Availability of land for agriculture in the northeastern region (21%) is limited due to geophysical parameters compared to other regions of India (54%), which puts pressure on the forests. The economics and efficiency of jhum cultivation[22] showed that jhum is a resourceful system of organic multiple cropping well suited to heavy-rainfall areas. The economic and energetic efficiency of jhum is higher than alternative forms of agriculture, such as terrace and valley cultivation with respect to expensive inputs such as fertilizers, and is thus followed by the tribals.

Figures 2 *a–d* and 3 *a–d* show 15-day composite images of DMSP–OLS-derived night-time fires over the study area from January to April 2005. DMSP–OLS analysis suggests enhanced fire activity during the first and second week of March in all the States. Mizoram, Nagaland, Meghalaya and Manipur showed fires during all the four months, with a peak in March and April.

1. Gubbi, S., *Deccan Herald*, Bangalore, available at http://wildlifefirst.info/images/wordfiles/fire.doc (accessed January 2004), 2003.
2. Stracey, P. D., *J. Bombay Nat. Hist. Soc.*, 1967, **64**, 440–446.
3. Hao, W. M., Ward, D. W., Olbu, G. and Baker, S. P., *J. Geophys. Res.*, 1996, **101**, 23577–23584.
4. Fearnside, P. M., *Climate Change*, 2000, **46**, 115–158.
5. Crutzen, P. J. and Andreae, M. O., *Science*, 1990, **250**, 1669–1678.
6. Dwyer, E., Gregoire, J. M. and Malingreau, J. P., *Ambio*, 1998, **27**, 175–181.
7. Hao, W. M. and Liu, M. H., *Global Biogeochem. Cycles*, 1994, **8**, 495–503.
8. Kaufman, Y. J. *et al.*, *J. Geophys. Res.*, 1998, **103**, 32215–32238.
9. Christopher, S. A., Chou, J., Zhang, J., Li, X. and Welch, R. M., *Geophys. Res. Lett.*, 2000, **27**, 2197–2200.
10. Reid, J. S. *et al.*, *Atmos. Chem. Phys.*, 2005, **5**, 827–849.
11. Kaufman, Y. J. *et al.*, *J. Geophys. Res.*, 1998, **103**, 31783–31808.
12. Levine, J. S., Cofer III, W. R., Cahoon, D. R. and Winstead, E. L., *Environ. Sci. Technol.*, 1995, **29**, 120A–125A.
13. Cofer III, W. R. *et al.*, *J. Geophys. Res. D*, 1989, **94**, 2255–2259.
14. Hurst, D. F., Griffith, D. W. T. and Cook, G. D., *J. Geophys. Res.*, 1994, **99**, 16441–16456.
15. Yokelson, R. J., Susott, R., Ward, D. E., Reardon, J. and Griffith, D. W. T., *J. Geophys. Res.*, 1997, **102**, 18865–18877.
16. Andrae, M. O. *et al.*, Trace gas and aerosol emissions from Savanna fires. In *Biomass Burning and Global Change, Remote Sensing, Modeling and Inventory Development and Biomass Burning* (ed. Levine, J. S.), MIT Press, 1996, pp. 278–295.
17. Ahern, F., Gregoire, J.-M. and Justice, C., Report of a workshop, Joint Research Center, ISPRS, Italy, 3–5 November 1999.
18. Korontzi, S., Justice, C. O. and Scholes, R., *J. Arid Environ.*, 2003, **54**, 395–404.
19. Champion, H. G. and Seth, S. K., *Revised Survey of the Forest Types of India*, Government of India, Delhi, 1968.
20. Elvidge, C. D., Baugh, K. E., Kihn, E. A., Kroehl, H. W. and Davis, E. R., *Photogramm. Eng. Remote Sensing*, 1997, **63**, 727–734.
21. Elvidge, C. D., Nelson, I., Hobson, V. R., Safran, J. and Baugh, K. E., Detection of fires at right using DMSP–OLS Data. *Global and Regional Fire Monitoring from Space*, MIT Press, 2001, pp. 125–144.
22. Ramakrishnan, P. S., *Shifting Agriculture and Sustainable Development: An Interdisciplinary Study from North–Eastern India*, MAB Series, UNESCO, Paris, 1992, vol. 10.

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Mutational analysis of H5N1 and H1H1 for ascertaining test systems

Bird flu (also known as avian influenza, avian flu, influenza virus A, type A flu, or genus A flu) is a type of influenza virus that is hosted by birds, but may infect several species of mammals. H5N1 is a highly pathogenic strain of bird flu. The first known appearance of this type of influenza in humans[1] was in Hong Kong during 1997. The name H5N1 refers to the subtypes of surface antigens present on the virus: hemagglutinin type 5 and neuraminidase type 1. Normally, avian flu viruses are transported worldwide in the intestines of wild birds, and are non-lethal. Infected birds pass on H5N1 through their saliva, nasal secretions and faeces. Because migratory birds are among the carriers of the H5N1 virus, it may spread to all parts of the world. There are three types of influenza viruses, namely A, B and C, which are classified on the basis of nucleoproteins. Among these, influenza A virus has a pandemic potential. There are two important surface glycoproteins, hemagglutinin (HA), and neuraminidase (NA), which are embedded in the virus membrane. Hemagglutinin mediates receptor binding and membrane fusion, whereas neuraminidase facilitates cleavage of the viral progeny from infected cells. There are 16 H and 9 N subtypes of the influenza A virus[2]. Totally 144 HA and NA combinations are possible, out of which 103 have been confirmed. The avian influenza A virus (AIV) that contains the HA subtypes H3, H4, H6 is the most frequently isolated, whereas AIV of subtypes H5 and H7 was less frequently encountered. All other HAs are rather rare. AIV that possesses the NA of subtypes N2, N1, N8 and N3 is frequent and all other NAs are rarely detected[3].

