the impact of plant integrative biology. In this regard the important question is what should be the relative criteria to select plant species for complete and/or partial genome sequencing?

The genome structural variations are reflected in sizes of individual chromosomes and the number of chromosomes in diploid genomes and additionally by levels of auto- or allo-ploidy in polyploid genomes. Complete genome sequences provide information about molecular processes responsible for diversity in genome structures. It will be necessary to obtain complete genome sequences of several to many diploid and auto- and allo-polyploid plant species varying in genome sizes, to comprehend the dynamics of plant genome structure evolution. Genomic analysis of polyploids is necessary to understand the impact of regional, as well as whole-chromosomal duplications. Among angiosperms, both monocotyledonous and dicotyledonous species need sampling. Species of gymnosperms, pteridophytes, bryophytes and eukaryotic algae must also be included. Their analyses will reveal the genome dynamics associated with gross changes in reproductive mechanisms and plant morphology. The cost estimates dictate that complete genome sequencing be limited to a rather small number of species. Sequencing of crop plant genomes of varying sizes is already in progress. The auto- and allo-polyploids may be chosen from among the relatives of plant species of heterologous genome sizes already sequenced or undergoing complete sequencing. It may also be possible to isolate inordinately long or short chromosomes from certain species on the basis of size-discriminative particle separation techniques. Sequencing of such chromosomes, in addition to complete sequencing of as many plant genomes as possible, will also be helpful in understanding the determinant features of chromosome size in plants. The sequencing of individual chromosomes will be cost-effective.

Sequencing of phylogenetically diverse plant species is desired to ultimately reveal variation in the structure, function and regulation of genes. Such information can largely be derived by the sequencing of euchromatic chromosomal regions of the genomes of chosen plant species. The plant species for genome sequencing should not only be selected on the basis of different phylogenetic lineages, but also some important additional criteria. These may include smallness of genome size, simple distribution of eu- and heterochromatic regions, sexual fertility and short seed-to-seed cycle, in each phylogenetic group. Among those that possess the above properties, the species that can vegetatively propagate may be preferred. To speed up and lower the cost of sequencing of coding regions, the selected species should be amenable to molecular marker linkage mapping and molecular-cum-cytogenetic karyotype analyses of eu- and heterochromatin regions. Partial sequencing will be meaningful and effective only if the boundaries of the euchromatic regions of chromosomes are molecularly marked in advance. The economically important species may be preferred in each phylogenetic group, provided they meet the various criteria listed above. Pyro-sequencing should help further reduce the cost of expanded comparative plant genomics enterprise.

Progress in plant genome biology is a pre-requisite for the breeding of new types of crop varieties that will meet the challenges of climate change, water scarcity, pollution, pathogen diversity and increased demands for food and feed, biofuels and industrial raw materials. Genome sequencing of phylogenetically diverse plant species selected by intelligent use of suitable features, some of them identified here, will help in the detection, marking, isolation and manipulation of agronomically and industrially important genes and their alleles to evolve crop varieties for future agriculture.

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Chikungunya outbreaks in Andhra Pradesh, South India

Chikungunya fever is caused by the chikungunya virus (CHIKV), which is spread to humans by mosquito bites. Chikungunya literally means bentover in the local Mekonde language. CHIKV is an *Alphavirus* belonging to the family Togaviridae[1]. It was isolated[2] for the first time from a Tanzanian outbreak in 1952. CHIKV is geographically distributed in Africa, India and Southeast Asia. In Africa, the virus is maintained through a sylvatic transmission cycle between wild primates and mosquitoes, such as *Aedes* species[3]. In Asia, CHIKV is transmitted to humans mainly by *Aedes aegypti* and to lesser extent by *Aedes albopictus* through an urban transmission cycle.

The most recent epidemic re-emergence was documented in 1999–2000 in Kinshasa, where an estimated 50,000 persons were infected[4]. The first Asian outbreak was recorded in 1958 in Bangkok, Thailand. Outbreaks were also reported in Cambodia, Vietnam, Laos, Myanmar, Malaysia, the Philippines and Indonesia[5]. CHIKV caused epidemics in India during 1824, 1871, 1901 and 1923. The most recent epidemic re-emergence was documented in 2001–03 in Java, and 2004 in an island of the Southwestern Indian Ocean. More recently an outbreak was reported in Madgascar[6].

