Bigi and A. Sanda). The angle α is notoriously difficult to measure because of some problem called penguin pollution and we do not know how to disentangle the penguin contamination and therefore considered to be not clean from theoretical point of view (although efforts are on to directly determine the same). So we are left with the option to measure the KM angle γ and there are many methods proposed to measure the same in the last two decades.

Before proceeding further let us emphasize the significance of KM angle γ. In the so-called Wolfenstein parameterization (which is a suitable one adopted by the high energy physics community to analyse the b-systems) the weak phase γ is associated with the $b \to u$ transitions and is the only angle (phase) associated with tree decay processes. This weak phase is also responsible for direct CP violation in B systems. Comparing the standard and Wolfenstein parameterizations it can be seen that the all important phase δ_{KM} is indeed the weak KM phase γ (the argument of $\rho + i\eta$) of the Wolfenstein parameterization that describes the CP violation in the SM.

For the first time, the KM angle γ has been measured by BELLE (KEK, Japan) and BABAR (SLAC, USA) B-factory experiments[4] based on the article written by A. Giri, Y. Grossman, A. Soffer and J. Zupan (GGSZ)[5], which is in agreement with the SM expectation and vindicates the KM phenomenon. There are other two competing methods for the determination of the KM angle γ. These are the method by M. Gronau, D. London and D. Wyler (GLW)[6] and another one by D. Atwood, I. Dunietz and A. Soni (ADS)[7]. The details of the methods are highly

technical and beyond the scope of this article. But let us briefly outline why GGSZ method became successful ahead of other plausible ones. In GGSZ, we used the interference of two Cabibbo allowed decay amplitudes (against the common wisdom that the interference must be with Cabibbo allowed and doubly Cabibbo suppressed ones or among two singly Cabibbo suppressed amplitudes), where we considered the multibody final state common to both D^0 and $\bar{D}^0$. Also the final decay products are charged particles which are easy to detect from the experimental point of view and moreover the multi-body final states can proceed through resonances which can provide us the crucial strong phase information. All the methods mentioned above are being employed now and also will be taken up at the LHC B-experiment along with some other methods[8].

CP violation observed in 1964 in the kaon system and the measurement of large $\sin 2\beta$, which confirmed the large CP violation in B system, are examples of indirect CP violation. After strenuous effort finally direct CP violation in the K system was established almost a decade ago by various Kaon experiments and first direct CP violation in B system (namely, in $B \to K\pi$ process) was observed only recently, which ruled out the super-weak model of CP violation. The KM phase is now measured, unitarity triangle has been constructed (area of the unitarity triangle is also a measure of the CP violation) out of the various measurements available and they are according to the SM expectations. Measurement of large KM phase, the evidence of direct CP violation in the B system along with results from K system have now firmly

established the KM mechanism of CP violation in the SM. M. Kobayashi and T. Maskawa have been awarded the Nobel prize in Physics in 2008 for their work on CP violation.

Note added: The interested readers may refer to a similar article[9] which appeared in the previous issue of *Current Science*.

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Genome sequencing of cells that live inside glass cages reveals their past history

B. Karthick

One-quarter of the total primary production on earth is contributed by diatoms[1]. These are photosynthetic, unicellular algae with ornamented silica shells found in all aquatic and moist environments. They form the base of energy-efficient food webs that support all aquatic life forms. More than 250 genera of living diatoms,

with as many as 100,000 species are known[2]. Fossil diatoms are known as early as the Cretaceous, 144–65 m.y. ago[3]. In India, deposits of diatoms occur in Rajasthan and are known as 'multani mitti'. Multani mitti or Indian Fuller's earth or diatomaceous earth as it is called in the West, is applied as a paste on the

surface of the skin for 15–20 min and then washed-off. This leaves the skin feeling smooth, soft, moist and rejuvenated. Diatomaceous earth is now being used in the formulation of soaps, cleansing products, face powders and skin-care preparations. Diatomaceous earth is a mineral material consisting mainly of

siliceous fragments of various species of fossilized remains of diatoms.

