RIBOSOMAL DNA: MOLECULAR EVOLUTION AND PHYLOGENETIC INFERENCE

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ABSTRACT

Ribosomal DNA (rDNA) sequences have been aligned and compared in a number of living organisms, and this approach has provided a wealth of information about phylogenetic relationships. Studies of rDNA sequences have been used to infer phylogenetic history across a very broad spectrum, from studies among the basal lineages of life to relationships among closely related species and populations. The reasons for the systematic versatility of rDNA include the numerous rates of evolution among different regions of rDNA (both among and within genes), the presence of many copies of most rDNA sequences per genome, and the pattern of concerted evolution that occurs among repeated copies. These features facilitate the analysis of rDNA by direct RNA sequencing, DNA sequencing (either by cloning or amplification), and restriction enzyme methodologies. Constraints imposed by secondary structure of rRNA and concerted evolution need to be considered in phylogenetic analyses, but these constraints do not appear to impede seriously the usefulness of rDNA.

An analysis of aligned sequences of the four nuclear and two mitochondrial rRNA genes identified regions of these genes that are likely to be useful to address phylogenetic problems over a wide range of levels of divergence. In general, the small subunit nuclear sequences appear to be best for elucidating Precambrian divergences, the large subunit nuclear sequences for Paleozoic and Mesozoic divergences, and the organellar sequences of both subunits for Cenozoic divergences. Primer sequences were designed for use in amplifying the entire nuclear rDNA array in 15 sections by use of the polymerase chain reaction; these "universal" primers complement previously described primers for the mitochondrial rRNA genes. Pairs of primers can be selected in conjunction with the analysis of divergence of the rRNA genes to address systematic problems throughout the hierarchy of life.

INTRODUCTION

DURING THE PAST three decades, the field of systematic biology has undergone several simultaneous revolutions. The three most significant changes have been in the development and refinement of systematic theory, the technical refinement of data analysis brought on by the development of computers, and the introduction of molecular analysis. Although molecular biology is not a panacea for systematics, molecular systematists can approach many problems previously considered intractable by morphologists (Hillis, 1987; Patterson, 1987). For instance, there are very few homologous morphological characters that can be compared among all living organisms. In contrast, a number of genes with fundamental biochemical functions are found in all species and they can be sequenced, aligned, and analysed to study phylogenetic relationships at the deepest part of the tree of life. Other genes can be used to study relationships among morphologically indistinguishable but otherwise distinct species (Hillis and Moritz, 1990). This

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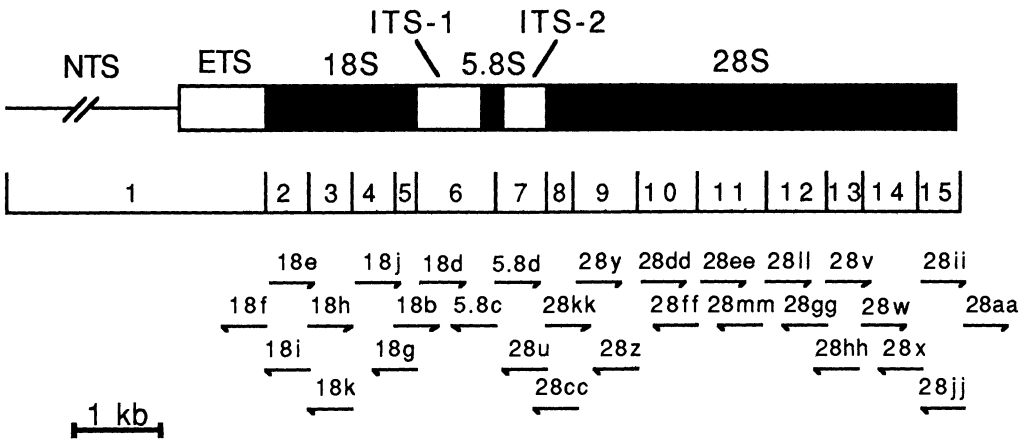

FIG. 1. THE rDNA ARRAY OF A EUKARYOTE.
The entire array can be amplified in sections (1-15) through the use of the primers indicated by arrows in polymerase chain reactions (primers are shown in Fig. 2).

entire range of applications, from the origin of life to relatively recent evolutionary events, has been addressed by studying the ribosomal RNA (rRNA) genes and their associated spacer regions, collectively called ribosomal DNA (Appels and Honeycutt, 1986; Mindell and Honeycutt, 1990).

This review is concerned with the inference of phylogenetic relationships from interspecific comparison of rDNA sequences. Some properties of rDNA are so sufficiently distinct from other molecular sequences that a number of special considerations are necessary or desirable when considering the use of rDNA in systematic studies. In addition, we will review the range of systematic problems to which studies of rDNA have been applied. The processes of rDNA evolution have been reviewed elsewhere (Gerbi, 1985, 1986), so these processes will be considered here only as they relate to phylogenetic inference.

Several distinct rRNAs combine with ribosomal proteins to form ribosomes, the organelles that direct protein synthesis from messenger RNA. Ribosomes are composed of two major subunits, each with distinct rRNAs and ribosomal proteins. The small ribosomal subunit contains a single type of rRNA and about 20 proteins in prokaryotes or 30 proteins in eukaryotes. The large ribosomal subunit contains two (prokaryotes) or three (eukaryotes) rRNAs and about 30 (prokaryotes) to 40 (eukaryotes) ribosomal proteins. A single copy of each of the proteins is present per ribosome. Because protein synthesis is a prerequisite for life as we know it, ribosomes (and hence rRNAs) are universally present in living systems.

The rDNA array of a eukaryote nuclear genome typically consists of several hundred tandemly repeated copies of the transcription unit and nontranscribed spacer shown in Figure 1 (see Long and Dawid, 1980, for a review). The number of copies of this transcription unit, however, may be as few as one (as in *Tetrahymena*, Yao and Gall, 1977), or as many as several thousand (e.g., see Appels et al., 1980). In prokaryotes there are one to several copies of the rRNA genes, and the genes may be organized in a single operon (in which they are usually separated by tRNA genes), or they may be dispersed throughout the genome (Hofman et al., 1979; Brosius et al., 1981; Morgan, 1982). There are usually three or four distinct nonorganellar rRNAs in a species (Long and Dawid, 1980; Gerbi, 1986). These rRNAs are often characterized in sedimentation velocity units (S, for Svedburg) (1) a large subunit rRNA, which ranges in size from 16S [≈1500 nucleotides (nt)] in vertebrate mitochondria to 23S (≈2900 nt) in most prokaryote genomes, and up to 28S (over 4000 nt) in eukaryote nuclear genomes (see Gutell and Fox, 1988, and Gutell et al.,

1990, for compilations of known sequences); (2) a 5.8S rRNA (≈160 nt) in eukaryotes, which is derived from a part of the 23S rRNA of prokaryotes (Cox and Kelly, 1981; Jacq, 1981; Walker, 1981; Clark and Gerbi, 1982) and is still structurally and functionally closely related to the large rRNA; (3) a small subunit rRNA, which ranges from 12S (≈900 nt) in vertebrate mitochondria to 16S (≈1500 nt) in prokaryotes and up to 18S (≈1800 nt) in eukaryotes (see Huysmans and DeWachter, 1987; Dams et al., 1988; Neefs et al., 1990); and (4) a 5S rRNA (≈120 nt), the gene of which is closely associated with the other rRNA genes in many prokaryotes but is found elsewhere in the nuclear genome of most eukaryotes (see Wolters and Erdmann, 1989). Although these are the most common themes, numerous variations have been discovered (e.g., Bobrova et al., 1987; Spencer et al., 1987). The large and small subunit rRNA genes of chloroplasts and mitochondria are more like those of their prokaryote ancestors than those of their eukaryote hosts (Schwarz and Kössel, 1980; Küntzel and Köchel, 1981; Grant and Lambowitz, 1982; Spencer et al., 1984; Palmer, 1985a,b; Evrard et al., 1990).

In eukaryotes, two internal transcribed spacers (ITS-1 and ITS-2) separate the 18S, 5.8S and 28S genes (or their homologs), and an external transcribed spacer (ETS) is located upstream of the 18S gene (Fig. 1). The transcribed spacers contain signals for processing the rRNA transcript. Adjacent copies of the rDNA repeat unit are separated by a nontranscribed spacer (NTS), also called an intergenic spacer by some workers. This region contains subrepeating elements that

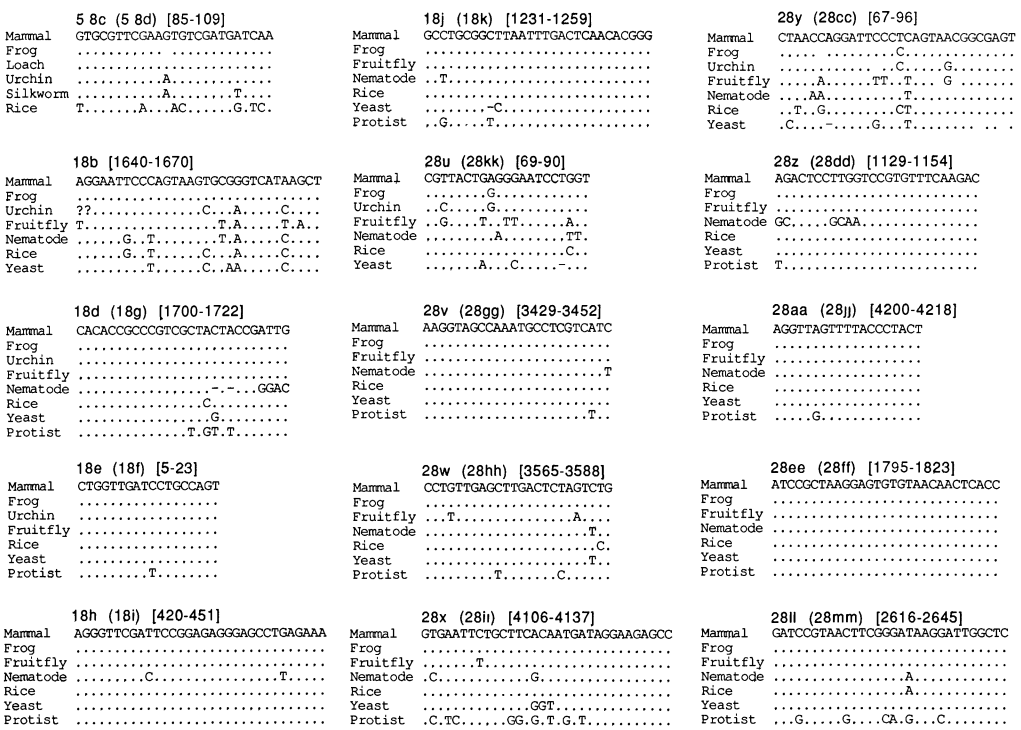

FIG. 2. PRIMERS FOR USE IN POLYMERASE CHAIN REACTIONS TO AMPLIFY SECTIONS OF rDNA ARRAYS SHOWN IN FIGURE 1.

These sequences can also be used as probes in Southern blotting experiments (see text). A dot indicates the nucleotide is the same as in the first sequence listed for the particular primer. The primer named in parentheses is the complement of the primer shown. Primers 18b and 28x contain the *Eco*RI sites in the 18S and 28S genes, and can be used to amplify a 5–6 kb fragment (sections 5–14) that is easily cloned into vectors with *Eco*RI cloning sites.

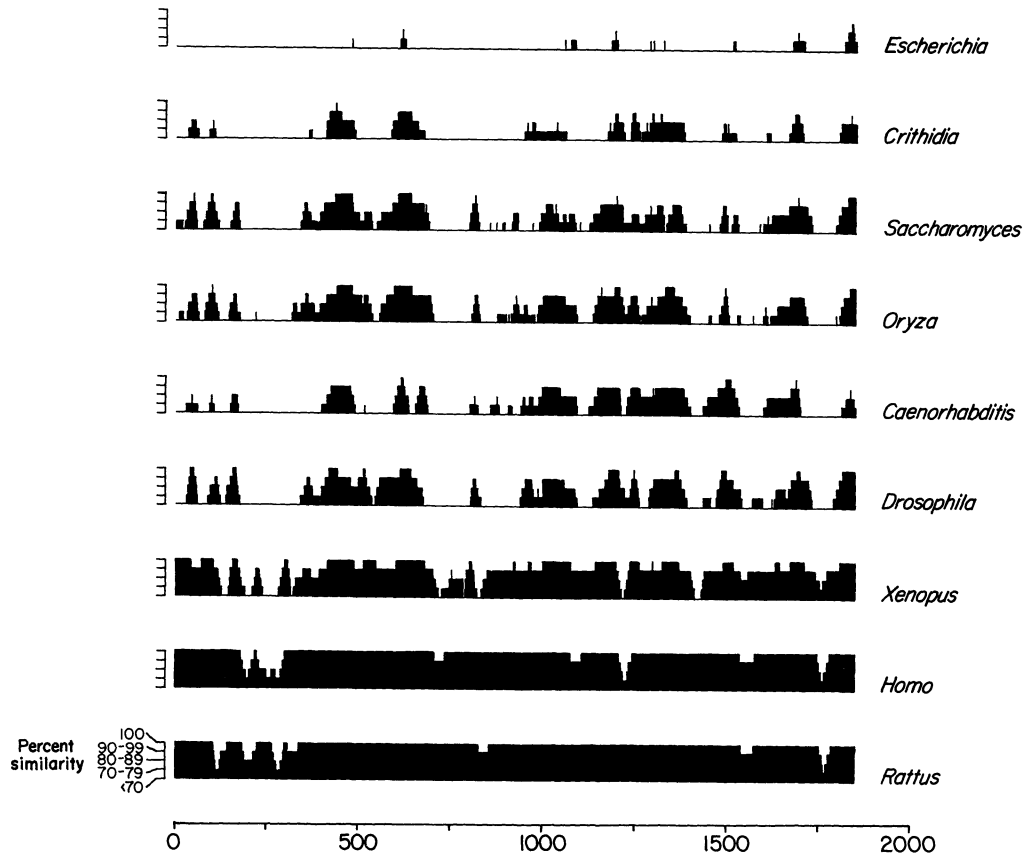

FIG. 3. SIMILARITY COMPARISONS OF THE NUCLEAR SMALL SUBUNIT rRNA GENE (16–18S).

All sequences were aligned with the *Mus musculus* (house mouse) sequence reported by Raynal et al., 1984. The scale on the horizontal axis shows the *Mus* nucleotide positions. The other sequences are from Brosius et al., 1978 (*Escherichia coli*, a eubacterium); Schnare et al., 1986 (*Crithidia fasciculata*, a trypanosome); Rubtsov et al., 1980 (*Saccharomyces cerevisiae*, brewer's yeast); Takaiwa et al., 1984 (*Oryza sativa*, domestic rice); Ellis et al., 1986 (*Caenorhabditis elegans*, a nematode); Tautz et al., 1988 (*Drosophila melanogaster*, common fruitfly); Salim and Maden, 1981 (*Xenopus laevis*, African clawed frog); Torczynski et al., 1985 (*Homo sapiens*, human); and Torczynski et al., 1983 (*Rattus norvegicus*, Norway rat). All sequences were as reported in GenBank. The graphs are based on a moving window of 30 bp recalculated ever 4 bp. Regions that are most likely to be useful for phylogenetic analysis are those within the similarity range of 70 to 90 percent.

serve as enhancers of transcription (Flavell and O'Dell, 1979; Kohorn and Rae, 1982, 1983; Reeder et al., 1983; Reeder, 1984).

