

al fluvial depositional systems.⁷

Second, as stated by Seeiand above, the depositional environment has been deduced to be fluvial, based on sandstone crossbeds and the grain-size and grain-shape distribution.⁸ Not only that, the thick coal beds are located parallel to and adjacent to the main 'palaeoriver' draining the basin. How flooding of debris into the peat beds is to be avoided is admittedly a problem.

Third, gradual subsidence of the peat beds must be at just the right rate for growth on the surface to continue unabated. The rate of subsidence must also be balanced by the build up of sediments in the adjacent river channels. Accumulation of peat layers hundreds of metres thick, subsiding gradually, in a fluvial environment for hundreds of thousands of years without collecting flood debris from a meandering river is an amazing coincidence.

Fourth, the purity of the coal eliminates practically all the many proposed theories, such as a low-lying swamp, transported vegetation into place, and a basin-wide lacustrine environment.⁹

Fifth, the most viable theory, the raised swamp environment, suffers

from too many special conditions. A raised swamp, which supposedly protects the peat from flooding, must be watered either through ground water seeping upward by capillary action, which is limited, or by rain water. If you have too much rain, there is flooding, either from the adjacent river or from flows from off the surrounding mountains. Special conditions already mentioned above would also apply. High biomass production with low rates of decay are also required. Based on pollen analysis, swamp cypress was a prime constituent of the vegetation. This tree generally grows in low-lying flooded swamps and not in raised mires.

Despite the divide and conquer proposal, it still seems that the 'law' of Uniformitarianism is violated by thick coal seams in the Powder River Basin. A Flood catastrophic mechanism, although difficult to explain in detail, is more likely. The Flood at least could have provided the ripped-up vegetation, much of which would have floated for a while during the Flood. In the right circumstances, it could have deposited the vegetation rapidly and then covered the plant material with thick sediments that would have aided in rapid coal formation.

REFERENCES

1. Seeiand, D., 1993. Origin of thick Lower Tertiary coal beds in the Powder River Basin, Wyoming and Montana — some paleogeographic constraints. **U.S. Geological Survey Bulletin 1917-Q**, U.S. Geological Survey, U.S. Government Printing Office, Washington D.C.
2. Anonymous, 1995. Mineral resource and reserve base estimates for Wyoming. **Wyoming Geo-notes**, No. 47, Wyoming State Geological Survey, Laramie, Wyoming, p. 46.
3. Moore, T. A. and Shearer, J. C., 1993. Processes and possible analogues in the formation of Wyoming's coal deposits. **In: Geology of Wyoming**, A. W. Snoke, J. R. Steidtmann and S. M. Roberts (eds), Geological Survey of Wyoming Memoir No. 5, pp. 874-896.
4. Seeiand, Ref. 1, p. 2.
5. Shearer, J. C., Staub, J. R. and Moore, T. A., 1994. The conundrum of coal bed thickness: a theory for stacked mire sequences. **Journal of Geology**, 102(5):611-617 (p. 611).
6. Moore and Shearer, Ref. 3, p. 892.
7. Seeiand, Ref. 1, p. 2.
8. Seeiand, D., 1992. Depositional system of a synorogenic continental deposit — the Upper Paleocene and Lower Eocene Wasatch Formation of the Powder River Basin, northeast Wyoming. **U.S. Geological Survey Bulletin 1917-H**, U.S. Geological Survey, U.S. Government Printing Office, Washington D.C.
9. Seeiand, Ref. 1.

M.J. O.

'Simple'? Whole Bacterial Genome Sequenced

A team of 40 scientists in the United States recently achieved a landmark with the sequencing of the whole of the genome of the bacterium *Haemophilus influenzae* Rd.¹ This is the first free-living bacterium to be fully sequenced. The team also proved the usefulness of the technique of random sequencing for sequencing bacterial genomes in particular and possibly eukaryotes as well.

Haemophilus influenzae was chosen for sequencing because no physical gene map existed and, with a genome size of about 1.8 million bases, it was considered 'typical among bacteria'.

The project involved an enormous amount of work and considerable computer analysis of the data generated by each of the laboratories involved. The DNA was physically chopped into random pieces, and pieces of a maximum of between 1,600 and 2,000 bases in length were selected for sequencing. Sufficient segments were sequenced to get the equivalent of six full genomes. The sequences were entered into a database and computer programmes used to match up the random segment sequences to derive the sequences for larger segments ('contigs') of the full genome. One part of this data analysis used 30 hours on a



SPARCenter 200 computer with 512 MB RAM. Statistical studies suggest that such a procedure is likely to result in a low level of gaps in the final sequence. These gaps were then filled by other techniques to complete the final sequence. The authors estimated their final error rate as between 1 base in 5,000 and 1 base in 10,000.