Photosynthesis by marine diatoms generates as much as 40% of the 45–50 billion metric tonnes of organic carbon produced each year in the sea[4], and their role in global carbon cycling is predicted to be comparable to that of all the terrestrial rainforests combined[5,6]. Over geological time, diatoms influenced the global climate by changing the flux of atmospheric carbon dioxide into the oceans[7]. The above numbers illustrate the quantitative significance of diatoms in the functioning of the earth's ecosystem. The diatoms are well known to adjusting their photosynthetic reactions to allow maximal growth rates over a wide range of light intensities[8]. Fossil diatoms have been known as early as 144– 65 m.y. ago[3], but their evolutionary history may extend back as far as 550 m.y. The endosymbiotic relationship between a cyanobacterium and a phagotrophic eukaryote gave rise to the red algae; this process is known as primary endosymbiosis. In the secondary endosymbiosis, the eukaryote engulfed a red alga to spawn a new lineage known as the chromalveolates, from which diatoms evolved eventually. The process of endosymbiosis has been responsible for the most significant events in eukaryotic evolution. The most celebrated products of endosymbiosis are plastids and mitochondria. The biochemical and molecular data in the plastids indicate that a prokaryotic relative of modern-day cyanobacteria was engulfed and retained by a heterotrophic eukaryote[9], and transformed into the photosynthetic organelle seen in the plants and algae of today. In spite of the enormous evolutionary and ecological importance of the diatoms, only in the past few years have molecular biologists been attracted towards this field.

The most fascinating features of diatoms are their SiO_2 (silica)-based cell walls, with dimensions in micrometres. Diatom silica is non-crystalline; yet it exhibits highly regular features on a nano to micron scale, such as patterns of pores, ridges, or tubular structures and often unusual shapes. Diatom cell walls are constructed like a petri dish, with one half (epitheca) overlapping the other half (hypotheca) (Figure 1). Each theca is composed of a valve, which is synthesized during cell division, and several girdle bands that are synthesized during interphase. The girdle bands are added to the valve in a step-wise manner, thus enabling cell expansion. Electron microscopic studies have revealed that valves and girdle bands are formed inside the cell within specialized, membrane-bound compartments termed silica deposition vesicles (SDV). After completion of the morphogenesis process, the silica parts are deposited on the cell surface through SDV exocytosis (Figure 2)[2]. At present, all we know is that silicon transporters and proteins called silaffins act as nucleation points for silica deposition. Knowing the genome will help us to figure out how to mimic the processes that diatoms use to construct their precise structures, and then we can learn how to create similarly precise structures ourselves. The details of silicon metabolism can help nanotechnologists to harness diatom proteins for the manufacture of nanodevices and details on the mechanism of gene expression of the diatoms at different water-quality conditions can answer many ecological questions. This is the first time that a eukaryotic genome has been interpreted in the ecological and application context. Apart from the evolutionary answers, diatom genomes also prove useful in applications-oriented issues, such as this study, which will help us understand how they can make these extremely fine structures at ambient temperatures and pressures, something that humans
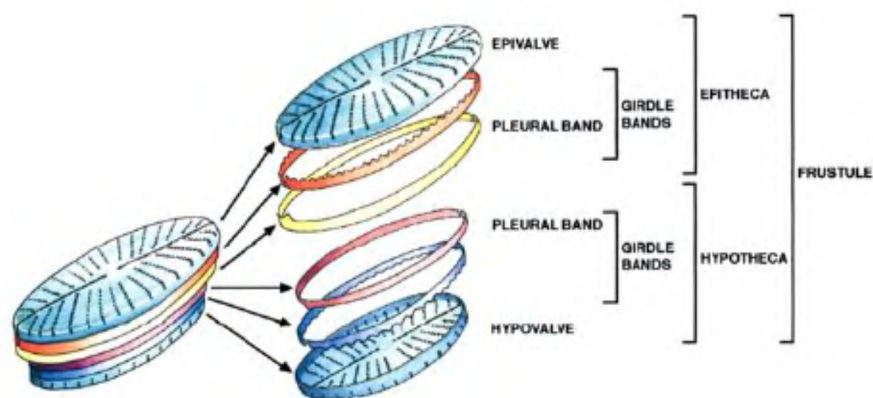
Figure 1. Schematic overview of siliceous components of diatom cell walls. (Drawing by Ian Nettleton[16] copyrighted by the American Society of Plant Biologists and reprinted with permission).
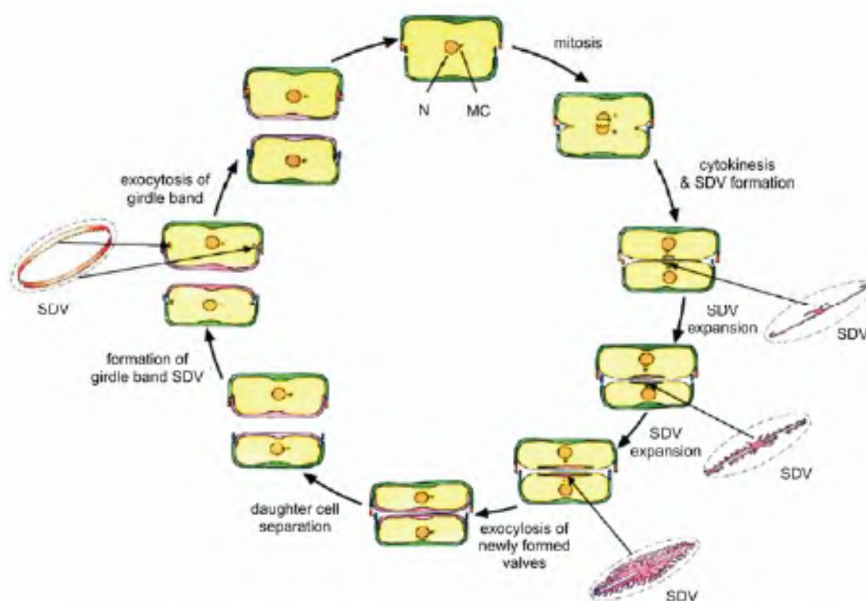
Figure 2. Schematic overview of mitotic cell division and hypovalve and girdle band formation. N, Nucleus; MC, Microtubule centre; SDV, Silica deposition vesicle. (Drawing by Ian Nettleton[16] copyrighted by the American Society of Plant Biologists and reprinted with permission).