STRUCTURE AND EVOLUTION OF rDNA: IMPLICATIONS FOR PHYLOGENETIC ANALYSIS

Rates of Evolution

One of the reasons why rDNA is useful for phylogenetic analysis is that different regions of the rDNA repeat unit evolve at very different rates. Thus regions of rDNA arrays that are particularly likely to yield informative data for almost any systematic question can be selected for analysis. In addition, the islands of highly conserved sequences within most rRNA genes are very useful for constructing "universal" primers that can be used for sequencing either rRNA or rDNA from many species, for amplifying regions of interest by use of the polymerase chain reaction, or for use as probes in restriction enzyme analyses (Kocher et al., 1989; Hillis et al., 1990; Simon et al., 1990; Fig. 2). Although intraindividual length heterogeneity causes problems for direct sequencing of amplified DNA in some regions of the repeat, the amplified DNA can be cloned and sequenced relatively easily.

The process of choosing a region that is likely to be appropriate for a particular systematic question is perhaps the most critical step in any phylogenetic analysis. If the region chosen is evolutionarily too conserved (i.e., the sequences are nearly the same in all study taxa), then considerable time will be wasted collecting invariant data. On the other hand, regions that differ among taxa to the extent that alignments are difficult or questionable also are unlikely to yield robust phylogenies (Swofford and Olsen, 1990). There are two reasons highly divergent sequences yield less robust results: (1) the level of homoplasy (parallelisms, convergences and reversals) increases as the probability for change at each position increases, and (2) the number of possible alignments that are nearly equally good becomes prohibitively large. Since alignment of positional homologs is an assumption of any phylogenetic analysis, it is best to delete from analyses any regions where the alignment is questionable (Swofford and Olsen, 1990).

Although there are no absolute rules, we have found that alignments are often ambiguous when paired sequences differ by more than about 30 percent in any given region. Therefore, regions of DNA that are best for phylogenetic studies are those that are greater than about 70 percent but less than 100 percent similar. We have aligned the complete sequences of the four nuclear rRNA genes and the two mitochondrial rRNA genes among a number of taxa of varying propinquity of relationship in order to identify the regions most useful for studies at a given level of divergence (Figs. 3–8). These figures can be used as a rough guide for choosing appropriate regions for phylogenetic analysis.

The most studied rRNA is the small subunit nuclear gene, 16–18S rRNA (Fig. 3). This gene has been studied most extensively because it is among the slowest evolving sequences found throughout living organisms, and has therefore been very useful for examining ancient evolutionary events. In addition, the slow rate of change permits the construction of many nearly universal primers, which facilitates sequencing efforts from groups that have not been studied previously. As one can see from Figure 3, aligned sequences of the small subunit gene provide relatively few variable sites even as far back as the divergence of mammals and amphibians, between 300 and 400 MYA. If the comparisons among mammals in Figure 3 are representative, this gene provides virtually no useful regions for comparisons involving taxa that diverged since the Cretaceous. Much of the gene is useful for comparisons among phyla of eukaryotes, however, and some comparisons among eukaryotes and prokaryotes are possible (Fig. 3). It has been used most successfully for reconstructing phylogenetic events from the Precambrian (see the Appendix and below).

The large subunit (23–28S) nuclear rRNA gene is larger and shows more variation in rates of evolution of its different domains than does the small subunit (Fig. 4). Although ancient comparisons are also possible with this gene (Lake, 1989a; Schleifer and Ludwig, 1989; Gouy and Li, 1989a), it primarily has been used to examine evolutionary events through the Paleozoic and Mesozoic (e.g., Guadet et al., 1989; Hillis and Dixon, 1989;

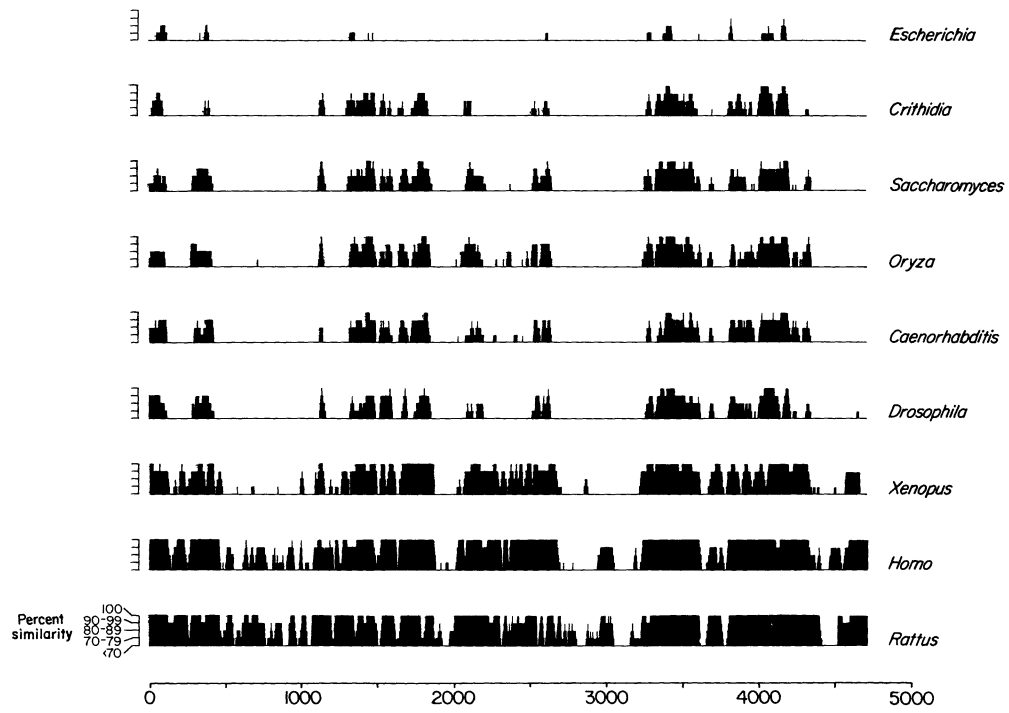

FIG. 4. SIMILARITY COMPARISONS OF THE NUCLEAR LARGE SUBUNIT rRNA GENE (23-28S).

All sequences were aligned with the *Mus musculus* sequence reported by Hassouna et al., 1984. The scale on the horizontal axis shows the *Mus* nucleotide positions. The aligned taxa are the same as in Figure 3; sources were Brosius et al., 1980 (*Escherichia coli*, a eubacterium); Spencer et al., 1987 (*Crithidia fasciculata*, a trypanosome); Georgiev et al., 1981 (*Saccharomyces cerevisiae*, brewer's yeast); Takaiwa et al., 1985 (*Oryza sativa*, domestic rice); Ellis et al., 1986 (*Caenorhabditis elegans*, a nematode); Tautz et al., 1988 (*Drosophila melanogaster*, common fruitfly); Ware et al., 1983 (*Xenopus laevis*, African clawed frog); Gonzalez et al., 1985 (*Homo sapiens*, human); and Chan et al., 1983 (*Rattus norvegicus*, Norway rat). Analysis was as described for Figure 3.

Larson and Wilson, 1989; Zimmer et al., 1989; de Sá and Hillis, 1990; Hillis, Dixon, and Ammerman, 1991). The large subunit rRNA gene has many divergent domains or expansion segments (Hassouna et al., 1984), so the size of the gene varies considerably among phyla (Gutell and Fox, 1988). These divergent domains are useful for reconstructing relatively recent events (into the Cenozoic), although regions for study must be chosen carefully if the taxa have recently diverged (Fig. 4).

The 5.8S rRNA gene of eukaryotes (and the corresponding region of the large subunit gene of prokaryotes) is similar to the small subunit gene in its useful phylogenetic range (Fig. 5), although the shortness of the sequence limits its effectiveness in inferring phylogeny across great time scales. It shows very little variation in comparisons of taxa that diverged after the Paleozoic (Nazar et al., 1976; Fig. 5). The 5S gene shows similar levels of variation, but it is even shorter than the 5.8S sequence (Fig. 6; Sankoff et al., 1973). The shortness of the sequence greatly restricts its phylogenetic usefulness (Halanych, 1991; Steele et al., 1991).

The mitochondrial rRNA genes evolve much more rapidly than the nuclear rRNA genes, and they can be used for most Cenozoic comparisons (Figs. 7 and 8). They are easily amplified through use of the polymerase chain reaction (Kocher et al., 1989; Simon et al., 1991). Even comparisons among taxa that have diverged within the past twenty million years (e.g., *Mus* versus *Rattus* in Figs. 7 and 8) are likely to show many changes. Studies that have successfully used the mitochondrial rRNA genes for phylogenetic reconstruction are concentrated on vertebrates (Appendix), but studies on other groups are beginning to appear (see Simon et al., 1991).

The spacer regions of rDNA arrays have been used less frequently for phylogenetic studies (Verbeet et al., 1984; McIntyre et al., 1988; Yokota et al., 1989; Gonzalez et al., 1990; Kjems and Garrett, 1990), except in restriction analyses of entire rDNA arrays (e.g., Nelkin et al., 1980; Wilson et al., 1984; Sytsma and Schaal, 1985; Hillis and Davis, 1986; Cracraft and Mindell, 1989; Mindell and Honeycutt, 1989; Sites and Davis, 1989; Allard and Honeycutt, 1991; Baker et al., in press). These studies have shown that the spacer regions can be used to infer phylogeny among closely related taxa (taxa that have diverged within the last 50 million years). In addition, variation in the spacer regions has been used to identify species or strains, to study hybridization, and as markers in population genetic studies (Toivonen et al., 1983; Saghai-Maroof et al., 1984; Rogers et al., 1986; Learn and Schaal, 1987; Schaal et al., 1987; Baker et al., 1989; King and Schaal, 1989; Sites and Davis, 1989; Hillis, Moritz, Porter, and Baker, 1991). Among the spacers, the NTS evolves most rapidly (Hoshikawa et al., 1983), and the transcribed spacers are somewhat more conserved (Appels and Dvořák, 1982a,b; Furlong and Maden, 1983). Amplification of the two internal transcribed spacers via the polymerase chain reaction is facilitated by conserved flanking regions of the 18S, 5.8S and 28S genes (Figs. 1 and 2), so the use of these spacers in studies involving closely related species is increasing (Appendix).

Concerted Evolution

As nuclear rRNA genes began to be studied in detail, it became clear that the multiple copies were not evolving independently, but in concert (Arnheim et al., 1980; Dover and Coen, 1981; Krystal et al., 1981; Coen, Strachan, and Dover, 1982; Coen, Thoday, and Dover, 1982; Arnheim, 1983). In other words, each copy of an rRNA array is usually very similar to the other copies within individuals and species, although differences among species accumulate rapidly in parts of the array. The differences among arrays within individuals are mostly length variation within the NTS (Wellauer, Dawid, Brown, and Reeder, 1976; Wellauer, Reeder, Dawid, and Brown, 1976; Stambrook, 1978; Arnheim et al., 1982; Cooper and Schmidtke, 1984; Yakura et al., 1984; Williams and Strobeck, 1985; Williams et al., 1985; Spencer et al., 1987), although smaller amounts of length variation also occur within individuals among the multiple copies of the genes (Gonzales et al., 1985). Nonetheless, the low variation among rDNA arrays within individuals (and throughout species) indicates that the multiple copies are homoge-

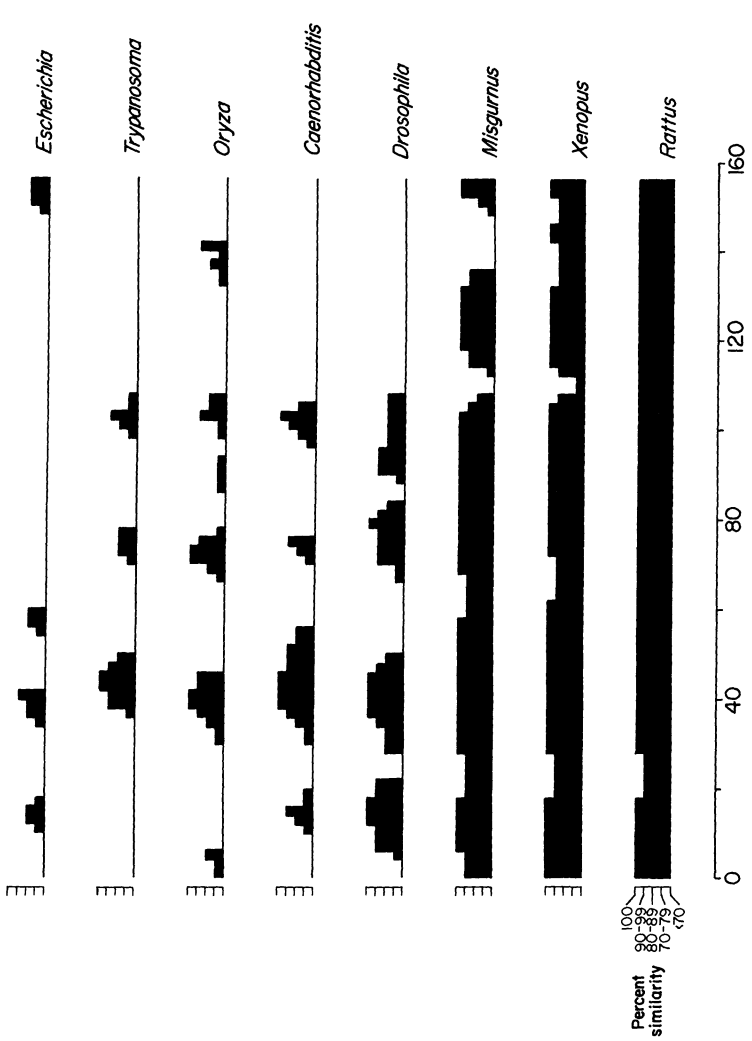

FIG. 5. SIMILARITY COMPARISONS OF THE 5.8S rRNA GENE (OR THE CORRESPONDING PORTION OF THE LARGE SUBUNIT GENE).

All sequences were aligned with the *Mus musculus* sequence reported by Walker et al., 1983. The scale on the horizontal axis shows the *Mus* nucleotide positions. The aligned taxa are the same as in Figure 3, except that the *Homo* and *Saccharomyces* sequences were not available, a different trypanosome (*Trypanosoma*) was used, and a ray-finned fish (*Misgurnus*) was included. Sources were Brosius et al., 1980 (*Escherichia coli*, a eubacterium); Dorfman et al., 1985 (*Trypanosoma brucei*, a trypanosome); Hariharan and Padayatty, 1987 (*Oryza sativa*, domestic rice); Ellis et al., 1986 (*Caenorhabditis elegans*, a nematode); Pavlakis et al., 1979 (*Drosophila melanogaster*, common fruitfly); Kupriyanova et al., 1985 (*Misgurnus fossilis*, a loach); Hall and Maden, 1980 (*Xenopus laevis*, African clawed frog); and Subrahmanyam et al., 1982 (*Rattus norvegicus*, Norway rat). Analysis was as described for Figure 3, except the window size was 10 bp, and similarity was calculated every 2 bp.

nized, among both homologous and nonhomologous chromosomes containing rDNA clusters. This phenomenon of homogenization is called concerted evolution (Arnheim et al., 1980).