Figure 1. Protein structure of *PB2* gene of H5N1 genome which has a mutation at position 627.

There are two models of mutations associated with influenza virus, namely antigen shift and antigen drift[4].

The H5N1 genome has eight segments (1–8), each segment codes for a protein: polymerase* (PB2), polymerase (PB1), polymerase (none), hemagglutanin (none), nucleocapsid (none), neuraminidase (NA), matrix protein 2(M) and nonstructural protein respectively.

Lysine (K) at position 627 of H1N1 (1918) has mutated to glutamic acid (E) in H5N1 (K627E), which is known to be pandemic for humans. This finding has resulted in a new approach of vaccine treatment for bird flu.

We notice one more mutation at position 628 which changes glutamine(Q) in H1N1 to proline(P) in H5N1 (Q627P), but this mutation has no effect on the protein function.

H1N1 *PB2* gene 'A(623)APP**K**(627)**Q**-(628)S' changes into 'A(623)APP**E**(627)-**P**(628)S'.

There are two domains present in segment of H5N1 genome, whose Prodom Domain ID is PD001667 and PD217887. However, position 627 comes under domain PD001667.

Secondary structure of segment 1 of H5N1 and H1N1 is almost similar according to the SOPMA secondary structure prediction. There are minor changes found in the extended strands and random coils, where the alpha helix is the same in H5N1 and H1N1.

Results have shown that the protein sequence of H5N1 is close to H1N1, but there are minor changes found due to a single mutation. Deletion of one amino acid at 627 is mainly responsible for the mutation. This leads to the new approach of vaccine treatment for bird flu. There are two domains found in segment 1 of H5N1 genome. The result of SOPMA shows that there are 284 alpha helices, 176 extended strands, 66 beta turns and 233 random coils present in the secondary structure.

1. Chan, P. K., *Clin. Infect. Dis.*, 2002, **34**, S58–S64.
2. Wu, Tsung-Zu and Huang, Li-Min, *Chang Gung Med. J.*, 11 November 2005, **28**.
3. Kaleta, E. F., Hergarten, G. and Yilmaz, A., *Dtsch. Tierarztl. Wochenschr.*, 2005, **112**, 448–456.
4. Nicholson, K. G., Wood, J. M. and Zambon, M., *Lancet*, 2003, **362**, 1733–1745.

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Isolation of halotolerant *Penicillium* species from mangroves and salterns and their resistance to heavy metals

Though it was believed that microbial communities at high salinities are dominated exclusively by archaea and bacteria and the eukaryotic species *Dunaliella salina*, studies on the microbial diversity in hypersaline environments revealed the presence of melanized fungi, 'considered as a new group of eukaryotic halophiles'[1], halotolerant black yeast and several other filamentous fungi[2–4], including *Penicillium* spp.[5].

Water bodies often become sinks for disposal of waste from effluent-treatment plants or run-offs from landfills, particularly during the rainy season. Much attention is given to heavy metal pollution because metals cannot be decomposed by *in situ* biological means[6]. Micro-organisms have been used at low costs to remove metals from effluents[7], with fungi known to be more tolerant to metals than bacteria or actinomycetes[8], and the *Penicillium* spp. being prominent[8–12] among these.

Although isolates of halophilic penicillia are reported from hypersaline environments, there has been little work done on this group of fungi from the coastal waters of Goa, India. Further, although the genus *Penicillium* has been studied and used for metal tolerance/removal, it has not been examined with respect to halophilic/halotolerant species possessing metal resistance. Here we report the isolation of extremely halotolerant penicillia from the mangroves and salterns of Goa; these species have the characteristic of being resistant to heavy metals such as Pb^{2+}, Cu^{2+} and Cd^{2+}.

Water samples were collected from a well (W) close to a copper-smelting plant and to the mouth of a river, from mangroves (M) and from solar salterns (S). These were filtered through a 0.45 µm filter, which was then placed over Czapek Dox Agar (CDA) containing 2% salt (S-CDA) for well-water and mangrove samples, while saltern samples were grown on CDA with 5% salt; observations were carried out for growth at room temperature (RT), i.e. 30°C. *Penicillium* species were selected and purified on isolation media containing 1 mM lead nitrate and maintained on S-CDA with lead.

The isolates were spot-inoculated onto CDA containing NaCl concentrations of 0, 2.0, 5.0, 7.5, 10.0, 12.5, 15.0, 17.5 and 20.0% (w/v) and assessed for growth in terms of colony diameter at RT up to 7 days for three sub-cultures.

The isolates were then spot-inoculated on S-CDA containing 0–10 mM Pb^{2+} as $Pb(NO_3)_2$, or 0–5.0 mM Cu^{2+} as $CuSO_4 \cdot 5H_2O$, or Cd^{2+} as $3CdSO_4 \cdot 8H_2O/Cd(NO_3)_2 \cdot 4H_2O$ and monitored for growth as above.

A total of forty-eight isolates were obtained from the samples screened, among which 12 belonged to the genus *Penicillium*: one from well-water, denoted as WP1, three from mangroves: MP2–MP4, and eight from salterns: SP5–SP12. SP10 and SP11 were monoverticillate; MP1, SP5–SP8 were biverticillate symmetric; MP2, MP3, SP9 and SP12 were biverticillate asymmetric and MP4 was triverticillate.