are not able to do. This could open new nanotechnologies, like those for building miniature silicon chips or for biomedical applications and the proteins that diatoms use to direct silica deposition could be useful to the semiconductor industry.

Thalassiosira pseudonana was the first diatom to be sequenced[10] because it has a small genome, and it represents a cosmopolitan genus of diatoms and its physiology has been well studied. Recently, *Nature*[11] carried an article on genomic sequence of a pennate diatom, *Phaeodactylum tricornutum* by researchers across continents. This is the first pennate diatom and the second diatom to be sequenced. *P. tricornutum is* the 'lab rat' of the diatom world; it is an attractive model because of its apparently small genome[12,13] and short generation time[14,15]. The *P. tricornutum* genome is approximately 27.4 megabases (Mb) in size, which is slightly smaller than *T. pseudonana* (32.4 Mb). *P. tricornutum* shares 57% of its genes with *T. pseudonana*, of which 1328 are absent from other sequenced eukaryotes. This diatom contains the genes of the former endosymbiont, host cell and interestingly, hundreds of bacterial genes. Among the 587 identified sequences, 42% is found only in *P. tricornutum*, whereas 56% is present in both diatoms, confirming their ancient origin. Around 73 sequences are shared between *P. tricornutum* and *Phytophthora* sp. (oomycetes, i.e. water moulds), 59 of which are also present in *T. pseudonana*, suggesting that the vast majority of gene transfers occurred after the divergence of photosynthetic heterokonts and oomycetes. The sequenced diatom chloroplast genomes have fewer genes than red algal chloroplast genomes, indicating that a number of chloroplast genes were transferred to the nucleus after secondary endosymbiosis, and a few more genes appear to be in the process of transfer in one diatom species or the other. The mitochondrion of diatom might have originated in the host, and its mitochondrial gene complement is almost identical to that of haptophytes and cryptophytes, which are other algal phyla that may have originated from the same secondary endosymbiotic event.