Several processes appear to be responsible for concerted evolution, but the most important appear to be unequal crossing over (Smith, 1973, 1976; Perelson and Bell, 1977; Petes, 1980; Szostak and Wu, 1980) and gene conversion (Nagylaki and Petes, 1982; Nagylaki, 1984; Enea and Corredor, 1991). The relative contribution of these two mechanisms is debated (Dover, 1982a,b), although relatively few empirical data have been collected that discriminate between the possibilities. Seperack et al. (1988) argued that unequal crossing over is likely to be far more important because it can result in duplication or elimination of many repeats at once, whereas gene conversion events are thought to affect only one or a few repeats. In addition, the number of rDNA repeats is known to vary widely among individuals within species that have been studied (e.g., Henderson et al., 1976), a pattern that would be expected if unequal crossing over is common. Although Coen and Dover (1983) showed that unequal crossing over probably is responsible for the coevolution of rRNA arrays on the X and Y chromosomes of *Drosophila melanogaster*, Coen, Thoday, and Dover (1982) argued that rates of unequal crossing over are insufficient to account for patterns of concerted evolution seen among closely related species of *Drosophila*. Lassner and Dvorak (1986) reported that the distribution of mutations within the subrepeats of the nontranscribed spacer support gene conversion as the operative mechanism of homogenization. Hillis, Moritz, Porter, and Baker (1991) studied triploid parthenogenetic lines of lizards formed through multiple hybridization events of two sexual species, designated as SM6 and CA6. Homogenization of the rDNA arrays always proceeded in the same direction, with fixation of SM6 rDNA on CA6 chromosomes, even if two of the three chromosomes bearing rRNA genes were of CA6 ancestry. They argued that these data were consistent with biased gene conversion as the operative mechanism; if unequal crossing over was responsible, then a mechanism must exist that consistently biases the unequal crossovers in favor of the SM6 genotype.

Whatever the mechanisms that account for the observed concerted evolution of rDNA arrays, the phenomenon has several effects on phylogenetic analyses. The ideal phylogenetic marker would evolve within species, but show little intraspecific variation compared to interspecific variation. For most single-copy genes, high levels of variation among species typically are accompanied by high variation within species, so that extensive sampling (among individuals and populations) is necessary to characterize a species. Among the rDNA genes, although intraspecific variation obviously occurs, it is greatly reduced compared to what would be expected based on observation of interspecific variation (because of concerted evolution). Thus, although some intraspecific sampling is still advisable in studies of closely related species, particularly studies involving the nontranscribed spacer (Williams et al., 1988), it is possible to use small sample sizes in most phylogenetic studies of rDNA (Hillis and Davis, 1988; Baverstock and Moritz, 1990).

A second advantage of a homogenized, multiple-copy gene family is ease of analysis. Since rRNA is so abundant and uniform, it can be sequenced directly using reverse transcriptase (Lane, Pace, Olsen, Stahl, Sogin, and Pace, 1985). Multiple copies and conserved restriction sites also aid in rapidly cloning rDNA repeats (Hillis and Dixon, 1989) or in amplifying regions of rDNA using the polymerase chain reaction (Medlin et al., 1988; Sogin, 1990). For restriction analyses, Southern blotting is greatly facilitated by the large number of relatively uniform fragments (Dowling et al., 1990).

Concerted evolution, however, undoubtedly imposes limitations on phylogenetic analyses as well. Evidence now exists that homogenization can also occur within, as well as among, rDNA repeats (Hancock and Dover, 1988). Hancock and Dover (1988) found that sequence similarity among divergent domains within the large subunit rRNA gene is often higher than is expected if the regions were evolving independently. If these regions are coevolving, then sequence positions within the regions cannot be treated as independent characters in a phylogenetic analysis (see the

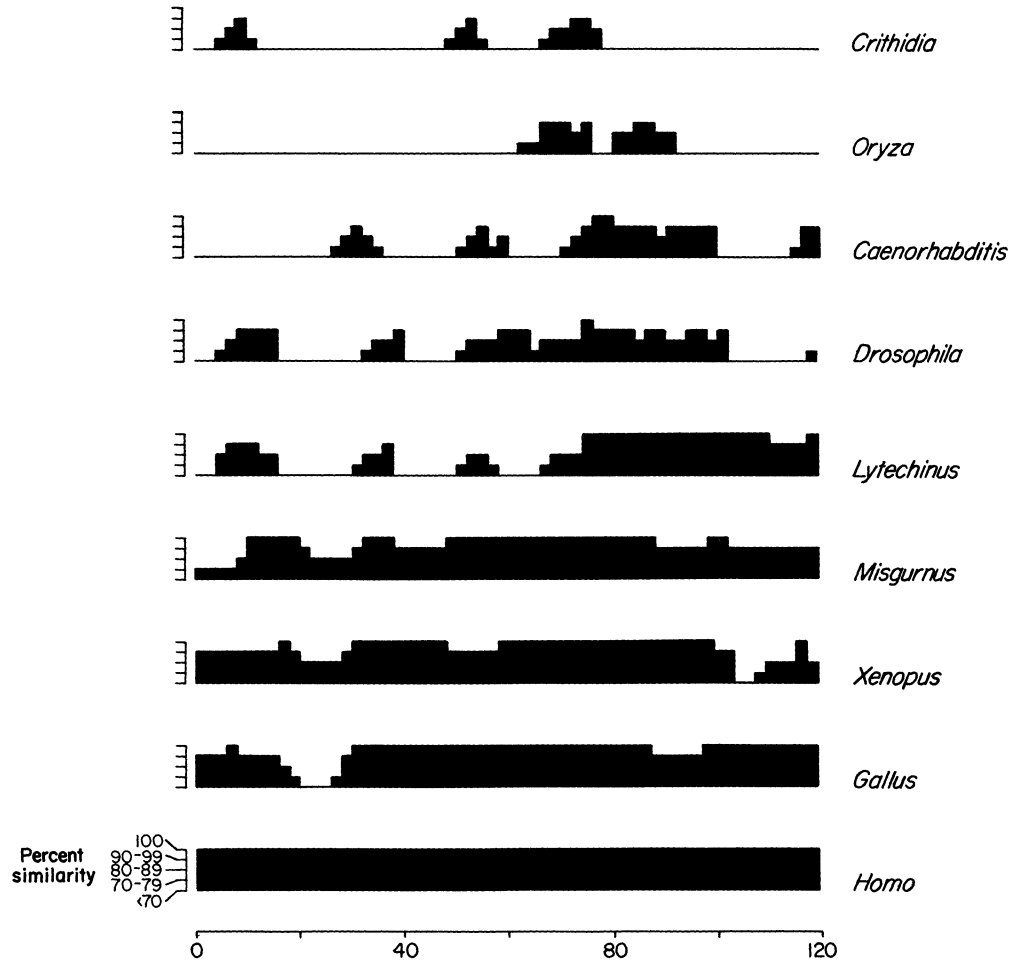

FIG. 6. SIMILARITY COMPARISONS OF THE NUCLEAR 5S rRNA GENE.

All sequences were aligned with the *Mesocricetus auratus* (Syrian hamster) sequence reported by Hart and Folk, 1982. The scale on the horizontal axis shows the *Mesocricetus* nucleotide positions. Sources were MacKay et al., 1980 (*Crithidia fasciculata*, a trypanosome); Hariharan et al., 1987 (*Oryza sativa*, domestic rice); Nelson and Honda, 1985 (*Caenorhabditis elegans*, a nematode); Tschudi and Pirrotta, 1980 (*Drosophila melanogaster*, common fruitfly); Simpson and Stafford, 1983 (*Lytechinus variegatus*, a sea urchin); Mashkova et al., 1981 (*Misgurnus fossilis*, a loach); Peterson et al., 1980 (*Xenopus laevis*, African clawed frog); Lazer et al., 1983 (*Gallus gallus*, chicken); and Forget and Weissman, 1969 (*Homo sapiens*, human). Analysis was as described for Figure 5.

discussion of weighting characters to account for nonindependence under *Secondary Structure*, below). In addition, if biases in gene conversion events are found to be sequence specific, then the possibility of parallel changes in multiple lineages will have to be considered.

It is important to recognize that although gene homogenization appears to be the rule, intragenomic variation is known. The most important cases seem to be growth-stage-specific rRNAs. This was first recognized in the existence of oocyte-specific 5S rRNA sequences (Wegnez et al., 1972; Mashkova et al., 1981). More recently, some *Plasmodium* species have been found to possess life-stage-specific small subunit rRNAs (Gunderson, Sogin, Wollett, Hollingdale, de la Cruz, Waters, and McCutchan, 1987; McCutchan et al., 1988). Although the number of sequence differences is substantial, they are concentrated in regions of rapid change, and are unlikely to interfere with the inference of distant relationships.

Given the number of unknowns associated with the processes responsible for concerted evolution of rDNA, some degree of caution probably is warranted in using rDNA for phylogenetic analysis (Rothschild et al., 1986). Results of phylogenetic studies based on rDNA, however, are generally consistent with those based on other sources of data in studies that involve multiple comparisons (Hillis, 1987), so it is likely that methods of phylogenetic inference are sufficiently robust to effectively handle the complexities of rDNA evolution. As new information becomes available on the constraints of concerted evolution, this information can be incorporated into phylogenetic analyses (e.g., through differential weighting of characters) for potentially increased resolution (see Swofford and Olsen, 1990).

Secondary Structure

To function properly within a ribosome, rRNA molecules must fold into a secondary structure that is directly dependent on the primary sequence (Noller, 1984). Although some secondary structure models are based on or tested with experimental evidence (e.g., Glotz and Brimacombe, 1980; Noller and Woese, 1981; Noller et al., 1981; Atmadja et al., 1984; Klein et al., 1984), most estimates of the secondary structure of rRNAs are based on comparative analysis (Nishikawa and Takemura, 1974; Fox and Woese, 1975). These models of secondary structure have been produced for all the rRNAs, both nuclear and organellar, for a wide diversity of organisms (e.g., Mankin and Kopylov, 1981; Chan et al., 1983, 1984; Maly and Brimacombe, 1983; Clark et al., 1984; Hadjiolov et al., 1984; Nelles et al., 1984; Gorski et al., 1987; Cummings, Domenico, and Nelson, 1989; Cummings, Domenico, Nelson, and Sogin, 1989). These studies have shown that major features of rRNA secondary structure are highly conserved throughout life (Zweib et al., 1981; Michot et al., 1984; Dunon-Bluteau and Brun, 1986; Michot and Bachellerie, 1987; Gutell et al., 1990). This maintenance of secondary structure occurs despite the continued evolution of the primary sequence, because compensatory mutations occur between the paired nucleotides (Ebel et al., 1983; Michel and Dujon, 1983; Curtiss and Vournakis, 1984; Torres et al., 1990).

Wheeler and Honeycutt (1988) examined 5S and 5.8S rRNA sequences from a wide diversity of organisms, and showed that phylogenetic analyses of nucleotide positions involved in base pairing produced different results than analyses based on unpaired positions. Furthermore, their analyses of unpaired positions produced results that were more like traditional hypotheses of relationships based on morphological data. Wheeler and Honeycutt (1988) concluded that the constraints of secondary structure were more likely to produce spurious phylogenetic conclusions in analyses of paired bases, and they recommended eliminating paired positions, or at least assigning them one-half weight to account for their nonindependence. In contrast, Smith (1989) suggested that paired nucleotides produced more reliable results than did unpaired positions (compared to well-established morphological phylogenies) in a study of 18S rRNA sequences in echinoderms.

We conducted an analysis similar to those of Wheeler and Honeycutt (1988) and Smith (1989) for 28S gene sequences of vertebrates (Dixon and Hillis, unpub.). We found that the analysis of paired positions produced a

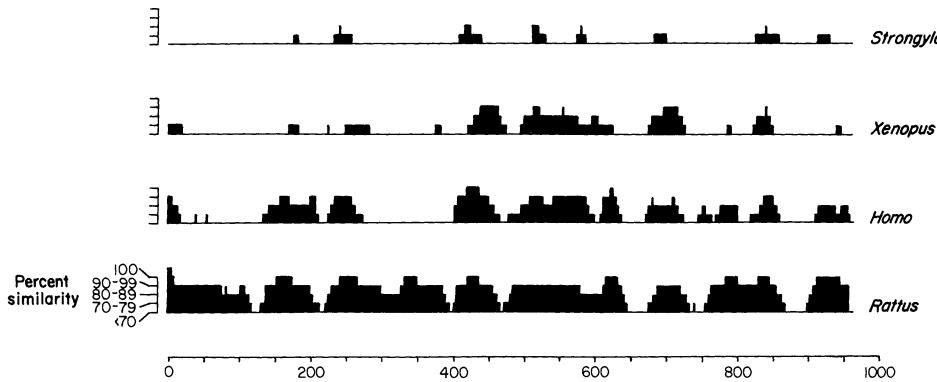

FIG. 7. SIMILARITY COMPARISONS OF THE 12S MITOCHONDRIAL rRNA GENE.
All sequences were aligned with the *Mus musculus* (house mouse) sequence reported by Bibb et al., 1981. The scale on the horizontal axis shows the *Mus* nucleotide positions. The other sequences are from Jacobs et al., 1988 (*Strongylocentrotus purpuratus*, a sea urchin); Roe et al., 1985 (*Xenopus laevis*, African clawed frog); Anderson et al., 1981 (*Homo sapiens*, human); and Kobayashi et al., 1981 (*Rattus norvegicus*, Norway rat). Analysis was as described for Figure 3.

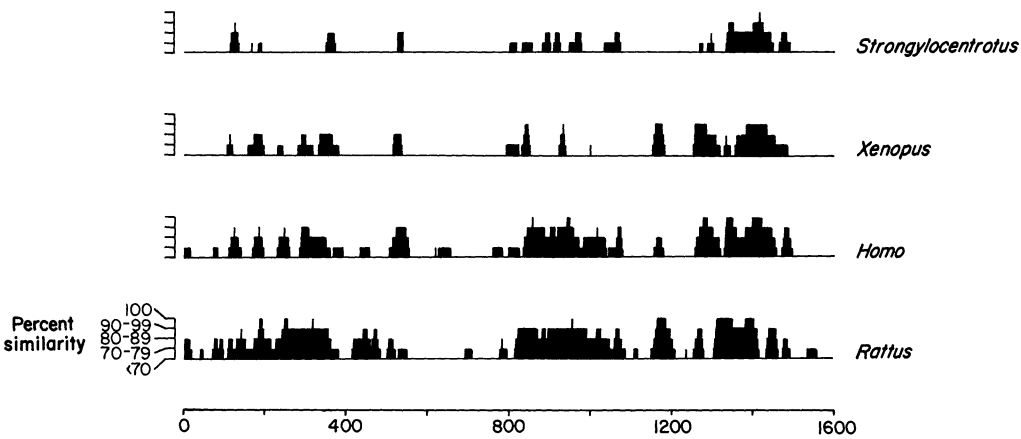

FIG. 8. SIMILARITY COMPARISONS OF THE 16S MITOCHONDRIAL rRNA GENE.
The aligned taxa, sources, and analysis are the same as in Figure 7 except that the *Rattus* sequence is from Saccone et al., 1981.

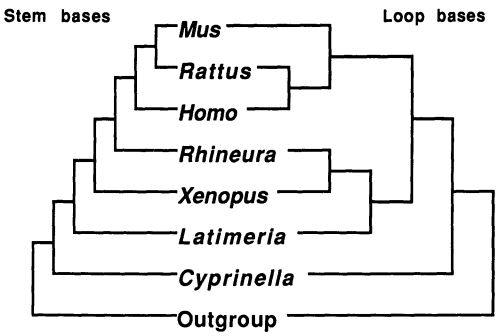

FIG. 9. RESULTS OF PHYLOGENETIC ANALYSIS OF NUCLEOTIDES THAT ARE PAIRED VERSUS UNPAIRED IN SECONDARY STRUCTURAL MODELS OF 28S RNA (SEE TABLE 1).