CHIKV was first isolated[7] in Calcutta in 1963, and the last outbreak[8] occurred in India in 1971. Presently there is an outbreak of chikungunya in several states of India. At present Andhra Pradesh and some neighbouring states like Karnataka, Tamil Nadu and Chhattisgarh are reeling under the epidemic of chikungunya. Millions of people have been affected mainly with morbidity and sporadically with mortality.

Currently, we have two full genomic sequences of CHIKVs, the first isolated

from the Tanzania outbreak in 1952, and the second from an outbreak in 1983 in Senegal. CHIKV strains are mainly of three types – Asian strains, western African strains and African strains. In most of the viral strains one particular gene part, i.e. E1 was extensively studied for phylogenetic relationships and pathogenicity, mutation rate and geographical distribution. Current studies proved that the 1950 virus belongs to A-type CHIKV, which mutated as a new viral strain, i.e. V-type which is attributed to the Indian Ocean outbreak[9].

Non-structural proteins of Nagpur (India) chikungunya viral strain are not detected in other isolates, i.e. West African phylogroup, other genotypes identified in East/South Africa, Central Africa and Congo, India Ocean group. Structural proteins of S27 viral strain, E2, E1 (GenBank accession no. AY726732) of Nagpur strain are closely related to West African chikungunya phylogroup virus, ross river virus. The first outbreak in Tanzania (1952) was less pathogenic because the first viral strain does not extensively replicate in the vector host, due to the cells having less cholesterol. However, in the recent outbreak in the Indian Ocean and other parts of the world, the genetic sequence from A-type virus 226 E_1 gene position was changed to V-type virus, a new viral strain which no longer requires cholesterol for replication in mosquito and human cells[10]. Johnston and Peters[5] suggested that mutation in CHIKV led to the emergence of ONNV virus and its ability to be transmitted by encephelinemosquitoes.

These phylogenetic studies prove that the present Indian epidemic viral strain may be from the mutated Nagpur strain (or) has independently entered from other parts of the world through tourist visits, migratory birds and other unknown viral reservoirs or vertebrate hosts, like monkeys, bats, rats, etc. This mutated pathogenic virus strain is causing a major public heath problem. In Andhra Pradesh, according to government statistics 1 million chikungunya cases were recorded in various hospitals. Reports from few voluntary organizations suggest that more than 10 million chikungunya cases have been recorded so far[11].

In India, particularly in Andhra Pradesh, chikungunya diagnostic tests like HMAF (Hyper Immune Ascetic Fluid), focus Immuna assay, and nucleotide sequencing test are not available, and there is lack of rapid diagnostic facilities. Cases are diagnosed based on clinical symptoms. High mutation rate is also a contributing factor in making studies on molecular virological aspects of the virus difficult. Chikungunya viral deaths reported in the Indian Ocean outbreak[9], suggest that above 50 deaths were recorded in various places in Andhra Pradesh, particularly in the Telangana region[12], where most of the area is covered with forest.

Clinical symptoms include high fever with shivering, severe joint pain (joint of hand and feet can be swollen and painful), erythematous rashes on feet, hand, neck, headache, red eyes, photophobia and itchy skin lesions. Clinically, the symptoms of chikungunya are difficult to distinguish from those of dengue fever and so may be misdiagnosed.

Patients with chikungunya also have rare secondary bacterial disease like leptospirosis. Some of the chikungunya cases also have hepatitis, kidney problems, dengue and malaria. Most cases are reported from the slums. Also rainy season contributes to mosquito breeding population. The treatment is purely supportive and symptomatic, and includes paracetomol, and Dicyclofenic. In the absence of an efficient vaccine (or) antiviral therapy, vector control is at present the only way to limit chikungunya. Personal hygiene, fogging larvicidals, and distribution of insecticide-treated mosquito nets are the simplest and most cost-effective to control the epidemic.

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