The genome of diatoms reveals 171 genes as being of red-algal origin, among which 108 were shared between the two diatoms. In addition, 11 of these genes were also present in oomycetes, which confirms that red algae were the common ancestors of diatoms and oomycetes. The results of this study support that diatom plastid has its origin from the red algae and many gene transfers have occurred from the red algae nucleus to the host nucleus. Interestingly, a large number of *P. tricornutum* genes appears to have been transferred between diatoms and bacteria. In the phylogenetic tree, 587 *P. tricornutum* genes clustered with bacteria-only clades. This finding indicates that horizontal gene transfer between bacteria and diatoms is pervasive and is much higher than has been found in other sequenced eukaryotes. This is the first time that horizontal gene transfer from bacteria to other organisms has been observed in such a scale. Bacterial genes in diatoms do not appear to be derived from any one specific source but from a range of origins, including proteobacteria, cyanobacteria and archaea (Figure 3). Heterotrophic bacteria and cyanobacteria, especially diazotrophs and planctomycetes, have been found in various close associations with diatoms, which explains the exceptional levels of horizontal gene transfer events that appear to have occurred. Although the transfer of bacterial genes into eukaryotes is generally regarded as a rare event, it seems that gene transfer is common in diatoms.

This leads to an unusual mixture of genes in diatoms that play an important role in managing nutrients such as carbon and nitrogen, and detecting changes in the inhabiting environment. Many of the genes shared between diatoms and bacteria encode components that are likely to provide novel metabolic capacities like organic carbon and nitrogen utilization, enzymes, functioning of the diatom urea cycle and diatom cell-wall silicification. Moreover, the diatoms have inherited photosynthesis from plants, and production of urea from animals. It is speculated that the diatoms use urea to store nitrogen, not to eliminate it like animals do, because nitrogen is a precious nutrient in the ocean. Diatoms draw the best of both kingdoms; they can convert fat into sugar, as well as sugar into fat, which is extremely useful in times of nutrient shortage.

The comparison of these two diatom genomes with other eukaryotes reveals the presence of many species-specific multicopy gene families, as well as a large number of species-specific single-copy genes. The higher number of species-specific gene families appearing in *P. tricornutum* may suggest that the recent pennate diatoms possess more specialized functions, which may be related to the heterogeneity of the benthic environments that they commonly inhabit.
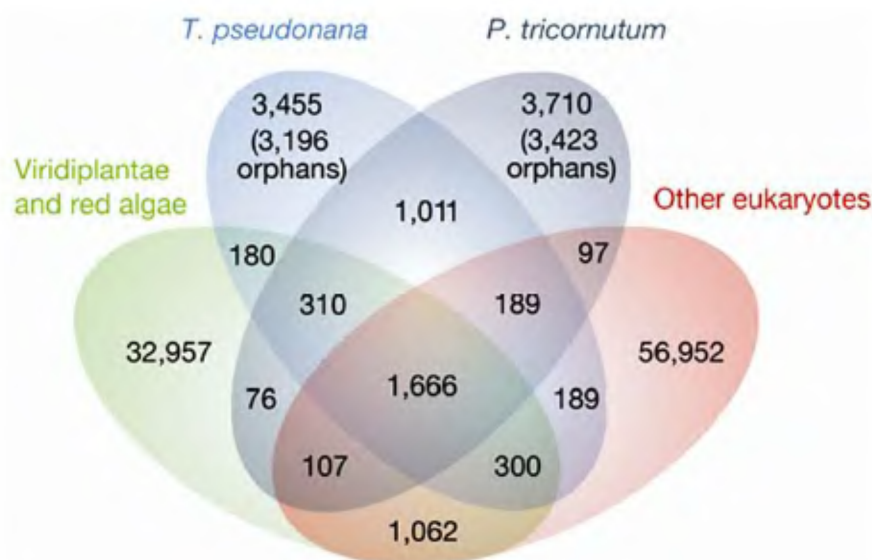