The tree on the left (based on the paired bases) is the same as in the analysis of the complete data set, and is also the commonly accepted tree based on morphology.

result that was better resolved than that obtained from analysis of unpaired positions (Fig. 9). Furthermore, the result from paired positions was identical to the result from the full data set, and also the same as the usually accepted tree from morphology. The percentage of phylogenetically informative characters that were paired positions is approximately the same as the percentage of paired positions in the total analysis (Table 1). The main difference between our analysis and that of Smith (1989) on the one hand, and the study by Wheeler and Honeycutt (1988) on the other hand, is the size of data sets. The results from analysis of the larger data sets, 18S sequences (Smith, 1989) and 28S sequences (our data) indicate that paired positions should not be eliminated from phylogenetic analyses—indeed, paired regions may contain most of the informative positions for some kinds of analyses.

The weighting scheme suggested by Wheeler and Honeycutt (1988)—assigning all paired bases one-half weight—assumes that compensatory changes to maintain secondary structure are perfect. In other words, if nearly every mutation immediately resulted in a compensatory mutation within paired regions, then adjusting the weighting in this manner would be a reasonable course of action. A simpler solution that would have the same effect (if compensation were perfect) would be to eliminate half of the paired sites from phylogenetic analysis. Compensation is far from perfect, however, and different taxa may show different compensatory changes (RNA pairing is slightly more complicated than DNA pairing, because uracil can pair with either guanine or adenine). Therefore, calculations of weights for paired versus unpaired bases should be based on observed levels of compensation, rather than on assumptions of perfect compensation. Analyses of vertebrate data sets indicate that the appropriate level of weighting for paired positions is closer to one than to one-half (Dixon and Hillis, unpub.).

STUDIES OF PHYLOGENY

Methods of Data Collection

There are four primary classes of data on rDNA arrays that have been used to infer phylogenetic relationships. The first two methods to be used, oligonucleotide catalogs (e.g., Sogin et al., 1972; Bonen and Doolittle, 1975; Zablen et al., 1975; Woese and Fox, 1977; Kössel et al., 1983) and hybridization studies (e.g., Pace and Campbell, 1971a,b; Palleroni et al., 1973; Johnson and Francis, 1975; de Smedt and de Ley, 1977; Moore, 1977; Stackebrandt et al., 1981), were largely

TABLE 1

The distribution of chordate 28S rDNA sequence data analysed in Figure 9, categorized by secondary structure

Information on the complete gene is from the *Xenopus laevis* sequence (Ware et al., 1983). The other columns are from the analysis of secondary structure of Dixon and Hillis (unpub.) based upon the data set of Hillis, Dixon and Ammerman (1991). Variable positions are homologous nucleotides that vary in at least one taxon and informative characters are those that can affect tree topology in a parsimony analysis. Secondary structure was based on the model for *Xenopus* by Clark et al. (1984).

	Complete gene	Aligned bases	Variable positions	Informative characters
Unpaired	1,866 (45.4%)	907 (45.6%)	221 (44.4%)	53 (47.7%)
Stems	2,244 (54.6%)	1,082 (54.4%)	277 (55.6%)	58 (52.3%)
Total	4,110	1,989	498	111

replaced by sequencing studies as methods for sequencing became increasingly easier. The fourth type of study, restriction site analysis, is especially useful in population studies or studies of closely related species where large numbers of individuals must be sampled (Dowling et al., 1990).

Among rDNA sequencing studies, three methods are commonly used to collect nucleotide sequences. The first method to be used regularly in comparative studies was direct RNA sequencing using reverse transcriptase (Lane, Pace, Olsen, Stahl, Sogin, and Pace, 1985; Hillis et al., 1990). The primary advantages of this method are ease of analysis (no cloning is required) and the obtainment of consensus sequences (if several nucleotides are present at a given position in different copies of the target gene, the most common will likely be recorded). Only one strand can be sequenced, however, so two-strand verification is not possible, and analyses are limited to transcribed portions of the array. In addition, the lack of a cloned sequence means that further studies require newly isolated RNA, and differences between studies may be the result of either errors or differences in the source RNA.

The more traditional approach of cloning and sequencing rDNA eliminates the disadvantages of direct RNA sequencing at the expense of greater effort per nucleotide. Also, each sequence obtained represents a single repeat rather than a consensus of the whole array. The ease of cloning multiple copy genes such as the rRNA genes greatly reduces the relative difficulty of the cloning approach (Hillis and Dixon, 1989).

The third method of obtaining sequence data is amplification via the polymerase chain reaction, or PCR (Medlin et al., 1988; Sogin, 1990). The amplified product can either be sequenced directly or cloned and then sequenced. This method is easily adaptable for comparative studies in which a particular region of one of the rRNA genes is to be targeted (see Fig. 1). For sequencing large regions of rDNA, however, it is less expensive and less time-consuming to clone, because amplification of an entire repeat at one time is not practical. The cost of repeated amplifications of many different small regions is high compared to the cost of cloning the entire repeat, and in the long run, cloning usually requires less time. For small-scale sequencing projects, on the other hand, PCR is highly time and cost effective.

Restriction analysis of rDNA is straightforward. Southern blots of rDNA can be screened using heterologous probes of cloned rDNA arrays (or parts thereof). If heterologous clones are used and length or sequence heterogeneity is present within individuals, mapping of restriction sites can be difficult (Hillis and Davis, 1988; Williams et al., 1988). An effective method for avoiding these problems is to use the oligonucleotide primers shown in Figure 2 as sequential probes on Southern blots. This has the advantage of reducing the region of comparison and thereby simplifying gel interpretation. Fine-scale restriction maps of regions of the repeat (the ITS regions, for instance) can be obtained by amplifying the regions using one biotinylated or radioactively labeled primer, followed by partial digestion and gel electrophoresis. The fragments so obtained immediately indicate the distance of each restriction site from the labeled primer, so restriction maps are relatively easy to construct.

Restriction mapping studies are useful not only for studying the phylogeny of relatively closely related species (Appendix), but also for any study in which many individuals need to be examined for a limited number of markers. For instance, restriction studies of rDNA have been used to study mechanisms of concerted evolution of ribosomal arrays (Hillis, Moritz, Porter, and Baker, 1991), interspecific hybridzation (Baker et al., 1989; Sites and Davis, 1989), population dynamics and gene flow (Learn and Schaal, 1987; Schaal et al., 1987; King and Schaal, 1989), and typing of strains of fungi (Lachance, 1990). The chief advantages restriction site mapping studies have over sequencing studies are that many individuals can be examined and scored quickly, the cost for these analyses is much less than for sequencing, and a much greater portion of the genome can be surveyed with less effort (albeit with less detail).

Small Subunit rRNA

The small subunit (16–18S) rRNA gene (nuclear version in eukaryotes) has been studied more extensively than any other rDNA

sequence (Appendix). The primary reason for the extensive attention on this gene is that it is the most slowly evolving of the rDNAs (Fig. 3), and therefore it is useful for addressing questions about ancient evolutionary events. Studies on the earliest branchings of life have focused on the small subunit, and these studies have documented the extensive phylogenetic diversity present among the prokaryotes (see references under "Major lineages of life," Appendix). As a result of these studies, it is now generally recognized that the "prokaryotes" do not form a natural group. Considerable controversy, however, still exists about the content and relationships of the primary lines of descent. One group supports the position that prokarotes consist of two lineages, the Archaebacteria and Eubacteria (e.g., Woese and Fox, 1977; Woese, 1987; Gouy and Li, 1989a). Under this system, Archaeabacteria include the highly thermophilic, sulphur-dependent eocytes, as well as methanogens and halobacteria. In contrast, Lake (1988, 1989a) considers the eocytes to be more closely related to eukaryotes and the halobacteria to be more closely related to Eubacteria. The results are somewhat dependent on the molecule selected for analysis, the method of analysis, and the method of alignment of the sequences (Gouy and Li, 1989a).

Small subunit rDNA sequences have also been extremely important for elucidating higher relationships within Archaebacteria and Eubacteria, as well as among the basal eukaryotes (see references under these headings in the Appendix). Until the widespread study of these sequences, there was little basis for ordering the diversity of prokaryotes or unicellular eukaryotes. As more rDNA sequences have become available for protists, the tremendous phylogenetic diversity of this paraphyletic assemblage has become increasingly clear (e.g., see Sogin, Edman, and Elwood, 1989; Sogin, Gunderson, Elwood, Alonso, and Peattie, 1989).

Most studies of phylogeny using small subunit rDNA sequences among the multicellular eukaryotes have concerned higher level relationships of phyla and classes (Appendix). For instance, seed plant relationships have been studied by Zimmer et al. (1989), and a major study of metazoans has been conducted by Field et al. (1988). The latter study has been one of the most controversial studies of phylogeny ever conducted, and has stimulated numerous reanalyses of the relevant data (e.g., Ghiselin, 1989; Lake, 1989b; Patterson, 1989; Lake 1990). The most surprising conclusion of Field et al. (1988) was that multicellular animals are polyphyletic, with coelenterates more closely related to plants and fungi than to other metazoans. This conclusion, however, was not well supported (Field et al., 1989), and reanalyses of these data (e.g., Patterson, 1989) support the more traditional arrangement of a monophyletic Animalia.

Large Subunit rRNA

The large subunit rRNA is the largest of the rRNAs, and contains regions that evolve more rapidly than the small subunit rRNA as well as some regions that evolve as slowly as those in the small subunit (Fig. 4). Thus a large subunit rRNA sequence can be used successfully to infer phylogenetic relationships among more closely related organisms (within eukaryote phyla, for instance). Fewer comparative studies of this gene have been conducted than for the small subunit gene, but it is beginning to be studied fairly extensively among the vertebrates (Appendix). Most of these studies are in fairly close agreement with traditional ideas about vertebrate phylogeny, although some differences do exist. For instance, the relationships of salamanders supported by 28S sequences are vastly different from those supported by morphology (Larson and Wilson, 1989; Hillis, 1991; Larson, 1991), and the resolution of relationships among the major clades of amniotes is poor (Hillis and Dixon, 1989; Hedges et al., 1990). Large subunit sequences, however, have been useful for distinguishing among a number of proposed alternatives at various levels of the vertebrate tree, such as the relationships within the pipid frogs (de Sá and Hillis, 1990), among orders of amphibians (Larson and Wilson, 1989), or among the basal sarcopterygians (Hillis, Dixon, and Ammerman, 1991).

5S and 5.8S rRNAs

The 5S and 5.8S rRNA genes are very short (Figs. 5 and 6), so the number of phylogenetically informative sites is quite limited

for most studies (Halanych, 1991; Steele et al., 1991). Nonetheless, some success has been obtained in using these sequences to examine relationships within major phyla of eukaryotes (e.g., Hendriks et al., 1986; Wheeler and Honeycutt, 1988; Steele et al., 1991) and occasionally at higher levels (e.g., Ohama et al., 1984). Comparisons across a wide spectrum of life (Figs. 5 and 6) reveal that at least some regions evolve quite slowly and can be aligned throughout living organisms. As argued by Halanych (1991), however, these sequences usually are too short to be used by themselves to produce robust phylogenetic results.

Organellar rRNAs

The rRNA genes of mitochondria and chloroplasts have been critical for inferring the origins of endosymbiosis of these organelles (Bonen and Doolittle, 1975, 1976; Küntzel and Köchel, 1981; Spencer et al., 1981; Yang, Oyaizu, Oyaizu, Olsen, and Woese, 1985; Evrard et al., 1990). In addition, these sequences can be studied within a particular group to elucidate phylogenies of more closely related taxa. The mitochondrial rRNA genes are particularly useful for looking at relationships with eukaryote groups that have diverged in the Cenozoic (Appendix), which makes them largely complementary to the nuclear rRNA genes. For instance, they have been sequenced for numerous species of mammals, and used to infer the phylogeny of groups within marsupials, artiodactyls, and primates (Hixson and Brown, 1986; Miyamoto et al., 1989, 1990; Thomas et al., 1989). Phylogenetic study of mitochondrial rDNA sequences, including the construction of appropriate primers for amplification, was recently reviewed by Simon et al. (1991).

THE FUTURE OF rDNA STUDIES

The Appendix documents the great range and utility of phylogenetic analyses of rDNA. One might assume from seeing such a long list of studies that analysis of rDNA has become mundane, and that there are no more real questions about the processes of rDNA evolution, just considerable cataloging ahead. This assumption is incorrect. The processes responsible for concerted evolution of rDNA arrays (or other repeated sequences) are still poorly known or documented, and the complexities of patterns of self-similarity are just beginning to be evaluated. Much work needs to be conducted on the rationale of weighting positions based on considerations of secondary structure, within-gene homogenization, subrepeats within repeats, and probability of change. Moreover, the spacer regions have received much less attention than the gene sequences, so the usefulness of comparative studies of rDNA spacers for investigations of closely related species and populations needs further evaluation.

Studies of rDNA sequences have changed the way we view organismal diversity. They have had the greatest systematic impact to date at the deepest levels of the tree of life, and for groups in which morphologies provide little information (e.g., unicellular organisms). They are also useful, however, at most other levels of phylogenetic divergence, from the Precambrian (small subunit), through the Paleozoic and Mesozoic (large subunit), to the Cenozoic (organellar genes and spacers regions). Thus, rRNA genes and their associated spacers are among the most versatile sequences for phylogenetic analysis of the history of life.

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REFERENCES

Abele, L. G., W. Kim, and B. E. Felgenhauer. 1989. Molecular evidence for the inclusion of the phylum Pentastomida in the Crustacea. *Mol. Biol. Evol.*, 6:685-691.

Achenbach-Richter, L., K. O. Stetter, and C. R. Woese. 1987. A possible biochemical missing link among archaebacteria. *Nature*, 327:348-349.

Achenbach-Richter, L., R. Gupta, K. O. Stetter, and C. R. Woese. 1987. Were the original eubacteria thermophiles? *Syst. Appl. Microbiol.*, 9: 34-39.

Achenbach-Richter, L., R. Gupta, W. Zillig, and C. R. Woese. 1988. Rooting the archaebacterial tree: the pivotal role of *Therococcus celer* in archaebacterial evolution. *Syst. Appl. Microbiol.*, 10:231-240.

Albrecht, W., A. Fischer, J. Smida, and E. Stackebrandt. 1987. *Verrucomicrobium spinosum*, a eubacterium representing an ancient line of descent. *Syst. Appl. Microbiol.*, 10:57-62.

Allard, M. W., and R. L. Honeycutt. 1991. Ribosomal DNA variation within and between species of rodents, with emphasis on the genus *Onychomys*. *Mol. Biol. Evol.*, 8:71-84.

Anderson, J., W. Andresini, and N. Delihas. 1982. On the phylogeny of *Phycomyces blakesleeanus*. *J. Biol. Chem.*, 257:9114-9118.

Anderson, S., A. T. Bankier, B. G. Barrell, M. H. L. de Bruijn, A. R. Coulson, J. Drouin, I. C. Eperon, D. P. Nierlich, B. A. Roe, F. Sanger, P. H. Schreier, A. J. H. Smith, R. Staden, and I. G. Young. 1981. Sequence and organization of the human mitochondrial genome. *Nature*, 290:457-465.

Appels, R., and J. Dvořák. 1982a. The wheat ribosomal DNA spacer region: its structure and variation in populations and among species. *Theor. Appl. Genet.*, 63:337-348.

———, and ———. 1982b. Relative rates of divergence of spacer and gene sequences within the rDNA region of species in the *Triticeae*: implications for the maintenance of homogeneity of a repeated gene family. *Theor. Appl. Genet.*, 63:361-365.

