primordia formation from nodal and internodal explants of cassava (cv. MCol 22) was justified. Nodal explants about 10 mm with an axillary bud developed adventitious roots in one step on MS basal medium containing 2% sucrose for 8 days of culture. But internodal segments without an axillary bud did not develop the adventitious roots on the same medium. However, most internodal segments excised from nodal explants after culture of 72-96 hours on MS basal medium developed adventitious roots. The segments rooted at 90% after culture on medium with 0.5 mg/L IBA for 132 hours, on medium with 1 mg/L IBA for 60 hours, and on medium with 2 mg/L IBA for 36 hours respectively. Thus the period of culture on IBA medium and IBA concentration affected the rooting rate. Anatomically root primordia were not formed in internodal segments cultured on medium with 2 mg/L IBA for 36 hours, but the primordia were formed when cultured on the medium longer than 72 hours. Therefore, it is suggested that the determination for root formation occurred before the differentiation of root primordia on medium with IBA, and root inducing factors from medium were absorbed and accumulated during the period of determination for root primordium differentiation in internodal segment of cassava.

D 207

Cloning of Cytosolic Ascorbate Peroxidase Gene in Embryogenic Callus of Pimpinella brachycarpa

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Ascorbate peroxidase is an important enzyme that detoxify hydrogen peroxide within the cytosol and chloroplasts of the plant cells. A full length cDNA clone(993 bp) encoding cytosolic ascrobate peroxidase from Pimpinella brachycarpa was isolated and its nucleotide sequence determined. The nucleotide sequences of Pbapx were highly homologous to those of apx from Nicotiana tabacum, Cucumic sativus, and Pisum sativum. Pbapx and apx from Nicotiana tabacum, apx from Cucumis sativus and apx from Pisum sativum are 80%, 78% and 77% identical in highly conserved region. The Pbapx contained an open reading frame encoding mature protein of 250 amino acids with calculated molecular mass of 27.8 kDa. According to the k-NN of PSORT program, Pbapx seemed to be located in cytosol. The Pbapx gene was expressed in all tested organs of Pimpinella brachycarpa; mRNA levels were low in petioles and high in embryogenic calli and roots.

D 301

A LAMMER Kinase Homologue of *Schizosaccharomyces pombe* Regulates Expression of Genes for Catalase and Glutathione Peroxidase

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Previously we have identified the *Schizosaccharomyces pombe lkh1+* gene encodes a dual-specificity kinase of LAMMER family having both serine/threonine kinase and tyrosine kinase activity. And also showed that the *lkh1* null mutant is viable but shows increased susceptibility towards a reactive oxygen generating compound, hydrogen peroxide. To investigate possible involvement of *lkh1* in expression of genes for defence mechanism against oxidative stress, northern analyses was performed.

Among the genes which have been known to play a role in defence mechanism against oxidative stress, the genes for catalase and glutathione peroxidase showed decreased level of expression in *lkh* null mutant. Our results indicate that LAMMER kinase may play a role not only in morphogenetic control but also in defense mechanism against oxidative stress in the fission yeast.

D 302

LAMMER Kinase Plays a Role in Morphogenesis of the Yeast

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We have previously cloned the *Schizosaccharomyces pombelkh1*$^{+}$ gene encoding a novel kinase belonging to the LAMMER kinase family. For fuctional analysis, we have constructed the *lkh1 D* null mutant. The cell lengths of *lkh1 D* changed through out the growth stages different from the wild type cells. Interestingly enough, the *lkh1 D* cells in liquid culture showed increased flocculation, in which, a Ca^{2+}-dependent galactose specific lectin-like proteins were involved. In addition, the prolonged cultivation of the *lkh1 D* cells on solid medium showed an abnormal colony margin and an invasion-like growth as the well-known invasive growth of haploid *Saccharomyces cerevisiae.*

S. cerevisiae gene, *KNS1*, which also know as the LAMMER kinase family was disrupted in this study. *D kns1* did not showed any differences from the wild type cells during normal growth conditions. Notably we have found when S 1278background cells and the *KNS1* disruptant were grown on minimal media containing 1% butanol, *D kns1* could not induce pseudohyphal growth, even in liquid medium. Furthermore, the *Sch. pombelkh1 D* transformed with *lkh1* and *KNS1* showed the morphological change including a functional complementation of flocculation. Together, these results suggest that the LAMMER kinase homologue in yeast may not fuction in exactly the same pathway, but it does have a role in regulation of morphology and the cell cycle. This is the first report on the fuction of LAMMER kinase homologue in the yeast.

D 303

Expression of *nsdD* that Controls Sexual Development of *Aspergillus nidulans*

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The *nsdD* encodes a GATA type transcription factor, carrying a type IVb zinc finger DNA binding domain, which functions in activating sexual development of *A. nidulans*. The *nsdD* over-expression by placing the gene downstream the *niiA* promotor resulted in the cleistothecial development even in the presence of 0.6 M KCl that inhibited sexual development specifically. The *nsdD* expression was repressed by 0.6M KCl. A lot of suppressors for D*nsdD* showed the common phenotype similar to that of *nsdD* over-expressed mutant,the salt independent sexual development. These results strongly suggest that the inhibition of sexual development by salts was carried out via *nsdD* involved regulatory network. In several allelic mutants of *nsdD* that resulted in non sense mutations and lacked C terminal zinc finger, the