

Figure 2. The onset T_c of 10.3 K for Bi-25 wt% Ni sample.

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MID-HOLOCENE FOSSIL WOOD FROM COLVA, GOA

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AMONG the major littoral formations of Goa, beaches form a prominent and a spectacular feature. The

beaches found along the Goa coast are notably extensive, especially to the south of Bombay (19°N). Interpretation of the nature and evolution of the Goan beaches is difficult, because no residual form of the palaeo-features are visible on the surface. However, a recent discovery of a fossil wood at Colva ($15^\circ 16' 55''\text{N}$ and $73^\circ 56' 18''\text{E}$) is useful in this respect.

The fossil wood, (the first to be reported from this part) was found in a well excavation, about 550 m from the present high tide line. This was associated with a "black sandy horizon", about 6.5 m below the surface of a coastal dune (figure 1). The horizon con-

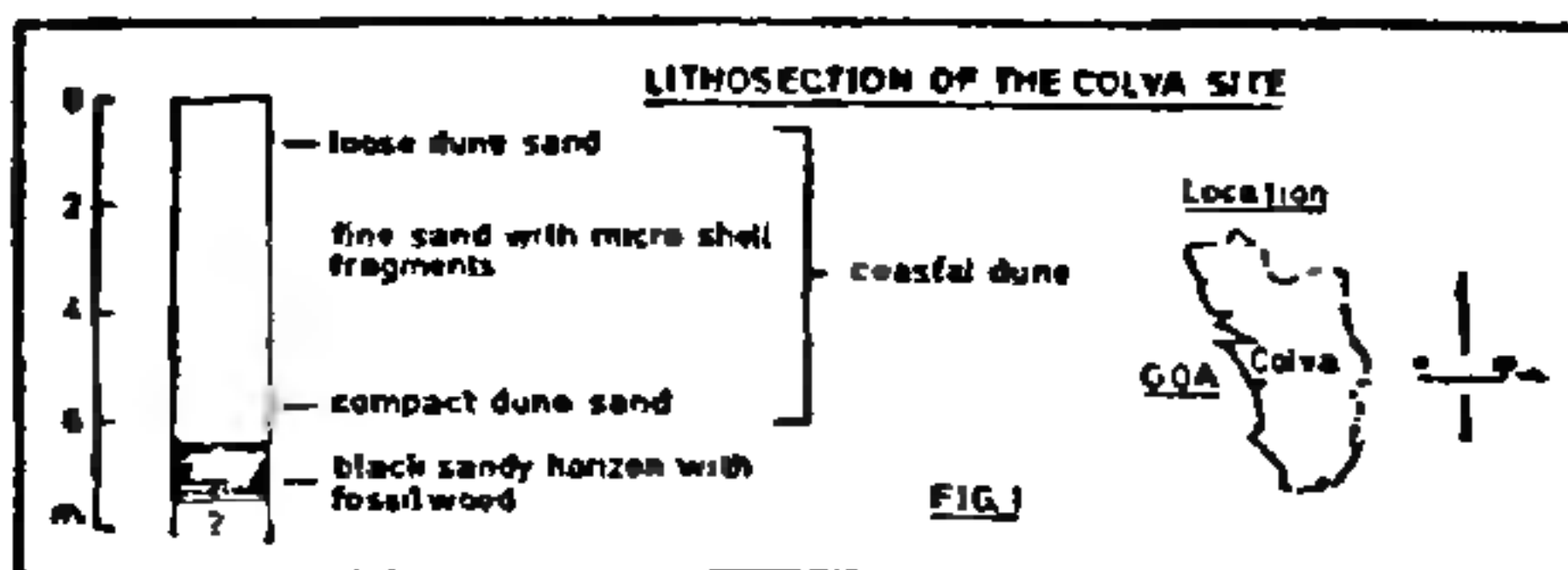


Figure 1. Location and the litho section of the Colva site.

stitutes, fossilized twigs in good proportion. The chemical analysis of the sample revealed that the pH was 2.9 and the conductivity was 4.2 millimhos/cm. The percentage of organic carbon was 0.336. Overlying this horizon is a layer of fine sand about 5 m in thickness. The fine sand also comprises microshell fragments. The dune sand is slightly hard, close to the fossil-wood-bearing horizon. Nevertheless, it loses its compactness at the top.