Appels, R., and R. L. Honeycutt. 1986. rDNA evolution over a billion years. In S. K. Dutta (ed.), *DNA Systematics*, pp. 81-135. CRC Press, Boca Raton.

Appels, R., W. L. Gerlach, E. S. Dennis, H. Swift, and W. J. Peacock. 1980. Molecular and chromosomal organization of DNA sequences coding for the ribosomal RNAs in cereals. *Chromosoma*, 78:293-311.

Arnheim, N. 1983. Concerted evolution of multigene families. In M. Nei and R. K. Koehn (eds.), *Evolution of Genes and Proteins*, pp. 38-61. Sinauer, Sunderland.

Arnheim, N., D. Treco, B. Taylor, and E. Eicher. 1982. Distribution of ribosomal gene length variants among mouse chromosomes. *Proc. Natl. Acad. Sci. USA*, 79:4677-4680.

Arnheim, N., M. Krystal, R. Schmickel, G. Wilson, O. Ryder, and E. Zimmer. 1980. Molecular evidence for genetic exchanges among ribosomal genes on nonhomologous chromosomes in man and ape. *Proc. Natl. Acad. Sci. USA*, 77: 7323-7327.

Atmadja, J., R. Brimacombe, and B. E. H. Maden. 1984. *Xenopus laevis* 18S ribosomal RNA: experimental determination of secondary structure elements and locations of methyl groups in the secondary structure model. *Nucleic Acids Res.*, 12:2649-2667.

Auling, G., J. Busse, M. Hahn, H. Hennecke, R.-M. Kroppenstedt, A. Probst, and E. Stackebrandt. 1988. Phylogenetic heterogeneity and chemotaxonomic properties of certain Gram-negative aerobic carboxydobacteria. *Syst. Appl. Microbiol.*, 10:264-272.

Baker, R. J., R. L. Honeycutt, R. A. Van Den Bussche. 1991. Examination of monophyly of bats: restriction map of the ribosomal DNA cistron. *Bull. Am. Mus. Nat. Hist.*, 206: 42-53.

Baker, R. J., S. K. Davis, R. D. Bradley, M. J. Hamilton, and R. A. Van Den Bussche. 1989. Ribosomal-DNA, mitochondrial-DNA, chromosomal, and allozymic studies on a contact zone in the pocket gopher, *Geomys*. *Evolution*, 43:63-75.

Balch, W. E., G. E. Fox, L. J. Magrum, C. R. Woese, and R. S. Wolfe. 1979. Methanogens: reevaluation of a unique biological group. *Microbiol. Rev.*, 43:260-296.

Balch, W. E., L. J. Magrum, G. E. Fox, R. S. Wolfe, and C. R. Woese. 1977. An ancient divergence among the bacteria. *J. Mol. Evol.*, 9:305-311.

Baroin, A., R. Perasso, L.-H. Qu, G. Brugerolle, J.-P. Bachellerie, and A. Adoutte. 1988. Partial phylogeny of the unicellular eukaryotes based on rapid sequencing of a portion of 28S ribosomal RNA. *Proc. Natl. Acad. Sci. USA*, 85: 3474-3478.

Barta, J. R., M. C. Jenkins, and H. D. Danforth. 1991. Evolutionary relationships of avian *Eimeria* species among other apicomplexan protozoa: Monophyly of the Apicomplexa is supported. *Mol. Biol. Evol.*, 8:345-355.

Bateson, M. M., K. Thibault, and D. M. Ward. 1990. Comparative analysis of partial 16S ribosomal RNA sequences of *Thermus* species. *Syst.*

Appl. Microbiol., 13:8-13.

Bateson, M. M., J. Wiegel, and D. M. Ward. 1989. Comparative analysis of 16S ribosomal RNA sequences of thermophilic fermentative bacteria isolated from hot spring cyanobacteria mats. *Syst. Appl. Microbiol.*, 12:1-7.

Baverstock, P. R., and C. Moritz. 1990. Sampling design. In D. M. Hillis and C. Moritz (eds.), *Molecular Systematics*, pp. 13-24. Sinauer Associates, Sunderland.

Baverstock, P. R., S. Illana, P. E. Christy, B. S. Robinson, and A. M. Johnson. 1989. srRNA evolution and phylogenetic relationships of the genus *Naegleria* (Protista:Rhizopoda). *Mol. Biol. Evol.*, 6:243-257.

Bellarosa, R., V. Delre, B. Schirone, and F. Maggini. 1990. Ribosomal RNA genes in *Quercus* spp. (*Fagaceae*). *Plant Syst. Evol.*, 172:127-139.

Bibb, M. J., R. A. Van Etten, C. T. Wright, M. W. Walberg, and D. A. Clayton. 1981. Sequence and gene organization of mouse mitochondrial DNA. *Cell*, 26:167-180.

Blair, D., and D. P. McManus. 1989. Restriction enzyme mapping of ribosomal DNA can distinguish between fasciolid (liver fluke) species. *Mol. Biochem. Parasitol.*, 36:201-208.

Blanz, P. A., and M. Gottschalk. 1986. Systematic position of *Septobasidium*, *Graphiola* and other basidiomycetes as deduced on the basis of their 5S ribosomal RNA nucleotide sequences. *Syst. Appl. Microbiol.*, 8:121-127.

Bobrova, V. K., A. V. Troitsky, A. G. Ponomarev, and A. S. Antonov. 1987. Low-molecular-weight rRNAs sequences and plant phylogeny reconstruction: nucleotide sequences of chloroplast 4.5S rRNAs from *Acorus calamus* (*Araceae*) and *Ligularia calthifolia* (*Asteraceae*). *Plant Syst. Evol.*, 156:13-27.

Bomar, D., S. Giovannoni, and E. Stackebrandt. 1988. A unique type of eubacterial 5S rRNA in members of the order Planctomycetales. *J. Mol. Evol.*, 27:121-125.

Bonen, L., and W. F. Doolittle. 1975. On the prokaryotic nature of red algal chloroplasts. *Proc. Nat. Acad. Sci. USA*, 72:2310-2314.

———, and ———. 1976. Partial sequence of 16S rRNA and the phylogeny of blue-green algae and chloroplasts. *Nature*, 261:669-673.

———, and ———. 1978. Ribosomal RNA homologies and the evolution of the filamentous blue-green bacteria. *J. Mol. Evol.*, 10:283-291.

Brayton, P. R., R. B. Bode, R. R. Colwell, M. T. MacDonell, H. L. Hall, D. J. Grimes, P. A. West, and T. N. Bryant. 1986. *Vibrio cincinnatiensis* sp. nov., a new human pathogen. *J. Clin. Microbiol.*, 23:104-108.

Bremer, B., and K. Bremer. 1989. Cladistic analysis of blue-green procaryote interrelationships and chloroplast origin based on 16S rRNA oligonucleotide catalogues. *J. Evol. Biol.*, 2:13-30.

Brosius, J., T. J. Dull, and H. F. Noller. 1980. Complete nucleotide sequence of a 23S ribosomal RNA gene from *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 77:201-204.

Brosius, J., T. J. Dull, D. D. Sleeter, and H. F. Noller. 1981. Gene organization and primary structure of a ribosomal RNA operon from *Escherichia coli*. *J. Mol. Biol.*, 148:107-127.

Brosius, J., M. L. Palmer, P. J. Kennedy, and H. F. Noller. 1978. Complete nucleotide sequence of a 16S ribosomal RNA gene from *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 75:4801-4805.

Bulygina, E. S., V. F. Galchenko, N. I. Govorukhina, A. I. Netrusov, D. I. Nikitin, Y. A. Trotsenko, and K. M. Chumakov. 1990. Taxonomic studies of methylotrophic bacteria by 5S ribosomal RNA sequencing. *J. Gen. Microbiol.*, 136:441-446.

Butler, M. H., S. M. Wall, K. R. Luehrsen, G. E. Fox, and R. M. Hecht. 1981. Molecular relationships between closely related strains and species of nematodes. *J. Mol. Evol.*, 18:18-23.

Catlin, B. W. 1991. *Branhamaceae* fam. nov., a proposed family to accommodate the genera *Branhamella* and *Moraxella*. *Int. J. Syst. Bacteriol.*, 41:320-323.

Cedergren, R., M. W. Gray, Y. Abel, and D. Sankoff. 1988. The evolutionary relationships among known life forms. *J. Mol. Evol.*, 28:98-112.

Chan, Y.-L., J. Olvera, and I. G. Wool. 1983. The structure of rat 28S ribosomal ribonucleic acid inferred from the sequence of nucleotides in a gene. *Nucleic Acids Res.*, 11:7819-7831.

Chan, Y.-L., R. Gutell, H. F. Noller, and I. G. Wool. 1984. The nucleotide sequence of a rat 18S ribosomal ribonucleic acid gene and a proposal for the secondary structure of 18S ribosomal ribonucleic acid. *J. Biol. Chem.*, 259:224-230.

Chen, M.-W., J. Anné, G. Volckaert, E. Huysmans, A. Vandenberghe, and R. de Wachter. 1984. The nucleotide sequences of the 5S rRNAs of seven molds and a yeast and their use in studying ascomycete phylogeny. *Nucleic Acids Res.*, 12:4881-4892.

Christen, R., A. Ratto, A. Baroin, R. Perasso, K. G. Grell, and A. Adoutte. 1991. An analysis of the origin of metazoans, using comparisons of partial sequences of the 28S RNA, reveals an early emergence of triploblasts. *EMBO (Eur. Mol. Biol. Organ.) J.*, 10:499-503.

Chuba, P. J., R. Bock, G. Graf, T. Adam, and

U. Göbel. 1988. Comparison of 16S rRNA sequences from the family Pasteurellaceae: phylogenetic relatedness by cluster analysis. *J. Gen. Microbiol.*, 134:1923-1930.

Clark, C. G., and G. A. M. Cross. 1988. Small subunit ribosomal RNA sequence from *Naegleria gruberi* supports the polyphyletic origin of amoebas. *Mol. Biol. Evol.*, 5:512-518.

Clark, C. G., and S. A. Gerbi. 1982. Ribosomal RNA evolution by fragmentation of the 23S progenitor: Maturation pathway parallels evolutionary emergence. *J. Mol. Evol.*, 18:329-336.

Clark, C. G., B. W. Tague, V. C. Ware, and S. A. Gerbi. 1984. *Xenopus laevis* 28S ribosomal RNA: a secondary structure model and its evolutionary and functional implications. *Nucleic Acids Res.*, 12:6197-6220.

Coen, E. S., and G. A. Dover. 1983. Unequal exchanges and the coevolution of X and Y rDNA arrays in *Drosophila melanogaster*. *Cell*, 33: 849-855.

Coen, E. S., T. Strachan, and G. A. Dover. 1982. Dynamics of concerted evolution of ribosomal DNA and histone gene families in the *melanogaster* species subgroup of *Drosophila*. *J. Mol. Biol.*, 158:17-35.

Coen, E. S., J. M. Thoday, and G. A. Dover. 1982. The rate of turnover of structural variants in the ribosomal gene family of *Drosophila melanogaster*. *Nature*, 295:564-568.

Collins, M. D., S. Wallbanks, D. J. Lane, J. Shah, R. Nietupski, J. Smida, M. Dorsch, and E. Stackebrandt. 1991. Phylogenetic analysis of the genus *Listeria* based on reverse transcriptase sequencing of 16S rRNA. *Int. J. Syst. Bacteriol.*, 41:240-246.

Cooper, D. N., and J. Schmidtke. 1984. DNA restriction fragment length polymorphisms and heterozygosity in the human genome. *Hum. Genet.*, 66:1-16.

Cox, R. A., and J. M. Kelly. 1981. Mature 23 S rRNA of prokaryotes appears homologous with the precursor of 25-28 S rRNA of eukaryotes: comments on the evolution of 23-28 S rRNA. *FEBS Lett.*, 130:1-6.

Coyne, V. E., C. J. Pillidge, D. D. Sledjeski, H. Hori, B. A. Ortiz-Conde, D. G. Muir, R. M. Wiener, and R. R. Colwell. 1989. Reclassification of *Alteromonas colwelliana* to the genus *Shewanella* by DNA-DNA hybridization, serology and 5S ribosomal RNA sequence data. *Syst. Appl. Microbiol.*, 12:275-279.

Cracraft, J., and D. P. Mindell. 1989. The early history of modern birds: a comparison of molecular and morphological evidence. In B. Fernholm, K. Bremer, and H. Jornval (eds.), *The Hierarchy of Life*, pp. 389-403. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Cummings, D. J., J. M. Domenico, and J. Nelson. 1989. DNA sequence and the secondary structures of the large subunit rRNA coding regions and its two class I introns of mitochondrial DNA from *Podospora anserina*. *J. Mol. Evol.*, 28:242-255.

Cummings, D. J., J. M. Domenico, J. Nelson, and M. L. Sogin. 1989. DNA sequence, structure, and phylogenetic relationship of the small subunit rRNA coding region of mitochondrial DNA from *Podospora anserina*. *J. Mol. Evol.*, 28: 232-241.

Curtiss, W. C., and J. N. Vournakis. 1984. Quantitation of base substitutions in eukaryotic 5S rRNA: selection for the maintenance of RNA secondary structure. *J. Mol. Evol.*, 20:351-361.

Dams, E., E. Huysmans, A. Vandenberghe, and R. de Wachter. 1987. Structure of Clostridial 5 S ribosomal RNAs and bacterial evolution. *Syst. Appl. Microbiol.*, 9:54-61.

Dams, E., L. Hendriks, Y. Van de Peer, J.-M. Neefs, G. Smits, I. Vandenbempt, and R. de Wachter. 1988. Compilation of small ribosomal subunit RNA sequences. *Nucleic Acids Res.*, 16:r87-r173.

Dekio, S., R. Yamasaki, J. Jidoi, H. Hori, and S. Osawa. 1984. Secondary structure and phylogeny of *Staphylococcus* and *Micrococcus* 5S rRNAs. *J. Bacteriol.*, 159:233-237.

de Ley, J., P. Segers, and M. Gillis. 1978. Intra- and intergeneric similarities of *Chromobacterium* and *Janthinobacterium* ribosomal ribonucleic acid cistrons. *Int. J. Syst. Bacteriol.*, 28:154-168.

Delihas, N., J. Anderson, W. Andresini, L. Kaufman, and H. Lyman. 1981. The 5S ribosomal RNA of *Euglena gracilis* cytoplasmic ribosomes is closely homologous to the 5S RNA of the trypanosomatid protozoa. *Nucleic Acids Res.*, 9: 6627-6633.

Demharter, W., R. Hensel, J. Smida, and E. Stackebrandt. 1989. *Sphaerobacter thermophilus* gen. nov., sp. nov. a deeply rooting member of the actinomycetes subdivision isolated from thermophilically treated sewage sludge. *Syst. Appl. Microbiol.*, 11:261-266.

Deming, J. W., H. Hada, R. R. Colwell, K. R. Luehrsen, and G. E. Fox. 1984. The ribonucleotide sequence of 5S rRNA from two strains of deep-sea barophilic bacteria. *J. Gen. Microbiol.*, 130:1911-1920.

Deming, J. W., L. K. Somers, W. L. Straube, D. G. Swartz, and M. T. MacDonell. 1988. Isolation of an obligately barophilic bacterium and description of a new genus, *Colwellia* gen. nov. *Syst. Appl. Microbiol.*, 10:152-160.

de Sá, R. O., and D. M. Hillis. 1990. Phylogenetic

relationships of the pipid frogs *Xenopus* and *Silurana*: an integration of ribosomal DNA and morphology. *Mol. Biol. Evol.*, 7:365-376.

