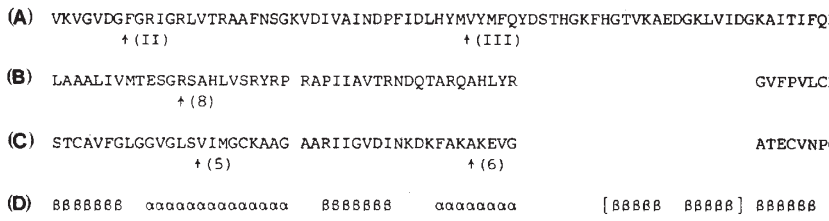

Intron arrangement in the mononucleotide binding-site region of pig glyceraldehyde 3-phosphate dehydogenase (A), chicken pyruvate kinase (B) and horse alcohol dehydrogenase (C), together with the consensus secondary structure (D) in terms of α-helices β-pleated sheets. Amino acids are designated by the one letter code; the positions of introns in the corresponding genes are shown by arrows and numbered according to the authors.

On page 498 of this issue, Schwartz and co-workers suggest that both kinds of intron are recognizable in the glyceraldehyde 3-phosphate dehydrogenase gene of the chicken. They classify the introns as type A, which result from the original assembly of the gene from smaller units, and type B, which have never had any function. Moreover, they believe that type A introns can be further classified according to whether they derive from the creation of a domain from smaller units (A1), from the duplication of a complete domain (A2), or from the joining of two dissimilar domains (A3). Classification of the three introns that occur at or near the boundaries of the four recognized structural domains of the enzyme is straightforward: one is type A2, two are type A3. In addition, the catalytic domain contains a region that makes about 85 per cent of its hydrogen bonds within itself and which also corresponds to an exon — the part of the gene that is translated into protein. Thus, the two introns that flank this exon can be regarded as resulting from the joining of protein domains and so of type A3.

Apart from one intron in the non-coding region of the mRNA, all of the remaining six introns occur within domains and are more difficult to classify, because both A1 and B type introns would be expected in similar positions. Nonetheless, Schwartz and co-workers believe that sub-domains can be recognized within the domains, and that several of the remaining introns can be interpreted as separating them, so that they are of type A1. Only one intron in the coding region is assigned to type B.

This type of classification can be tested by examining the genes of comparable proteins. Types A2 and A3 introns should occur in other genes at domain boundaries; type A1 introns should occur at homologous positions within homologous domains; but type B introns should occur at arbitrary and unrelated positions. It is of interest, therefore, to examine the hypothesis of Schwartz and co-workers in relation to new work by Lonberg & Gilbert (*Cell* **40**, 81; 1985). These workers have determined the structure of the gene for chicken pyruvate kinase and compared it with that of the gene for maize alcohol dehydrogenase (Dennis E.S.*et al.*, *Nucleic Acids Res.* **12**, 3983; 1984). All three proteins contain a mononucleotide binding domain with alternating regions of β-pleated sheet and α-helix, though this domain in glyceraldehyde 3-phosphate dehydrogenase is considerably longer because it contains an extra piece of β-sheet (which does not interfere with the structure of the rest of the domain). The comparison shown in the figure, with arrows indicating the location of introns, is disappointing: intron II of the glyceraldehyde 3-phosphate dehydrogenase gene, classified as type A1 by Schwartz and co-workers, occurs at the boundary between β and α regions, but there is no intron at this boundary in either of the other two genes; intron III, on the other hand, suggested to be of type B, corresponds almost exactly to an intron of the alcohol dehydrogenase gene.

Examining the pyruvate kinase gene as a whole, it is clear that introns are not placed at random in the sequence, and at least two systematic characteristics are evident. The ten exons are of a much more uniform length than one would expect if the coding region were interrupted at random, and the introns tend to fall between discrete regions of secondary structure in the protein. Surprisingly, there is little tendency for introns to occur at domain boundaries: most noticeably, the boundary between domains B and A_2 occurs near the middle of exon 5, the longest exon in the gene. It would be appealing, though entirely speculative, to suggest that an intron at this boundary has been lost, because if it were present it would not only separate the two domains but would also make the exon size even more uniform.

Although there is now much to suggest that introns are an ancient relic of primordial genes, convincing proof must await the discovery of clearly corresponding intron arrangements in genes for that arose by duplication before the separation of prokaryotes and eukaryotes. □

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100 years ago

THE LIFE HISTORY OF THE LYCOPODIACEAE

THE area within which really notable discoveries are possible — at any rate amongst the higher plants — in the field of vegetable morphology is becoming very circumscribed. For some time the complete life-history of the *Lycopodiaceae* has been a missing chapter in our text-books. A paper which will mark its epoch in the history of Lycopodium is that for a separate copy of which I am indebted to my friend, Dr. Treub, the accomplished director of the Botanic Garden at Buitenzorg in Java. On his arrival at Buitenzorg, he lost no time in endeavouring to find the prothallia of tropical species. He seems to have all but succeeded in discovering those of *Lycopodium cernuum* in the first year of his residence there. Subsequently, he sowed the spores on the trunks of trees, and after a delay which led him to abandon any hope of success, he obtained satisfactory results from one of the sowings.

In the present paper, Dr. Treub gives an exhaustive account of the prothallium of *Lycopodium cernuum*. It is curious to observe, however, that in artificial cultures he did not succeed in carrying the development further than DeBary had done some time ago with *L. inundatum*. Fortunately, prothallia which he discovered under spontaneous conditions of development exactly fitted in where the others stopped. W. T. THISELTON DYER

From *Nature* **31**, 5 February 1885.

Palaeontology

Back to the trees for *Archaeopteryx* in Bavaria

from Michael E. Howgate

NOBODY expected the latest *Archaeopteryx* conference* to answer all the problems thrown up by this unique intermediate fossil. Indeed some of the more sceptical participants doubted if any of the problems would be nearer resolution after the event. However, a consensus of sorts emerged; several theories met their Waterloo; agreement was reached on some outstanding problems; and other contentious areas were set for resolution in the forseeable future.

To help the proceedings, three of the six specimens of *Archaeopteryx* were present: the counterpart of the isolated feather imprint; the incomplete Tyler specimen; and the perfectly preserved (apart from the feather impressions) Eichstätt specimen accompanied by a specimen of the small dinosaur *Compsognathus* from the same Upper Jurassic formation. The Berlin specimen of *Archaeopteryx* was unable to attend, as it is on loan to Japan; the British Museum (Natural History) specimen was in too fragile a condition to travel, but an excellent video and slides were sent instead;

* 'The International *Archaeopteryx* Conference', Eichstätt, FRG, 11-15 September 1984. The conference proceedings will be available through Dr. G. Viohl, Jura Museum, Willibaldsburg, 8078 Eichstätt, FRG.