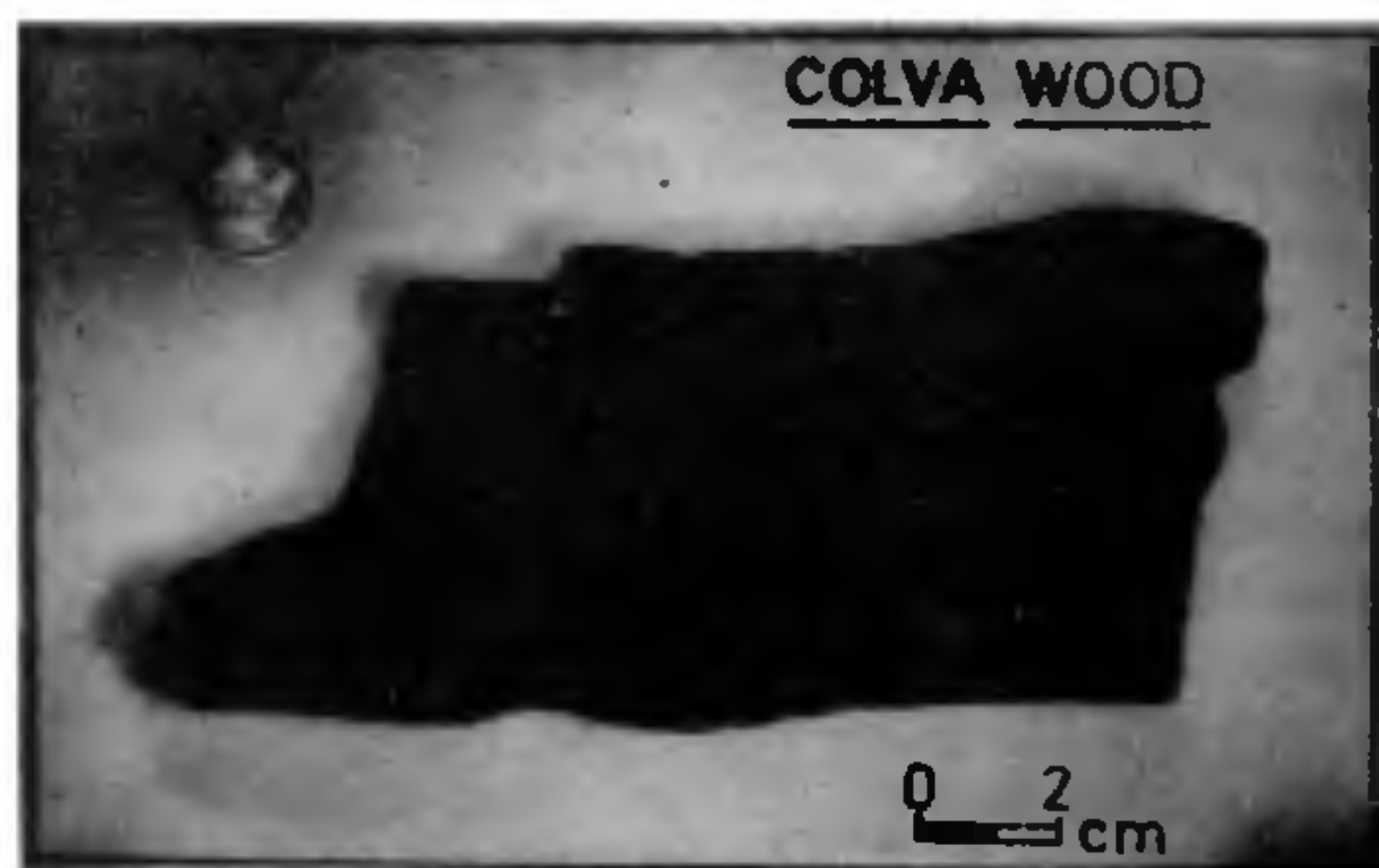


Figure 2. The Colva fossil wood

The fossil wood was dated by the radiocarbon method as 6430 ± 110 years B.P. (BS-343). The location of the fossil wood in the lithosection demonstrates that the horizon lies about 1.5 to 2.5 m below the present sea level. Thus, the stratigraphic location of the Colva wood and the radiocarbon date of the wood suggest that during mid-Holocene the sea level was lower than the present.

