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Super-linear speed-up on Flosolver

Parallel computing is widely used to reduce the time required for large numerical computations. The popular view was that the maximum speed-up one can obtain on N processors is N . Speed-ups greater than N have, however, been reported for certain problems on modern parallel computers. Recently, for JNCASR's multigrid Navier–Stokes code, a speed-up of eleven was obtained using NAL's eight-processor Flosolver system (page 589). This result was a surprise, especially because



multigrid codes are considered difficult to scale due to global dependencies. Many believe that super-linear speed-ups are possible only when the problem size is sufficiently small, and all the data required for computing is available in the processor's cache memory itself. According to Venkatesh *et al.*, the NAL–JNCASR experience now indicates that the algorithm can also play a role in the speed-ups. It would therefore appear that a right combination of algorithm and architecture results in the best parallel efficiencies.

Cloning of defence-related genes

Plants respond to invasion by pathogens with an array of biochemical and genetic changes. Salicylic acid (SA) plays a key role in disease resistance. Dicto and Manjula (page 624), aimed at identifying and characterizing SA induction-specific defence-related genes from the resistant wild *Piper*, *P. colubrinum* using Suppression Subtractive Hybridization (SSH) strategy. Using this technique a subtracted cDNA

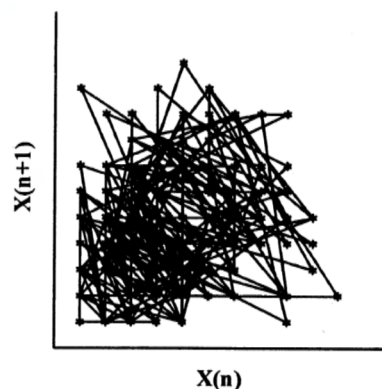


library was constructed with SA-treated leaf sample as tester and fresh untreated leaf sample as driver to identify genes specifically induced or over-expressed by SA treatment. Results indicate that in using SSH differentially expressed genes are enriched in the subtracted library. One of the subtracted clones showed sequence homology to osmotin (PR 5). Northern analysis confirms that SSH can be efficiently used to identify and clone defence-related genes in *P. colubrinum*.

Earthquake dynamics in major tectonic zones

The mega tectonic units of Himalayas, e.g. Northeast Himalayas (NEH), Central

Himalayas (CH) and Western Himalayas (WH) are considered to be some of the most seismically active regions of the world. The earthquake processes present very complex and mixed responses having stochastic and chaotic/deterministic behaviour. Characterization of the nature of dynamical behaviors is quite important for the purpose of modeling and hence for predictions. The modern nonlinear forecasting time series analyses are used to characterize these distinctive patterns. Tiwari and Sri Lakshmi (page 640) in the study of temporal evolution of seismicity (magnitude ≥ 4) of the CH, WH and NEH



for the period of 1960–2003 show that the earthquake processes in all three regions evolved on a high dimensional chaotic plane, however, with a contrasting predictive pattern. In particular, the predictive correlation analysis suggests that the earthquake dynamics in the NEH and WH are better ‘organized’ than in the central region. The significant distinction in the earthquake dynamical patterns seems to be associated with the underlying seismotectonics of these three regions. These results place significant constraints for developing criteria for testing the models of Himalayan earthquakes on a more rigorous and quantitative basis.