DeSalle, R., T. Freedman, E. M. Prager, and A. C. Wilson. 1987. Tempo and mode of sequence evolution in mitochondrial DNA of Hawaiian *Drosophila*. *J. Mol. Evol.*, 26:157-164.

de Smedt, J., and J. de Ley. 1977. Intra- and intergeneric similarities of *Agrobacterium* ribosomal ribonucleic acid cistrons. *Int. J. Syst. Bacteriol.*, 27:222-240.

de Smedt, J., M. Bauwens, R. Tytgat, and J. de Ley. 1980. Intra- and intergeneric similarities of ribosomal ribonucleic acid cistrons of free-living, nitrogen-fixing bacteria. *Int. J. Syst. Bacteriol.*, 30:106-122.

Devereux, R., A. R. Loeblich III, and G. E. Fox. 1990. Higher plant origins and the phylogeny of green algae. *J. Mol. Evol.*, 31:18-24.

Devereux, R., M. Delaney, F. Widdel, and D. A. Stahl. 1989. Natural relationships among sulfate-reducing eubacteria. *J. Bacteriol.*, 171: 6689-6695.

Devereux, R., S.-H. He, C. L. Doyle, S. Orkland, D. A. Stahl, J. LeGall, and W. B. Whitman. 1990. Diversity and origin of *Desulfovibrio* species: phylogenetic definition of a family. *J. Bacteriol.*, 172:3609-3619.

Dewhirst, F. E., B. J. Paster, and P. L. Bright. 1989. *Chromobacterium, Eikenella, Kingella, Neisseria, Simonsiella*, and *Vitreoscilla* species comprise a major branch of the beta group *Proteobacteria* by 16S ribosomal ribonucleic acid sequence comparison: transfer of *Eikenella* and *Simonsiella* to the family *Neisseriaceae* (emend.). *Int. J. Syst. Bacteriol.*, 39:258-266.

Dewhirst, F. E., B. J. Paster, S. La Fontaine, and J. I. Rood. 1990. Transfer of *Kingella indologenes* (Snell and Lapage 1976) to the genus *Suttonella* gen. nov. as *Suttonella indologenes* comb. nov.; transfer of *Bacteroides nodosus* (Beveridge 1941) to the genus *Dichelobacter* gen. nov. as *Dichelobacter nodosus* comb. nov.; and assignment of the genera *Cardiobacterium, Dichelobacter*, and *Suttonella* to *Cardiobacteriaceae* fam. nov. in the Gamma division of *Proteobacteria* on the basis of 16S rRNA sequence comparisons. *Int. J. Syst. Bacteriol.*, 40:426-433.

Distel, D. L., D. J. Lane, G. J. Olsen, S. J. Giovannoni, B. Pace, N. R. Pace, D. A. Stahl, and H. Felbeck. 1988. Sulfur-oxidizing bacterial endosymbionts: analysis of phylogeny and specificity by 16S rRNA sequences. *J. Bacteriol.*, 170:2506-2510.

Doolittle, W. F., C. R. Woese, M. L. Sogin, L. Bonen, and D. Stahl. 1975. Sequence studies on 16S ribosomal RNA from blue green alga. *J. Mol. Evol.*, 4:307-315.

Döpfer, H., E. Stackebrandt, and F. Fiedler. 1982. Nucleic acid hybridization studies on *Microbacterium, Curtobacterium, Agromyces* and related taxa. *J. Gen. Microbiol.*, 128:1687-1708.

Dorfman, D. M., M. J. Lenardo, L. V. Reddy, L. H. T. Van der Ploeg, and J. E. Donelson. 1985. The 5.8S ribosomal RNA gene of *Trypanosoma brucei*: structural and transcriptional studies. *Nucleic Acids Res.*, 13:3533-3549.

Dover, G. 1982a. A molecular drive through evolution. *BioScience*, 32:526-533.

———. 1982b. Molecular drive: a cohesive mode of species evolution. *Nature*, 299:111-117.

Dover, G., and E. Coen. 1981. Springcleaning ribosomal DNA: a model for multigene evolution? *Nature*, 290:731-732.

Dowling, T. E., C. Moritz, and J. D. Palmer. 1990. Nucleic acids II: restriction site analysis. In D. M. Hillis and C. Moritz (eds.), *Molecular Systematics*, pp. 250-317. Sinauer Associates, Sunderland.

Dunon-Bluteau, D., and G. Brun. 1986. The secondary structures of the *Xenopus laevis* and human mitochondrial small ribosomal subunit are similar. *FEBS Lett.*, 198:333-338.

Ebel, J.-P., C. Branlant, P. Carbon, B. Ehresmann, C. Ehresmann, A. Krol, and P. Stiegler. 1983. Sequence and secondary structure conservation in ribosomal RNAs in the course of evolution. In B. Pullman and J. Jortner (eds.), *Nucleic Acids: The Vectors of Life*, pp. 387-401. D. Reidel, Dordrecht.

Eden, P. A., T. M. Schmidt, R. P. Blakemore, and N. R. Pace. 1991. Phylogenetic analysis of *Aquaspirillum magnetotacticum* using polymerase chain reaction-amplified 16S rRNA-specific DNA. *Int. J. Syst. Bacteriol.*, 41:324-325.

Edman, J. C., J. A. Kovaks, H. Masur, D. V. Santi, H. J. Elwood, and M. L. Sogin. 1988. Ribosomal RNA sequence shows *Pneumocystis carinii* to be a member of the Fungi. *Nature*, 334: 519-522.

Ehlers, R.-U., U. Wyss, and E. Stackebrandt. 1988. 16S rRNA cataloguing and the phylogenetic position of the genus *Xenorhabdus*. *Syst. Appl. Microbiol.*, 10:121-125.

Ellis, R. E., J. E. Sulston, and A. R. Coulson. 1986. The rDNA of *C. elegans*: sequence and structure. *Nucleic Acids Res.*, 14:2345-2367.

Elwood, H. J., G. J. Olsen, and M. L. Sogin. 1985. The small-subunit ribosomal RNA gene sequences from the hypotrichous ciliates *Oxytricha nova* and *Stylonychia pustulata*. *Mol. Biol. Evol.*, 2:399-410.

Embley, M. T., J. Smida, and E. Stackebrandt. 1988a. The phylogeny of Mycolate-less wall chemotype IV actinomycetes and description of *Pseudocardiaceae* fam. nov. *Syst. Appl. Microbiol.*,

11:44-52.

———, ———, and ———. 1988b. Reverse transcriptase sequencing of 16S ribosomal RNA from *Faenia rectivirgula, Pseudonocardia thermophila* and *Saccharopolyspora hirsuta*, three wall type IV actinomycetes which lack mycolic acids. *J. Gen. Microbiol.*, 134:961-966.

Enea, V., and V. Corredor. 1991. The evolution of plasmodial stage specific rRNA genes is dominated by gene conversion. *J. Mol. Evol.*, 32:183-186.

Erdmann, V. A., J. Wolters, E. Huysmans, and R. de Wachter. 1985. Collection of published 5S, 5.8S and 4.5 S ribosomal RNA sequences. *Nucleic Acids Res.*, 9:r105-r153.

Erwin, D. H. 1991. Metazoan phylogeny and the Cambrian radiation. *Trends Ecol. & Evol.*, 6: 131-134.

Eschbach, S., J. Wolters, and P. Sitte. 1991. Primary and secondary structure of the nuclear small subunit ribosomal RNA of the cryptomonad *Pyrenomonas salina* as inferred from the gene sequence: evolutionary implications. *J. Mol. Evol.*, 32:247-252.

Evrard, J. L., M. Kuntz, and J. H. Weil. 1990. The nucleotide sequence of five ribosomal protein genes from the *Cyanophora paradoxa*: implications concerning the phylogenetic relationship between *Cyanelles* and chloroplasts. *J. Mol. Evol.*, 30:16-25.

Field, K. G., G. J. Olsen, S. J. Giovannoni, E. C. Raff, N. R. Pace, and R. A. Raff. 1989. Response to comments on Field et al., 1988. *Science*, 243:550-551.

Field, K. G., G. J. Olsen, D. J. Lane, S. J. Giovannoni, M. T. Ghiselin, E. C. Raff, N. R. Pace, and R. A. Raff. 1988. Molecular phylogeny of the animal kingdom. *Science*, 239:748-753.

Flavell, R. B., and M. O'Dell. 1979. The genetic control of nucleolus formation in wheat. *Chromosoma*, 71:135-152.

Forget, B. G., and S. M. Weissman. 1969. The nucleotide sequence of ribosomal 5 S ribonucleic acid from KB cells. *J. Biol. Chem.*, 244: 3148-3165.

Fowler, V. J., N. Pfennig, W. Schubert, and E. Stackebrandt. 1984. Towards a phylogeny of phototrophic purple sulfur bacteria—16S rRNA oligonucleotide cataloguing of 11 species of Chromatiaceae. *Arch. Microbiol.*, 139:382-387.

Fox, G. E., and C. R. Woese. 1975. 5S RNA secondary structure. *Nature*, 256:505-507.

Fox, G. E., K. R. Leuhrsen, and C. R. Woese. 1982. Archaebacterial 5 S ribosomal RNA. *Zentralbl. Bakteriol. Mikrobiol. Hyg. Abt. 1 Orig.*, C3: 330-345.

Fox, G. E., K. R. Pechman, and C. R. Woese. 1977. Comparative cataloging of 16S ribosomal ribonucleic acid: molecular approach to procaryotic systematics. *Int. J. Syst. Bacteriol.*, 27:44-57.

Fox, G. E., L. J. Magrum, W. E. Balch, R. S. Wolfe, and C. R. Woese. 1977. Classification of methanogenic bacteria by 16S ribosomal RNA characterization. *Proc. Natl. Acad. Sci. USA*, 74:4537-4541.

Fox, G. E., E. Stackebrandt, R. B. Hespell, J. Gibson, J. Maniloff, T. A. Dyer, R. S. Wolfe, W. E. Balch, R. S. Tanner, L. J. Magrum, L. B. Zablen, R. Blakemore, R. Gupta, L. Bonen, B. J. Lewis, D. A. Stahl, K. R. Luehrsen, K. N. Chen, and C. R. Woese. 1980. The phylogeny of prokaryotes. *Science*, 209:457-463.

Fox, K. F., and A. Brown. 1989. Partial sequence analysis of the 16S-rRNA of Legionellae: taxonomic implications. *Syst. Appl. Microbiol.*, 11: 135-139.

Fox, K. F., A. Brown, A. Fox, and G. Schnitzer. 1991. *Tatlockia*, a genetically and chemically distinct group of bacteria. Proposal to transfer *Legionella maceachernii* (Brenner et al.) to the genus *Tatlockia*, as *Tatlockia maceachernii* comb. nov. *Syst. Appl. Microbiol.*, 14:52-56.

Franzmann, P. D., U. Wehmeyer, and E. Stackebrandt. 1988. *Halomonadaceae* fam. nov., a new family of the class *Proteobacteria* to accommodate the genera *Halomonas* and *Deleya*. *Syst. Appl. Microbiol.*, 11:16-19.

Franzmann, P. D., E. Stackebrandt, K. Sanderson, J. K. Volkman, D. E. Cameron, P. L. Stevenson, T. A. McMeekin, and H. R. Burton. 1988. *Halobacterium lacusprofundi* sp. nov., a halophilic bacterium isolated from Deep Lake, Antarctica. *Syst. Appl. Microbiol.*, 11:20-27.

Furlong, J. C., and B. E. H. Maden. 1983. Patterns of major divergence between the internal transcribed spacers of ribosomal DNA in *Xenopus borealis* and *Xenopus laevis*, and of minimal divergence within ribosomal coding regions. *EMBO (Eur. Mol. Biol. Organ.) J.*, 2:443-448.

Georgiev, O. I., N. Nikolaev, A. A. Hadjiolov, K. G. Skryabin, V. M. Zakharyev, and A. A. Bayev. 1981. The structure of the ribosomal RNA genes. 4. Complete sequence of the 25 S rRNA gene from *Saccharomyces cerevisiae*. *Nucleic Acids Res.*, 9:6953-6958.

Gerbi, S. A. 1985. Evolution of ribosomal DNA. In R. J. MacIntyre (ed.), *Molecular Evolutionary Genetics*, pp. 419-517. Plenum Press, New York.

———. 1986. The evolution of eukaryotic ribosomal DNA. *BioSystems*, 19:247-258.

Ghiselin, M. T. 1988. The origin of molluscs in

light of molecular evidence. *Oxf. Surv. Evol. Biol.*, 5:66-95.

———. 1989. Summary of our present knowledge of metazoan phylogeny. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 261-272. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Gibson, J., W. Ludwig, E. Stackebrandt, and C. R. Woese. 1985. The phylogeny of the green photosynthetic bacteria: absence of a close relationship between *Chlorobium* and *Chloroflexus*. *Syst. Appl. Microbiol.*, 6:152-156.

Gibson, J., E. Stackebrandt, L. B. Zablen, R. Gupta, and C. R. Woese. 1979. A phylogenetic analysis of the purple photosynthetic bacteria. *Curr. Microbiol.*, 3:59-64.

Gillis, M., and J. de Ley. 1980. Intra- and intergeneric similarities of the ribosomal ribonucleic acid cistrons of *Acetobacter* and *Gluconobacter*. *Int. J. Syst. Bacteriol.*, 30:7-27.

Giovannoni, S. J., S. Turner, G. J. Olsen, S. Barns, D. J. Lane, and N. R. Pace. 1988. Evolutionary relationships among cyanobacteria and green chloroplasts. *J. Bacteriol.*, 170:3584-3592.

Glotz, C., and R. Brimacombe. 1980. An experimentally-derived model for the secondary structure of the 16S ribosomal RNA from *Escherichia coli*. *Nucleic Acids Res.*, 8:2377-2395.

Gomez, E., A. M. Valdes, D. Piñero, and R. Hernandez. 1991. What is a genus in the Trypanosomatidae family? Phylogenetic analysis of two small rRNA sequences. *Mol. Biol. Evol.*, 8:254-259.

Gonzalez, I. L., J. E. Sylvester, T. F. Smith, D. Stambolian, and R. D. Schmickel. 1990. Ribosomal RNA gene sequences and hominoid phylogeny. *Mol. Biol. Evol.*, 7:203-219.

Gonzalez, I. L., J. L. Gorski, T. J. Campen, D. J. Dorney, J. M. Erickson, J. E. Sylvester, and R. D. Schmickel. 1985. Variation among human 28S ribosomal RNA genes. *Proc. Natl. Acad. Sci. USA*, 82:7666-7670.

Gorski, J. L., I. L. Gonzalez, and R. D. Schmickel. 1987. The secondary structure of human 28S rRNA: the structure and evolution of a mosaic rRNA gene. *J. Mol. Evol.*, 24:236-251.

Gottschalk, M., and P. A. Blanz. 1984. Highly conserved 5S ribosomal RNA sequences in four rust fungi and atypical 5S rRNA secondary structure in *Microstroma juglandis*. *Nucleic Acids Res.*, 12:3951-3958.

———, and ———. 1985. Untersuchungen und 5S ribosomalen ribonukleinsaeuren als beitrag zur klaerung von systematik und phylogenic der basidiomyceten. *Z. Mykol.*, 51:205-255.

Gouy, M., and W.-H. Li. 1989a. Phylogenetic analysis based on rRNA sequences supports the archaebacterial rather than the eocyte tree. *Nature*, 339:145-147.