The resulting genome has 1,830,137 base pairs coding for an estimated 1,743 coding regions ('genes'). The sequence was compared with the sequences in a published database of gene sequences called GeneBank 87. From this, 1,007, or 58 per cent, of the coding regions were tentatively assigned a role, but 736, or 42 per cent, could not be assigned a role. In other words, there is an

enormous amount of work yet to be done to confirm and elucidate the functions of each of the coding regions identified.

The putatively identified coding regions were categorised as to their functions into 102 biological roles, and further into 14 broader role categories. It is interesting to see that some 87 genes code for proteins/enzymes involved in DNA replication alone. There are many more involved in transcription and translation, not to mention biosynthesis, energy metabolism, transport, etc. How many of the 1,743 genes are essential for life?

It is clearly becoming more and more untenable to believe that any sort of self-reproducing cell could ever have been 'simple' so as to allow for its

naturalistic origin. Anyone who believes in 'simple' bacteria should look at the genome map for *Haemophilus influenzae* — it should cure them for good. Furthermore, if a prokaryote such as a typical bacterium were to be transformed into a human over some billions of years, one has to add the information for about a further 100,000 genes — an impossible task for mutations to achieve.

REFERENCES

1. Fleischmann, R. D., Adams, M. D., 1995. Whole-genome sequencing and assembly of *Haemophilus influenzae* Rd. *Science*, 269:496-512.

D.B.

What do Ocean Bottom Pits Tell Us?

Soon after the development of side-scan sonar in oceanographic research, V-shaped pits on the bottom of the ocean were discovered on the continental shelf off Nova Scotia.¹ These pits, called pockmarks, were soon found to be relatively common on the ocean bottom where detailed surveys have been made.² A density as high as 240 per km² has been

reported,³ making the ocean bottom appear heavily cratered like the moon. Pockmarks average 50 to 100 m in diameter and 2 to 3 m in depth.⁴ However, they range in size from quite small to as large as 700 m long in one oval-shaped pockmark.⁵ In Belfast Bay, Maine, pockmarks as deep as 35 m have been noted (see Figure 1).⁶

Pockmarks occur at shallow to

moderate ocean depths and are more frequently found in muddy sediments. One of the latest discoveries was made from 2,167 metres depth on the continental rise off the Carolinas, USA.⁷ The origin of pockmarks appears to be fluid and gas escape from the sediments.

There are many marine, sedimentary rocks on the continents that are supposed to have formed slowly over long periods of time, often at shallow depths. If this were true, pockmarks should be common in these sedimentary rocks, and due to their size and abundance in some areas today, they could hardly be missed. However, pockmarks **are not found in any pre-Pleistocene marine sedimentary rock**. Eyles states:

*'The style of sediment deformation below surface pockmarks is not known and such structures await identification in pre-Pleistocene glaciogenic marine sediments.'*⁸

Hovland and Judd corroborate and suggest that pockmarks should be common in the geological column back to the Precambrian:

'It is unfortunate that pockmarks have not as yet been discovered

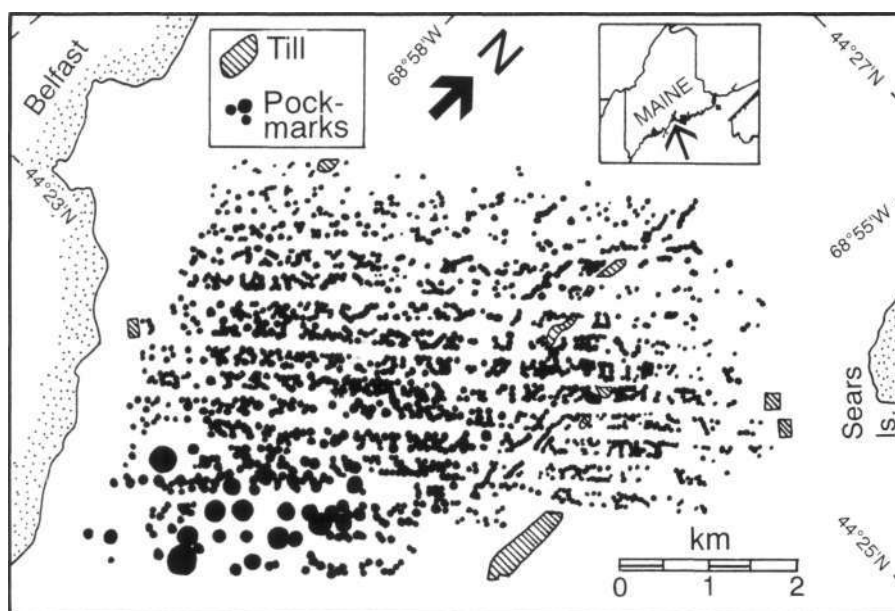


Figure 1. Map of the sea-floor pockmarks in Belfast Bay, Maine.