investigations in all known cases of code violations. If enduring traditions are to be evolved, establishing the image of impartiality is as essential as the impartial action itself.

Some of the recommendations resulting from the SSV seminar are worth noting:

'Since there are a large number of universities and research institutions in India, it was suggested that each and every organization must have an Ethics Committee of its own to look into any complaint. The inquiries conducted by them should not be secretive. It should follow transparent procedures. In case a *prima facie* case is established, the matter should be referred to a formal inquiry. The organization may form a committee of scientists well known for their integrity and independent views for making reliable and impartial inquiries. Their reports should be made public and proper and effective action must be taken on their recommendations'.

'Scientific academies/societies, organizations, and government establishments should take the following action against guilty scientists:

Science academies and societies should withdraw fellowships/memberships granted to such scientists; Academic degrees, awards and prizes based on fraudulent work should be withdrawn; Scientific journals should take note of such cases and take appropriate action such as refusal of publications of papers authored by such scientists; Such persons should not be invited to present papers or chair sessions in scientific seminars, symposia, and conferences; Scientific community should boycott an institution that does not take required action against its staff found guilty of misconduct of science; Various government funding agencies and university grants commission responsible for giving grants should ensure that the organization being given the grant has a transparent mechanism for investigating cases of scientific misconduct.'

If the Indian scientific community believes in the cause of science and establishing healthy foundations for its practice and management, it would find these recommendations of SSV unexceptional. The primary responsibility to assure that they are implemented in the spirit in which they are conceived rests solely with them. This cause cannot triumph unless they become the faithful agents to carry the message through. It was precisely because they did not care enough as a body in the past, the cancer of unethical practices in science and its management has grown over the years. Like corruption in society, such practices too will spread with increasing frequency if not checked decisively.

The Academies among themselves represent the top senior scientific community of India. It will be appropriate, if they take the initiative to implement a uniform code of ethics for the practice and management of science, perhaps along the lines recommended by SSV, and monitor its implementation. In a sense, such a move by the Academies will be a measure of their own commitment to inculcate healthy practices in science. If they are not willing, perhaps a time has already come as suggested by Vittal, to have the government pass appropriate legislation.

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## SCIENTIFIC CORRESPONDENCE

# Identity of subsequences of some pregnancy-associated proteins with SERPIN signature sites of some serine protease inhibitors and a carcinoma antigen

The foetus is an allograft in the uterus. Yet it is not rejected by the immunocompetent mother. Understanding of the exact mechanism of foetal survival is limited and the unequivocal evidence still seems elusive. It is proposed that one of the possible reasons for evasion of maternal lymphocyte-mediated lysis by the foetus could be local inactivation of serine proteases, secreted on the target trophoblast cells by cytotoxic lymphocytes during lethal hit, by some pregnancy-associated proteins which contain amino acid subsequences (and presumably function) identical to those of some serine protease inhibitors (SERPINs).

In this study, the amino acid subsequences of three pregnancy-associated proteins – human pregnancy zone protein (H. PZP), sheep uterine milk protein (S. UTMP) and pig uteroferrin-associated protein (P. UFAP), were found to be identical to tri-, tetra-, penta-, hexa- and heptapeptide sequences of SERPINs like human plasma serine protease (Protein C) inhibitor, and Rat SERPINs 1, 2.1 and 3, respectively. The overall identity of sequences of pregnancy-associated proteins with SERPINs ranged from 15.27% to 28.97%.

Interestingly, among the identical sequences, one tripeptide (RPF) and one hexapeptide stretch (FNRPFL) of human plasma SERPIN, two tripeptide subsequences (FNR and RPF) of rat SERPIN 1 and a tetrapeptide (RPFL) and a pentapeptide subsequence (FDRPF) of rat SERPIN 3 were found to be parts of SERPIN signature sites of the respective inhibitors.

Human squamous cell carcinoma antigen (H. SCCA) is a tumour marker. The amino acid sequences of S. UTMP and H. SCCA, H. PZP and H. SCCA as well as P. UFAP and H. PZP available in the Protein Sequence Database were aligned using the PC GENE software.

Interestingly, the sequence of a pregnancy-associated protein, S. UTMP was found to have an identity of 20.51% with that of carcinoma antigen, H. SCCA whereas, the sequences of H. PZP and H. SCCA were only 9.74% identical to each other. Five tripeptides (Leu–Asp–Ala, Leu–Val–Asn, Phe–Lys–Gly, Met–Met–Arg and Pro–Phe–Leu) were found

to be identical between S. UTMP and H. SCCA. The tripeptide sequence Pro–Phe–Leu happens to be a part of the SERPIN signature site of both, S. UTMP and H. SCCA. On the other hand, the sequence of P. UFAP, which is known to be similar to S. UTMP, was found to have only 9.35% identity with H. PZP even though both are pregnancy-associated proteins having SERPIN activity.