The geographical features like beach morphology of Colva, the absence of beach cusps and the absence of extensive beach rocks¹ indicate that the site of the fossil wood, was not occupying a palaeo-tidal channel. This leads to the inference that the Colva beach is prograding at a rapid rate.

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GENOME SIZE OF SLOW GROWING SPECIES OF RHIZOBIUM

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KNOWLEDGE of bacterial genome size which is the total molecular weight of haploid unreplicated bacterial genome DNA is known to be useful to assess the average number of genes and the phenotypic potential of an organism as well as the evolutionary relationships¹. This knowledge also has taxonomic implications and the values are indispensable to calculate possible DNA sequence between organisms². Britten and Kohne³ established an apparent proportionality between the genome size and its $C_{0t_{1/2}}$ corresponding to the C_{0t} (moles nucleotides/lit \times sec) at which a given DNA sample attains 50% renaturation. Bacterial genome size can thus be measured from the $C_{0t_{1/2}}$ of its DNA by comparing it to that of a standard bacteria whose genome size is precisely known. This method has been successfully used for many organisms⁴⁻⁸. *Escherichia coli* B has a genome of about 1100 μ in length⁹ and its genome size has been estimated to be 2.2×10^9 daltons¹⁰. As such *E. coli* B DNA can serve as a primary molecular weight standard in DNA renaturation studies. In our endeavour, as a prelude to the studies of evolutionary relationships of rhizobia, the genome sizes of three slow-growing species of *Rhizobium*, e.g. *R. lupini* 3001, *R. sp.* Cowpea U₈ and *R. japonicum* CC409 were measured.

E. coli was grown in nutrient broth and rhizobia were propagated in Ashby's Mannitol Medium at 28°C and harvested during the stationary phase of growth. DNA was extracted and purified by a modification of Marmur's method¹¹. The final DNA preparation had an $A_{260\text{nm}}/A_{230\text{nm}}$ value of about 2 and

$A_{260\text{nm}}/A_{230\text{nm}}$ value of more than 2. The preparation had an RNA contamination of less than 4% as estimated by solubility in cold normal perchloric acid¹². DNA was sheared by partial depurination and alkali cleavage¹³ and hybridizations were performed at 60°C in 0.12 M phosphate buffer, pH 6.8 (0.18 M Na⁺). For the reassociation kinetics, fractionation of reassociated DNA was carried out by chromatography on columns of hydroxyapatite as described earlier¹⁴⁻¹⁷ at the desired C_{0t} values. The C_{0t} values were conveniently calculated by use of the formulae—optical density at 260 nm \times time of incubation in hr/2. The concentration of single-stranded and reassociated DNA was determined from the eluates by their absorbance at 260 nm and the percent of reassociation was calculated.