———, and ———. 1989b. Molecular phylogeny of the kingdoms Animalia, Plantae and Fungi. *Mol. Biol. Evol.*, 6:109-122.

Grant, D. M., and A. M. Lambowitz. 1982. Mitochondrial ribosomal RNA genes. In H. Busch and L. Rothblum (eds.), *The Cell Nucleus: rDNA*, Vol. X, Part A, pp. 387-408. Academic Press, New York.

Gray, M. W., and D. F. Spencer. 1981. Is wheat mitochondrial 5S ribosomal RNA prokaryotic in nature? *Nucleic Acids Res.*, 95:3523-3529.

Gray, M. W., D. Sankoff, and R. J. Cedergren. 1984. On the evolutionary descent of organisms and organelles: a global phylogeny based on a highly conserved structural core in small subunit ribosomal RNA. *Nucleic Acids Res.*, 12:5837-5852.

Guadet, J., J. Julien, J. F. Lafay, and Y. Brygoo. 1989. Phylogeny of some *Fusarium* species, as determined by large-subunit rRNA sequence comparison. *Mol. Biol. Evol.*, 6:227-242.

Guého, E., C. P. Kurtzman, and S. W. Peterson. 1990. Phylogenetic relationships among species of *Sterigmatomyces* and *Fellomyces* as determined from partial rRNA sequences. *Int. J. Syst. Bacteriol.*, 40:60-65.

Gunderson, J. H., T. F. McCutchan, and M. L. Sogin. 1986. Sequence of the small subunit ribosomal RNA gene expressed in the bloodstream stages of *Plasmodium berghei*: evolutionary implications. *J. Protozool.*, 33:525-529.

Gunderson, J. H., H. Elwood, A. Ingold, K. Kindle, and M. L. Sogin. 1987. Phylogenetic relationships between chlorophytes, chrysophytes, and oomycetes. *Proc. Natl. Acad. Sci. USA*, 84:5823-5827.

Gunderson, J. H., M. L. Sogin, G. Wollett, M. Hollingdale, V. F. de la Cruz, A. P. Waters, and T. F. McCutchan. 1987. Structurally distinct, stage-specific ribosomes occur in *Plasmodium*. *Science*, 238:933-937.

Gupta, R., J. M. Lanter, and C. R. Woese. 1983. Sequence of the 16S ribosomal RNA from *Halobacterium volcanii*, an archaebacterium. *Science*, 221:656-659.

Gutell, R. R., and G. E. Fox. 1988. A compilation of large subunit RNA sequences presented in a structural format. *Nucleic Acids Res.*, 16:r175-r269.

Gutell, R. R., M. N. Schnare, and M. W. Gray. 1990. A compilation of large subunit (23S-like) ribosomal RNA sequences presented in a secondary structure format. *Nucleic Acids Res.*, 18s:2319-2330.

Hadjiolov, A. A., O. I. Georgiev, V. V. Nosikov, and L. P. Yavachev. 1984. Primary and secondary structure of rat 28S ribosomal RNA.

Nucleic Acids Res., 12:3677-3693.

Hahn, D., M. P. Lechevalier, A. Fischer, and E. Stackebrandt. 1989. Evidence for a close phylogenetic relationship between members of the genera *Frankia, Geodermatophilus*, and *"Blastococcus"* and emdendation of the family *Frankiaceae. Syst. Appl. Microbiol.*, 11:236-242.

Halanych, K. M. 1991. 5S ribosomal RNA sequences inappropriate for phylogenetic reconstruction. *Mol. Biol. Evol.*, 8:249-253.

Hall, L. M. C., and B. E. H. Maden. 1980. Nucleotide sequence through the 18S-28S intergene region of a vertebrate ribosomal transcription unit. *Nucleic Acids Res.*, 8:5993-6005.

Hamby, R. K., and E. A. Zimmer. 1988. Ribosomal RNA sequences for inferring phylogeny within the grass family (Poaceae). *Plant Syst. Evol.*, 160:29-37.

Hancock, J. M., and G. A. Dover. 1988. Molecular coevolution among cryptically simple expansion segments of eukaryotic 26S/28S rRNAs. *Mol. Biol. Evol.*, 5:377-391.

Hancock, J. M., D. Tautz, and G. A. Dover. 1988. Evolution of the secondary structures and compensatory mutations of the ribosomal RNAs of *Drosophila melanogaster. Mol. Biol. Evol.*, 5: 393-414.

Hariharan, N., and J. D. Padayatty. 1987. Ribosomal RNA gene repeat units in rice embryos. *Indian J. Biochem. Biophys.*, 24:157-164.

Hariharan, N., P. S. Reddy, and J. D. Padayatty. 1987. 5S-rRNA genes in rice embryos. *Plant Mol. Biol.*, 9:443-451.

Hart, R. P., and W. R. Folk. 1982. Structure and organization of a mammalian 5 S gene cluster. *J. Biol. Chem.*, 257:11706-11711.

Hartmann, R. K., J. Wolters, B. Kröger, S. Schultze, T. Specht, and V. A. Erdmann. 1989. Does *Thermus* represent another deep eubacterial branching? *Syst. Appl. Microbiol.*, 11: 243-249.

Hasegawa, M., Y. Iida, T. Yano, F. Takaiwa, and M. Iwabuchi. 1985. Phylogenetic relationships among eukaryotic kingdoms inferred from ribosomal RNA sequences. *J. Mol. Evol.*, 22:32-38.

Hassouna, N., B. Michot, and J.-P. Bachellerie. 1984. The complete nucleotide sequence of mouse 28S rRNA gene. Implications for the process of size increase of the large subunit rRNA in higher eukaryotes. *Nucleic Acids Res.*, 12:3563-3583.

Hedges, S. B., K. D. Moberg, and L. R. Maxson. 1990. Tetrapod phylogeny inferred from 18S and 28S ribosomal RNA sequences and a review of the evidence for amniote relationships. *Mol. Biol. Evol.*, 7:607-633.

Henderson, A. S., E. M. Eicher, M. T. Yu, and K. C. Atwood. 1976. Variations in RNA gene number in mouse chromosomes. *Cytogenet. Cell Genet.*, 17:307-316.

Hendriks, L., E. Huysmans, A. Vandenberghe, and R. de Wachter. 1986. Primary structures of the 5S ribosomal RNAs of 11 arthropods and applicability of 5S RNA to the study of metazoan evolution. *J. Mol. Evol.*, 24:103-109.

Hendriks, L., R. de Baere, Y. Van De Peer, J. Neefs, and A. Goris. 1991. The evolutionary position of the rhodophyte *Porphyra umbilicalis* and the basidiomycete *Leucosporidium scottii* among other eucaryotes as deduced from complete sequences of small ribosomal subunit RNA. *J. Mol. Evol.*, 32:167-177.

Hendriks, L., C. Van Broeckhoven, A. Vandenberghe, Y. Van De Peer, and R. de Wachter. 1988. Primary and secondary structure of the 18S ribosomal RNA of the bird spider *Eurypelma californica* and evolutionary relationships among eukaryotic phyla. *Eur. J. Biochem.*, 177: 15-20.

Herzog, M., and L. Maroteaux. 1986. Dinoflagellate 17S rRNA sequence inferred from the gene sequence: evolutionary implications. *Proc. Natl. Acad. Sci. USA*, 83:8644-8648.

Hespell, R. B., B. J. Paster, T. J. Macke, and C. R. Woese. 1984. The origin and phylogeny of the bdellovibrios. *Syst. Appl. Microbiol.*, 5: 196-203.

Hillis, D. M. 1987. Molecular versus morphological approaches to systematics. *Annu. Rev. Ecol. Syst.*, 18:23-42.

———. 1991. The phylogeny of amphibians: current knowledge and the role of cytogenetics. In D. M. Green and S. K. Sessions (eds.), *Amphibian Cytogenetics and Evolution*, pp. 7-31. Academic Press, New York.

Hillis, D. M., and S. K. Davis. 1986. Evolution of ribosomal DNA: fifty million years of recorded history in the frog genus *Rana. Evolution*, 40: 1275-1288.

———, and ———. 1987. Evolution of the 28S ribosomal RNA gene in anurans: regions of variability and their phylogenetic implications. *Mol. Biol. Evol.*, 4:117-125.

———, and ———. 1988. Ribosomal DNA: intraspecific polymorphism, concerted evolution, and phylogeny reconstruction. *Syst. Zool.*, 37:63-66.

Hillis, D. M., and M. T. Dixon. 1989. Vertebrate phylogeny: evidence from 28S ribosomal DNA sequences. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 355-367. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Hillis, D. M., and C. Moritz. 1990. An overview of applications of molecular systematics. In

D. M. Hillis and C. Moritz (eds.), *Molecular Systematics*, pp. 502-515. Sinauer Associates, Sunderland.

Hillis, D. M., M. T. Dixon, and L. K. Ammerman. 1991. The relationships of the coelacanth *Latimeria chalumnae*: evidence from sequences of vertebrate 28S ribosomal RNA genes. *Envir. Biol. Fishes*, 32:119-130.

Hillis, D. M., A. Larson, S. K. Davis, and E. A. Zimmer. 1990. Nucleic Acids III: sequencing. In D. M. Hillis and C. Moritz (eds.), *Molecular Systematics*, pp. 318-370. Sinauer Associates, Sunderland.

Hillis, D. M., C. Moritz, C. A. Porter, and R. J. Baker. 1991. Evidence for biased gene conversion in concerted evolution of ribosomal DNA. *Science*, 251:308-310.

Hinnebusch, A. G., L. C. Klotz, R. L. Blanken, and A. R. Loeblich III. 1981. An evaluation of the phylogenetic position of the dinoflagellate *Crypthecodinium cohnii* based on 5S rRNA characterization. *J. Mol. Evol.*, 17:334-347.

Hixson, J. E., and W. M. Brown. 1986. A comparison of the small ribosomal RNA genes from the mitochondrial DNA of the great apes and humans: sequence, structure, evolution, and phylogenetic implications. *Mol. Biol. Evol.*, 3: 1-18.

Hofman, J. D., R. H. Lau, and W. F. Doolittle. 1979. The number, physical organization and transcription of ribosomal RNA cistrons in an archaebacterium: *Halobacterium halobium*. *Nucleic Acids Res.*, 7:1321-1333.

Hori, H., and S. Osawa. 1979. Evolutionary change in 5S RNA secondary structure and a phylogenetic tree of 54 5S RNA species. *Proc. Natl. Acad. Sci. USA*, 76:381-385.

———, and ———. 1986. Evolutionary change in 5S rRNA secondary structure and a phylogenetic tree of 352 5S RNA species. *BioSystems*, 19:163-172.

———, and ———. 1987. Origin and evolution of organisms as deduced from 5S ribosomal RNA sequences. *Mol. Biol. Evol.*, 4:445-472.

Hori, H., B.-L. Lim, and S. Osawa. 1985. Evolution of green plants as deduced from 5S rRNA sequences. *Proc. Natl. Acad. Sci. USA*, 82:820-823.

Hori, H., S. Osawa, F. Takaiwa, and M. Sugiura. 1984. The nucleotide sequence of 5S rRNAs from a fern *Dryopteris acuminata* and a horsetail *Equisetum arvense*. *Nucleic Acids Res.*, 12:1573-1576.

Hoshikawa, Y., Y. Iida, and M. Iwabuchi. 1983. Nucleotide sequence of the transcriptional initiation region of *Dictyostelium discoideum* rRNA gene and comparison of the initiation regions of three lower eukaryotes' genes. *Nucleic Acids Res.*, 11:1725-1734.

Huss, V. A. R., and M. L. Sogin. 1990. Phylogenetic position of some *Chlorella* species within the Chloroccales based upon complete small subunit ribosomal RNA sequences. *J. Mol. Evol.*, 31:432-442.

Huysmans, E., and R. de Wachter. 1987. Compilation of small ribosomal subunit RNA sequences. *Nucleic Acids Res.*, 14s:r73-r118.

Huysmans, E., E. Dams, A. Vandenberghe, and R. de Wachter. 1983. The nucleotide sequences of the 5S rRNAs of four mushrooms and their use in studying the phylogenetic position of basidiomycetes among the eukaryotes. *Nucleic Acids Res.*, 11:2871-2880.

Jacobs, H. T., D. J. Elliott, V. B. Math, and A. Farquharson. 1988. Nucleotide sequence and gene organization of sea urchin mitochondrial DNA. *J. Mol. Biol.*, 202:185-217.

Jacq, B. 1981. Sequence homologies between eukaryotic 5.8S rRNA and the 5' end of prokaryotic 23S rRNA: evidences for a common evolutionary origin. *Nucleic Acids Res.*, 9:2913-2932.

Jarsch, M., and A. Böck. 1985. Sequence of the 16S ribosomal RNA gene from *Methanococcus vannielii*: evolutionary implications. *Syst. Appl. Microbiol.*, 6:54-59.

Johansen, T., S. Johansen, and F. B. Haugli. 1988. Nucleotide sequence of the *Physarum polycephalum* small subunit ribosomal RNA as inferred from the gene sequence: secondary structure and evolutionary implications. *Curr. Genet.*, 14:265-273.

Johnson, A. M., S. Illana, P. Hakendorf, and P. R. Baverstock. 1988. The phylogenetic relationships of the apicocomplexan protist *Sarocystis* as determined by small subunit ribosomal RNA comparison. *J. Parasitol.*, 74:847-860.

Johnson, A. M., P. J. Murray, S. Illana, and P. R. Baverstock. 1987. Rapid nucleotide sequence analysis of the small subunit ribosomal RNA of *Toxoplasma gondii*: evolutionary implications for the Apicomplexa. *Mol. Biochem. Parasitol.*, 25: 239-246.

Johnson, A. M., A. Thanou, P. F. L. Boreham, and P. R. Baverstock. 1989. *Blastocystis hominis*: phylogenetic affinities determined by rRNA sequence comparison. *Exp. Parasitol.*, 68:283-288.

Johnson, J. L., and B. S. Francis. 1975. Taxonomy of the Clostridia: ribosomal ribonucleic acid homologies among the species. *J. Gen. Microbiol.*, 88:229-244.

Jupe, E. R., R. L. Chapman, and E. A. Zimmer. 1988. Nuclear ribosomal RNA genes and algal phylogeny—the *Chlamydomonas* example. *BioSystems*, 21:223-230.

Katoh, K., H. Hori, and S. Osawa. 1983. The

nucleotide sequences of 5S ribosomal RNAs from four bryophyta-species. *Nucleic Acids Res.*, 11:5671-5674.

Kim, W., and L. G. Abele. 1990. Molecular phylogeny of selected decapod crustaceans based on 18S rRNA nucleotide sequences. *J. Crustacean Biol.*, 10:1-13.

Kimura, M., and T. Ohta. 1973. Eukaryotes-prokaryotes divergence estimated by 5.8S ribosomal RNA sequences. *Nature New Biol.*, 243: 199-200.

King, L. M., and B. A. Schaal. 1989. Ribosomal-DNA variation and distribution in *Rudbeckia missouriensis*. *Evolution*, 43:1117-1119.

Kistler, H. C., P. W. Bosland, U. Benny, S. Leong, and P. H. Williams. 1987. Relatedness of strains of *Fusarium oxysporum* from crucifers measured by examination of mitochondrial and ribosomal DNA. *Genetics*, 77:1289-1293.

Kjems, J., and R. A. Garrett. 1990. Secondary structural elements exclusive to the sequences flanking ribosomal RNAs lend support to the monophyletic nature of the archaebacteria. *J. Mol. Evol.*, 31:25-32.