In the present study, the overall identity of sequences of pregnancy-associated proteins with SERPINs and of a pregnancy-associated protein with a carcinoma antigen were quite significant. An unrelated protein c-myb oncoprotein used as a control, when compared with the pregnancy-associated proteins, was found to have identities of only 3.96%, 4.32% and 5.30% with sheep uterine milk protein, pig uteroferrin-associated protein and human pregnancy zone protein, respectively. This relationship is not only statistically significant but also important biologically.

Similarities between pairs of protein sequences are potentially important because they may indicate some functional, structural or evolutionary relationship between the proteins. Biological significance of this kind does not necessarily imply a strong statistical significance.

A low statistical significance does not imply that a similarity is not biologically important; on the other hand, a similarity which is very improbable does imply that sequences are related, even if this relationship is not yet understood. The main value of assessment of the statistical significance of a similarity is therefore to provide additional evidence that a biological relationship exists[1].

The immunoglobulin superfamily includes certain receptor proteins like the PDGF receptor. The sequence resemblances in members of this family are very low, often amounting to as few as 10 or 12 residues per 100, but they are consistent enough across a large number of comparisons that the statistical likelihood is compelling.

In the case of G-protein (transducer)-linked receptor proteins, the per cent identity of the most distant pairs is well below 25, however, all these proteins appear to have seven segments rich in hydrophobic amino acids. In case of the most distant members of the group, the major evidence for divergence is not statistical, it is physiological[1].

The present findings support the hypothesis proposed above as well as the possibility of a common mechanism of evasion of host immune response in tumour and pregnancy since the immune-mediated lysis of target cells in both involves serine protease-based lytic systems.

1. Collins, J. F. and Coulson, A. F. W., *Methods Enzymol.*, 1990, **183**, 474–487.

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# A rapid and efficient method for isolation of RNA from bark tissues of *Hevea brasiliensis*

Efficient extraction of high quality RNA from a variety of plant tissues including bark is very important and is the first step in many molecular biology techniques, such as analysis of gene expression, cDNA library construction, *in vitro* translation, etc. Preparation of high quality RNA from tissues containing high levels of polyphenols such as bark of *Hevea brasiliensis* is difficult because of RNA degradation mediated by secondary plant products like phenolics, terpenoids and tannins which may bind to RNA after cell lysis. In the recent past, different protocols have been described for the isolation of RNA from various tissues[1-4] except bark tissues. When we tried to apply these methods for the isolation of RNA from *Hevea* bark tissues, they failed either due to degradation or very low yield of the RNA. RNA degradation may be due to the increase of RNAses and RNA degrading compounds (like polyphenols) in wounded slices[2,5]. The low yield of RNA might be due to the fact that after wounding, insoluble starch is converted into soluble polysaccharides which contaminate the RNA as they display very similar physicochemical properties[6].

*Hevea brasiliensis* is the commercial source of natural rubber, *cis*-1,4 polyisoprene, present in latex, the milky cytoplasm of specialized cells called laticifers located adjacent to phloem vessels. The latex is collected by the controlled wounding of the bark of the main trunk. Upon wounding, the cytoplasmic contents of these cells are expelled and sealing of wound sites occurs by coagulation of flowing latex. The extensive tapping of latex causes certain disorders in the bark characterized by browning and drying followed by cessation of latex flow, a physiological disorder called tapping panel dryness (TPD). There is an urgent need to study the molecular mechanism of wound healing, the stability of bark tissues during latex tapping, control of tapping panel dryness, etc. in the bark of *H. brasiliensis*. A pre-requisite for successful use of the molecular biology techniques to study the function of bark is a simple and reliable method for the isolation of RNA from bark tissues. There were a few reports on RNA isolation and cDNA library construction in *Hevea* in the past[7-10]. However, in all these reports RNAs were isolated either from latex or leaf. To our knowledge there are no reports on RNA isolation from bark tissues in general and *Hevea* in particular. We, therefore, attempted to develop a simple and efficient method for the isolation of large quantities of good quality and undegraded RNA from wounded *Hevea* bark tissues.

Initially, four protocols published earlier were tried for the isolation of RNA from *Hevea* bark tissues. First, the method of Palmiter[1] was tried followed by the methods of Logemann *et al.*[2], Verwoerd *et al.*[3] and Shirzadegan *et al.*[4]. None of these protocols could yield good