virus 40, SV-40).

CHO cells were grown in the dark in presence of 5-bromodeoxyuridine (1 μg/ml) for 2 cell cycles during logarithmic phase. One set of cultures was inoculated by adsorption method with 3 dex $TCID_{50}$/ml of each of the following viruses: Vaccinia (671061), HSV-1 (753166), HSV-2 (753167) and SV-40 (776), and the cultures were incubated for about 10 hr thereafter. Mock-infected and uninfected cultures were used as controls. c-Metaphase chromosome preparations were made with a 2 hr colchicine (0.05 μg/ml) treatment. The slides were coded for temporarily masking their identity. Sister chromatid differential staining was performed following the 'fluorescence-plus-Giemsa' technique[1] with minor modifications. Thirty well-spread metaphase plates, each containing 21 chromosomes, were scored from each slide. The slides were then decoded and the results were analyzed.

The average SCE increase, obtained from 3 identical experiments, in Vaccinia-, HSV-1-, HSV-2- and SV-40-infected cultures was about 2.77, 3.0, 3.85 and 2.76 exchanges per cell over the control base levels, respectively (Student's t-test, $p < 0.01$). There was no significant difference between uninfected control and mock-infected control cultures. Other chromosome abnormalities were not observed in any of these cultures.

Brown and Crossen[2] reported elevation in the SCE frequencies but not chromosome aberrations in a mouse embryo cell line (JLS-V16) infected with Rauscher leukemia virus; on the other hand, Kato and Sandberg[3] have shown that infection of human diploid fibroblasts with HSV-1 and HSV-2 viruses induces chromosome aberrations but not SCEs. The present observations therefore agree with the view that the mechanisms leading to SCEs and to chromosome aberrations are distinct[3].

It is interesting to note that the induction of SCEs in CHO cultures was observed with all the viruses tested, irrespective of the differences among their nature, replication mechanisms and lytic/transformation cycles: Vaccinia virus multiplies in cytoplasm while HSV-1 and HSV-2 multiply in nucleus; CHO cells are non-permissive to SV-40 virus multiplication, but can be transformed by this virus. It is therefore apparent that some as yet unidentified virus-specific event(s), common to all these viruses, may play an important role in the induction of SCEs in CHO cells. Attempts to resolve this issue will be described elsewhere.

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XYLANOLYTIC ACTIVITY OF *ASPERGILLUS OCHRACEUS*-42

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MANY studies have been carried out concerning the industrial use of amylase and cellulase. However, only a few reports are available on xylanase which degrades xylan to xylose. Xylan is a polymer of xylose containing β-1, 4-xylosidic linkages and is widely distributed in plant cell walls and forms a primary part of the hemicellulose portion. In some higher plants and agricultural wastes, xylan is 20–40% of dry weight[1]. Because of its natural abundance, xylan, like cellulose, is potentially a good fermentation substrate for production of feedstuff[2].

In recent years, interest has increased in the use of microbial xylanase for the economical production of xylose, a sweetening and antidiabetic agent, for clarification of fruit juices. It is also used as digestive aid in pharmaceutical industry. Various microorganisms such as *Aspergillus niger*[3,4], *Chaetomium trilaterale*[5], *Streptomyces xylophagus*[6], *Cryptococcus albidus*[7], *Irpex lacteus*[8], *Bacillus*. sp[9], *Bacillus subtilis*[10], have been reported to be sources of xylanases. *Aspergillus ochraceus*-42 has outstanding ability to produce sufficient xylanolytic enzymes in xylan medium. But it has not been reported earlier. Therefore the present paper deals for the first time with the xylanolytic activity of *A. ochraceus*-42.

The strain was isolated during a screening programme for xylanase producing microorganisms from soils of W. Bengal. It possesses appreciable xylan decomposing activity. Colonies on CD-medium attain a diameter of 2–3 cm in 6 days at 28°C, usually plane or slightly furrowed, less zonate, characterized by a tough basal mycelium that is submerged. Conidial structures are crowded. It appears as brownish yellow. Conidial