

infection during 2005–06. Similar results were reported with isolates from the other three South Indian states by sequencing the *E1* and *NS4* genes⁶. However, the earlier Indian Nagpur isolate of 1965 (sequences submitted in 2003) grouped with the Asian genotype CHIKV (Malaysian lineage). Determining the genotypes of viruses circulating in the different states of India and South East Asia and the conditions favouring such large-scale outbreaks are required to be constantly monitored to control the spread of CHIKV and in the long run to evolve optimum and adequate control strategies.

This study confirms that Chikungunya infection in Tamil Nadu is caused by the African genotype of CHIKV, similar to the ones in the other southern states of Andhra Pradesh, Karnataka and Maharashtra.

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Morphogenetic somatic sieve facilitates ‘genomic shock’ transmission across cell lineage in plants

The finding by Molinier *et al.*¹ that the capacity of stress-induced increased genomic flexibility is passed onto the successive generations, is a new observation in plant genetics. A parallel to such transgenerational memory could be seen in continual recovery of *in situ* somatic variants that occur in asexual progenies of stressed vegetative propagules². The latter suggests that transgenerational memory of genomic stress owe its genesis to the inbuilt mechanism of ‘morphogenetic somatic sieve’ in plants.

Incidence of rapid changes in plant genomes to environmental stress has attracted wide attention in recent years, adding to baffling new observations in plant genetics that continue to challenge the current concepts. Particular mention is made of two specific instances: one about heritable phenotypic and genetic alterations that are continuously produced in flax under changed environment³, and the other about the reversion of mutations in the *Arabidopsis* *HOTHEAD* gene at an extraordinary high frequency with genome-wide effects⁴. The critical analysis⁵ underpinned the significance of consistent reductions in ribosomal gene copy number and widespread insertion events

distributed throughout the genome under changed nutritional regimen to bring about sudden but consistent appearance of large element in the genome in flax, and occurrence of extragenomic inheritance in the form of RNA cache of correction templates in *Arabidopsis* respectively, as the possible mechanisms to facilitate rapid changes in plant genomes. However, in the latter this tendency of wild-type reversion of the *HOTHEAD* mutants has been attributed to their predominant out-crossing nature, since the *HOTHEAD* plants when grown in isolation exhibit completely stable genetic inheritance⁶. Also, an RNA cache of epigenetic information involving RNA-dependent RNA polymerase to direct paramutation has been experimentally demonstrated in maize to define stability of chromatin states associated with paramutation⁷.

Notwithstanding, the experimental demonstration that the plants could inherit even the capacity of stress-induced increased genomic flexibility across generations is quite intriguing¹. The study pinpoints that in order to cope with the abiotic and biotic stresses, not only do plants activate their own defences, but also manage to pass on a possible protective

strategy to their descendants^{1,8}. Axiomatically, the ability to increase the frequency of genetic mutation in response to stress has transgenerational memory. Subjecting the *Arabidopsis thaliana* plants to short-wavelength radiation (ultraviolet-C) or flagellin (an elicitor of plant defences), it has been shown that somatic, homologous recombination of a transgenic reporter is increased in the treated population and these increased levels of homologous recombination persist in the subsequent, untreated generations as well¹. How plants pass down this information is unknown, but Molinier *et al.*¹ opine that the mechanism is ‘epigenetic’. Further analysis of RNA directed changes in chromatin structure that cause paramutation lead to speculate that changes in chromatin structure could play a role in passing on the ‘memory’ of being expressed to environmental stress⁹. The demonstrated genomic change of enhanced homologous recombination is heritable at least to four generations, and could be transmitted through either of the parent regardless of its gender¹. Concluding their findings, Molinier *et al.*¹ propose that the environmental influences which lead to increased genomic dynamics even in successive,

untreated generations, may increase the potential of adaptive evolution.