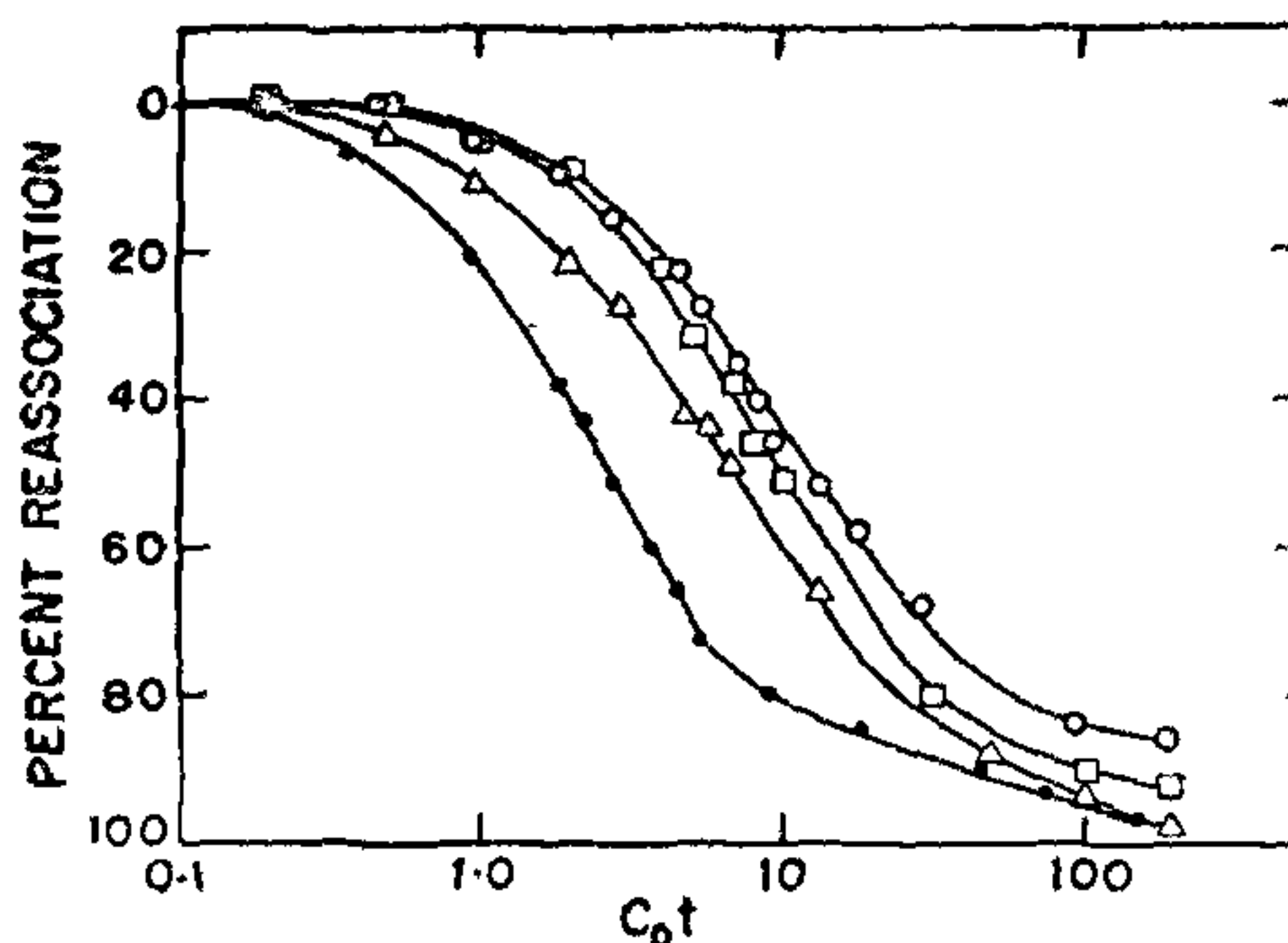


Figure 1. The kinetics of reassociation of the DNAs of *Rhizobium* species and of *E. coli*. The samples were sheared by partial depurination and alkaline cleavage, made to 0.12 M phosphate buffer, pH 6.8, denatured by heat and incubated at 60°C. Kinetic points were then taken. Each point was analysed by fractionation on hydroxyapatite. *E. coli* B, (closed circle) *R. lupini* 3001, (open triangle) *R. sp.* Cowpea U₈, (open square) *R. japonicum* CC 409, (open circle).

Figure 1 presents the reassociation kinetic profiles of DNAs obtained from the three species of rhizobia. The kinetics followed a second order pattern and all the DNAs hybridized to the extent of about 90% at a C_{0t} of 100. No significant hybridizations were observed below a C_{0t} of 0.1. From the figure it is apparent that DNAs from *E. coli* and the three species of rhizobia attained 50% of maximum hybridization at a C_{0t} of 2.8, 6.9, 8.8 and 9.7 respectively. This suggests that the genomes of *R. lupini* 3001, Cowpea U₈ and *R. japonicum* CC 409 are respectively almost 2.46, 3.14 and 3.46 times greater than that of *E. coli* B and, therefore, renatured as many times slower. The molecular weight of *E. coli* B DNA is 2.2×10^9 daltons