Figure 3. Venn diagram representation of shared/unique gene families in *Phaeodactylum tricornutum*, *Thalassiosira pseudonana*, Viridiplantae (plants and green algae) and red algae, and other eukaryotes (i.e. other chromalveolates and Opisthokonta (fungi and metazoa)). In addition to the total number of gene families specific to *P. tricornutum* and *T. pseudonana*, the number of families consisting of a single gene (denoted 'orphans') is also indicated. For example, among the 3710 gene families that are only found in *P. tricornutum*, 3423 consist of single-copy genes whereas 287 gene families have at least two members[11].

On the other hand, the centric diatom retained more features found in other eukaryotes such as the flagellar apparatus, which may be functional in planktonic life. The detection of a similar number of diatom-specific gene families and eukaryotic gene families not found in diatoms, reveals that the rates of gene gain and gene loss are similar and consistent with the high diversification rates observed in diatoms. It is also confirmed that diatom-specific genes are evolving faster than other genes in diatom genomes, providing a further explanation for the rapid diatom divergence rates. Moreover the presence of 10 and 42 diatom-specific cyclin genes in *P. tricornutum* and *T. pseudonana* respectively reflects the unusual characteristics of diatom life cycles due to the rigid silica cell walls, such as the control of cell-size reduction, activation of sexual reproduction at a critical size threshold, and life in rapidly changing and unpredictable environments.

This study suggests that genes acquired after secondary endosymbiosis by gene transfer from bacteria are pervasive in diatoms and represent at least 5% of their gene repertoires. Findings show that gene transfer between diatoms and other organisms has been extremely common, making diatoms 'transgenic by nature'.

The study also proposes that gene transfer from bacteria to diatoms, and perhaps vice versa, has been a common event in marine environments and has been a major driving force during diatom evolution. It has also brought together highly unorthodox combinations of genes permitting non-canonical management of carbon and nitrogen in primary metabolism and the sensing of external stimuli adapted to aquatic environments. The combination of mechanisms reported here may underlie the rapid diversification rates observed in diatoms and may explain why they have come to dominate contemporary marine ecosystems in a relatively short period of time.

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Perilous outcomes of arsenic

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The benign staple of rice may be a carrier of cancer risk, if latest research is to be believed. The wonder grain that feeds a large chunk of the Asian populace is said to contain ten-fold higher arsenic concentrations than wheat and other cereals[1]. It is speculated that rice sourced from arsenic-polluted groundwater exceeds an upper limit of 50 µg arsenic and may stretch to 400 µg per kg. Contaminated wells contain arsenic levels that are manifold compared to the permissible limits of 10 µg per litre set by the World Health Organization (WHO).

Arsenic is present in high concentrations in well water in many parts of the western United States, South America and Taiwan. Industrial use of arsenic along with its extensive use in plant sprays leading to its assimilation into feed of livestock and poultry are the reasons for the environmental dispersion of this compound. Environmental arsenic is also known to occur in some species of fish and shellfish. Inhalation of arsenic-polluted air, smoke as well as ingestion of contaminated food, air and water are also said to cause arsenic-related ailments[2]. The average daily human intake of arsenic[3] through food and water is pegged at 300 µg.

History of skin afflictions due to arsenic dates back to 1556. Investigations later have shown that ingestion of inorganic arsenic can cause skin cancer and inhalation of inorganic arsenic can cause lung cancer. Though both inorganic and organic arsenic occur in varying amounts in food, the inorganic counterpart is considered more dangerous than its organic form[4].

Recently, scientists have undone the contradiction of the carcinogenic poison being used as a treatment for acute promyelocytic leukaemia. Arsenic, by virtue of its glue-like property, attaches itself to SUMO – a type of molecule involved in leukaemia, which is later attacked by an enzyme called RNF4, in a process known to destroy the cancer-causing proteins. A treatment for blood cancer was success-