With this experimental demonstration of transgenerational memory of stress in plants¹, there is a need to search for a probable phenomenon underlying such heritable 'genomic shock'-related epigenetic messages. New traits arising in meristematic tissue in plants could be subject of selection, because a sort of germ-line is created late in the plant development¹⁰. There are reasons to believe that the unique occurrence of continual organogenesis in plants¹¹ owes to the inherent potential for epigenetic transfer of acquired changes across the generations. In all probability, the genesis of transgenerational capacity of stress-induced, increased genomic flexibility lay in the unique developmental property of plants rather than to any unusual genetic phenomenon. Unlike animals, there are no germ lines in plants, but the latter are uniquely armed with inbuilt mechanism of continual somatic organogenesis. Plants display profound genomic plasticity as a sequel to abiotic and biotic stresses, and readily generate 'genomic shock'-mediated epigenetic and genotypic variations in their somatic tissues. The potential variation-prone cells from within the somatic tissues carrying the so-called epigenetic factor, could be differentially selected during continual somatic organogenesis and transmitted to the progeny. In the vegetative progenies the transmission of variation-prone cell is facilitated by morphogenetic selection through somatic cell lineages entering into differentiating shoots, and in seed progenies through its

selective passage to pre-meiotic L-II sub-epidermal layer. In both the situations the potential somatic selection of variation-prone cell for epigenetic/genomic variation is the determining factor for transgenerational of induced variation.

As such, it is the continual organogenesis and morphogenetic somatic sieve that offers plants the opportunity to unravel a range of variations that are generated *in situ* and accumulated during growth and development. Such accumulated build-up of potential hidden variation could be transgenerational even in seed progenies, and more so in vegetative progenies.

A practical corollary to the said findings¹ could be seen in asexual plants if the succession potential of stress-induced somatic changes were studied in segregating clonal progenies. Using a palaeopolyploid plant species, *Mentha arvensis* L. (family Lamiaceae), we have demonstrated that somatic mutations caused by genomic shock are selectively passed through the somatic sieve and potentially transmitted to subsequent vegetative generations through propagule-mediated clonal progenies². The vegetative propagules (i.e. suckers) of this species when administered genomic stress, accumulate/acquire genomic changes, but the same is not revealed in a growing plant, albeit differentially transmitted to its fast proliferating suckers and unravelled in subsequent sucker-mediated clonal progenies. This clearly suggests transgenerational capacity of stress-induced genomic changes in vegetatively propagating plants. Such 'genomic shock'-induced changes could serve as a valu-

able resource for realizing variation in plants where sexual recombination is lacking or deficient.

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On the estimation of evapotranspiration, water-use efficiency and crop coefficient of lucerne (*Medicago sativa* L.) in central India

Lucerne or alfalfa (*Medicago sativa* L.) is a major irrigated forage crop attaining high yields with high-forage quality potential. Its versatility in utilization, adaptations to a wide range of climate and soil conditions, soil improvement capability and symbiotic N₂ fixation make it preferable choice in intensive agricultural production system¹. In India, it is grown successfully even in the low rainfall areas with assured irrigation². The crop has relatively high-water demand and long production season and is exposed to periodic harvesting.

Efficient water management is key to success in augmenting crop production. Increasing the irrigation water-use efficiency necessitates improved irrigation scheduling techniques based on integrated effect of climate, soil and crop characteristics. Reliable estimate of evapotranspiration as a function of crop stage is important for determining crop water use and efficient irrigation management. Water stress in the plant can be quantified by actual evapotranspiration rate, as the level of evapotranspiration is related to the evaporative demand of the air³. Eva-

potranspiration loss and rate of evapotranspiration indicate the amount of water required at different growth periods for its satisfactory growth and optimum production. Crop coefficient represents crop specific water use and facilitates estimation of irrigation water requirements. Its significance for scheduling irrigation is shown earlier^{4,5}. Experimentally determined crop coefficient values for North Indian^{6–8} and Gujarat⁹ region have been reported for different crops. However, the information on these aspects in relation to lucerne crop for the Indian region is