Kjems, J., R. A. Garrett, and W. Ansorge. 1987. The sequence of the 16S RNA gene and its flanking region from the archaebacterium *Desulfurococcus mobilis*. *Syst. Appl. Microbiol.*, 9:22-28.

Klein, B. K., P. Forman, Y. Shiomi, and D. Schlessinger. 1984. Electron microscopy of secondary structure in partially denatured *Escherichia coli* 16S rRNA and 30S subunits. *Biochemistry*, 23: 3927-3933.

Klenk, H.-P., B. Haas, V. Schwass, and W. Zillig. 1986. Hybridization homology: a new parameter for the analysis of phylogenetic relations, demonstrated with the urkingdom of the archaebacteria. *J. Mol. Evol.*, 24:167-173.

Kobayashi, M., T. Seki, K. Yaginuma, and K. Koike. 1981. Nucleotide sequences of small ribosomal RNA and adjacent transfer RNA genes in rat mitochondrial DNA. *Gene*, 16:297-307.

Köchel, H. G., and H. Küntzel. 1982. Mitochondrial L-rRNA from *Aspergillus nidulans*: potential secondary structure and evolution. *Nucleic Acids Res.*, 10:4795-4801.

Kocher, T. D., W. K. Thomas, A. Meyer, S. V. Edwards, S. Paabo, F. X. Villablanca, and A. C. Wilson. 1989. Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. *Proc. Natl. Acad. Sci. USA*, 86:6196-6200.

Kohorn, B. D., and P. M. M. Rae. 1982. Non-transcribed spacer sequences promote *in vitro* transcription of *Drosophila* ribosomal DNA. *Nucleic Acids Res.*, 10:6879-6886.

———, and ———. 1983. Localization of DNA sequences promoting RNA polymerase I activity in *Drosophila*. *Proc. Natl. Acad. Sci. USA*, 80: 3265-3268.

Komiya, H., and S. Takemura. 1981. The nucleotide sequence of 5S ribosomal RNA from slime mold *Physarum polycephalum*. *J. Biochem.*, 90: 1577-1581.

Komiya, H., M. Hasegawa, and S. Takemura. 1983. Nucleotide sequences of 5S rRNAs from sponge *Halichondria japonica* and tunicate *Halocynthia roretzi* and their phylogenetic positions. *Nucleic Acids Res.*, 11:1969-1974.

Komiya, H., N. Shimizu, M. Kawakami, and S. Takemura. 1980. Nucleotide sequence of 5S ribosomal RNA from *Lingula anatina*. *J. Biochem.*, 88:1449-1456.

Kössel, H., K. Edwards, E. Fritzsche, W. Koch, and Z. Schwarz. 1983. Phylogenetic significance of nucleotide sequence analysis. In U. Jensen and D. E. Fairbrothers (eds.), *Protein and Nucleic Acids in Plant Systematics*, pp. 36-57. Springer-Verlag, Berlin.

Kraus, F., and M. M. Miyamoto. 1991. Rapid cladogenesis among the pecoran ruminants: evidence from mitochondrial DNA sequences. *Syst. Zool.*, 40:117-130.

Krishnan, S., S. Barnabas, and J. Barnabas. 1990. Interrelationships among major protistan groups based on a parsimony network of 5S rRNA sequences. *BioSystems*, 24:135-144.

Krystal, M., P. D'Eustachio, F. H. Ruddle, and N. Arnheim. 1981. Human nucleolus organizers on nonhomologous chromosomes can share the same ribosomal gene variants. *Proc. Natl. Acad. Sci. USA*, 78:5744-5748.

Kumazaki, T., H. Hori, and S. Osawa. 1983. Phylogeny of protozoa deduced from 5S rRNA sequences. *J. Mol. Evol.*, 19:411-419.

Kumazaki, T., H. Hori, S. Osawa, N. Ishii, and K. Suzuki. 1982. The nucleotide sequence of 5S rRNAs from a rotifer, *Brachionus plicatilis*, and two nematodes, *Rhabditis tokai* and *Caenorhabditis elegans*. *Nucleic Acids Res.*, 10:7001-7004.

Kumazaki, T., H. Hori, S. Osawa, T. Mita, and T. Higashinakagawa. 1982. The nucleotide sequences of 5S rRNAs from three ciliated protozoa. *Nucleic Acids Res.*, 10:4409-4412.

Küntzel, H., and H. G. Köchel. 1981. Evolution of rRNA and origin of mitochondria. *Nature*, 293:751-755.

Küntzel, H., B. Piechulla, and U. Hahn. 1983. Consensus structure and evolution of 5S rRNA. *Nucleic Acids Res.*, 11:893-900.

Kupriyanova, N. S., T. I. Serenkova, A. M. Mazo, and M. Y. Timofeeva. 1985. Investigation of a cloned portion of the ribosomal operon

coding the 5.8S rRNA of the loach *Misgurnus fossilis* L. *Mol. Biol.*, 18:1126-1134.

Laaser, G., E. Möller, K.-D. Jahnke, G. Bahnweg, H. Prillinger, H. H. Prell. 1989. Ribosomal DNA restriction fragment analysis as a taxonomic tool in separating physiologically similar basidiomycetous yeasts. *Syst. Appl. Microbiol.*, 11:170-175.

Lachance, M.-A. 1990. Ribosomal DNA spacer variation in the cactophilic yeast *Clavispora opuntiae*. *Mol. Biol. Evol.*, 7:78-193.

La Fontaine, S., and J. I. Rood. 1990. Evidence that *Bacteroides nodosus* belongs in subgroup Gamma of the class *Proteobacteria*, not in the genus *Bacteroides*: partial sequence analysis of a *B. nodosus* 16S rRNA gene. *Int. J. Syst. Bacteriol.*, 40:154-159.

Lake, J. A. 1987. Prokaryotes and archaebacteria are not monophyletic: Rate invariant analysis of rRNA genes indicates that eukaryotes and eocytes form a monophyletic taxon. *Cold Spring Harbor Symp. Quant. Biol.*, 52:839-846.

———. 1988. Origin of the eukaryotic nucleus determined by rate-invariant analysis of rRNA sequences. *Nature*, 331:184-186.

———. 1989a. Origin of the eukaryotic nucleus determined by rate-invariant analyses of ribosomal RNA genes. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 87-101. Elsevier Science Publishers (Biomedical Division), Amsterdam.

———. 1989b. Origin of the multicellular animals. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 273-278. Elsevier Science Publishers (Biomedical Division), Amsterdam.

———. 1990. Origin of the Metazoa. *Proc. Natl. Acad. Sci. USA*, 87:763-766.

Lake, J. A., V. F. de la Cruz, P. C. G. Ferreira, C. Morel, and L. Simpson. 1988. Evolution of parasitism: kinetoplastid protozoan history reconstructed from mitochondrial rRNA gene sequences. *Proc. Natl. Acad. Sci. USA*, 85:4779-4783.

Lane, D. J., D. A. Stahl, G. J. Olsen, D. J. Heller, and N. R. Pace. 1985. A phylogenetic analysis of the genera *Thiobacillus* and *Thiomicrospira* by 5S rRNA sequences. *J. Bacteriol.*, 163:75-81.

Lane, D. J., B. Pace, G. J. Olsen, D. A. Stahl, M. L. Sogin, and N. R. Pace. 1985. Rapid determination of 16S ribosomal RNA sequences for phylogenetic analyses. *Proc. Natl. Acad. Sci. USA*, 82:6955-6959.

Larson, A. 1991. A molecular perspective on the evolutionary relationships of the salamander families. In M. K. Hecht, B. Wallace, and R. J. Macintyre (eds.), *Evolutionary Biology*, Vol. 25, pp. 211-277. Plenum Press, New York.

Larson, A., and A. C. Wilson. 1989. Patterns of ribosomal RNA evolution in salamanders. *Mol. Biol. Evol.*, 6:131-154.

Lassner, M., and J. Dvorak. 1986. Preferential homogenization between adjacent and alternate subrepeats in wheat rDNA. *Nucleic Acids Res.*, 14:5499-5512.

Lazar, E., B. Haendler, and M. Jacob. 1983. Two 5S genes are expressed in chicken somatic cells. *Nucleic Acids Res.*, 11:7735-7741.

Le, H. L. V., R. Perasso, and R. Billard. 1989. Phylogénie moléculaire préliminaire des <<poissons>> basée sur l'analyse de séquences d'ARN ribosomique 28S. *C. R. Acad. Sci. Paris*, 309: 493-498.

Learn, G. H., Jr., and B. A. Schaal. 1987. Population subdivision for ribosomal DNA repeat variants in *Clematis fremontii*. *Evolution*, 41:433-438.

Lechner, K., G. Wich, and A. Böck. 1985. The nucleotide sequence of the 16S rRNA gene and flanking regions from *Methanobacterium formicicum*: the phylogenetic relationship between methanogenic and halophilic Archaebacteria. *Syst. Appl. Microbiol.*, 6:157-163.

Leffers, H., J. Kjems, L. Østergaard, N. Larsen, and R. A. Garrett. 1987. Evolutionary relationships amongst Archaebacteria. A comparative study of 23S ribosomal RNAs of a sulphur-dependent extreme thermophile, an extreme halophile and a thermophilic methanogen. *J. Mol. Biol.*, 195:43-61.

Leinfelder, W., M. Jarsch, and A. Böck. 1985. The phylogenetic position of the sulfur-dependent Archaebacterium *Thermoproteus tenax*: sequence of the 16S rRNA gene. *Syst. Appl. Microbiol.*, 6:164-170.

Lenaers, G., L. Maroteaux, B. Michot, and M. Herzog. 1989. Dinoflagellates in evolution: a molecular phylogenetic analysis of large subunit ribosomal RNA. *J. Mol. Evol.*, 29:40-51.

Lenaers, G., H. Nielsen, J. Engberg, and M. Herzog. 1988. The secondary structure of large-subunit rRNA divergent domains, a marker for protist evolution. *BioSystems*, 21:215-222.

Lenaers, G., C. Scholin, Y. Bhaud, D. St. Hilaire, and M. Herzog. 1991. A molecular phylogeny of dinoflagellate protists (Pyrrhophyta) inferred from the sequence of the 24S rRNA divergent domains D1 and D8. *J. Mol. Evol.*, 32: 53-56.

Liebl, W., M. Ehrmann, W. Ludwig, and K. H. Schleifer. 1991. Transfer of *Brevibacterium divaricatum* DSM 20297^T, "*Brevibacterium flavum*" DSM 20411, "*Brevibacterium lactofermentum*" DSM 20412 and DSM 1412, and *Corynebacterium lilium* DSM 20137^T to *Corynebacterium glutamicum* and their distinction by rRNA gene restriction

patterns. *Int. J. Syst. Bacteriol.*, 41:255-260.

Lim, B.-L., H. Kawai, H. Hori, and S. Osawa. 1986. Molecular evolution of 5S ribosomal RNA from red and brown algae. *Jpn. J. Genet.*, 61:169-176.

Lim, P.-O., and B. B. Sears. 1989. 16S rRNA sequence indicates that plant-pathogenic mycoplasma-like organisms are evolutionarily distinct from animal mycoplasmas. *J. Bacteriol.*, 171:5901-5906.

Long, E. O., and I. B. Dawid. 1980. Repeated genes in eukaryotes. *Annu. Rev. Biochem.*, 49: 727-764.

Ludwig, W., K.-H. Schleifer, H. Reichenbach, and E. Stackebrandt. 1983. A phylogenetic analysis of the myxobacteria *Myxococcus fulvus, Stigmatella aurantiaca, Cystobacter fuscus, Sorangium cellulosum* and *Nannocystis exedens*. *Arch. Microbiol.*, 135:58-62.

Ludwig, W., K.-H. Schleifer, G. E. Fox, E. Seewaldt, and E. Stackebrandt. 1981. A phylogenetic analysis of staphylococci, *Peptococcus saccharolyticus* and *Micrococcus mucilaginosus*. *J. Gen. Microbiol.*, 125:357-366.

Lynn, D. H., and M. L. Sogin. 1988. Assessment of phylogenetic relationships among ciliated protists using partial ribosomal RNA sequences derived from reverse transcripts. *BioSystems*, 21:249-254.

MacDonell, M. T., and R. R. Colwell. 1985a. Phylogeny of the Vibrionaceae, and recommendation for two new genera, *Listonella* and *Shewanella*. *Syst. Appl. Microbiol.*, 6:171-182.

———, and ———. 1985b. Phylogeny of the *Vibrionaceae*. *Ukr. Biokhim. Zh.*, 6:171-182.

MacKay, R. M, and W. F. Doolittle. 1981. Nucleotide sequences of *Acanthamoeba castellanii* 5S and 5.8S ribosomal ribonucleic acids: phylogenetic and comparative structural analyses. *Nucleic Acids Res.*, 9:3321-3334.

MacKay, R. M., M. W. Gray, and W. F. Doolittle. 1980. Nucleotide sequence of *Crithidia fasciculata* cytosol 5S ribosomal ribonucleic acid. *Nucleic Acids Res.*, 8:4911-4917.

Maly, P., and R. Brimacombe. 1983. Refined secondary structure models for the 16S and 23S ribosomal RNA of *Escherichia coli*. *Nucleic Acids Res.*, 11:7263-7286.

Mankin, A. S., and A. M. Kopylov. 1981. A secondary model for mitochondrial 12S rRNA: an example of economy in rRNA structure. *Biochem. Int.*, 3:587-593.

Maroteaux, L., M. Herzog, and M.-O. Soyer-Gobillard. 1985. Molecular organization of dinoflagellate ribosomal DNA: evolutionary implications of the deduced 5.8S rRNA secondary structure. *BioSystems*, 18:307-319.

Mashkova, T. D., T. I. Serenkova, A. M. Mazo, T. A. Avdonina, M. Ya. Timofeyeva, and L. L. Kisselev. 1981. The primary structure of oocyte and somatic 5S rRNAs from the loach *Misgurnus fossilis*. *Nucleic Acids Res.*, 9:2141-2151.

McCarroll, R., G. J. Olsen, Y. D. Stahl, C. R. Woese, and M. L. Sogin. 1983. Nucleotide sequence of the *Dictyostelium discoideum* small-subunit ribosomal ribonucleic acid inferred from the gene sequence: evolutionary implications. *Biochemistry*, 22:5858-5868.

McCutchan, T. F., V. F. de la Cruz, A. A. Lal, J. H. Gunderson, H. J. Elwood, and M. L. Sogin. 1988. The primary sequences of the small subunit ribosomal RNA genes from *Plasmodium falciparum*. *Mol. Biochem. Parasitol.*, 28: 63-68.

McGill, T. J., J. Jurka, J. M. Sobieski, M. H. Pickett, C. R. Woese, and G. E. Fox. 1986. Characteristic archaebacterial 16S rRNA oligonucleotides. *Syst. Appl. Microbiol.*, 7:194-197.

McIntyre, C. L., B. C. Clarke, and R. Appels. 1988. DNA sequence analyses of the ribosomal spacer regions in the *Triticeae*. *Plant Syst. Evol.*, 160:91-104.

Medlin, L., H. J. Elwood, S. Stickel, and M. L. Sogin. 1988. The characterization of enzymatically amplified eukaryotic 16S-like rRNA-coding regions. *Gene*, 71:491-499.

Meyer, A., and A. C. Wilson. 1990. Origin of tetrapods inferred from their mitochondrial DNA affiliation to lungfish. *J. Mol. Evol.*, 31: 359-364.

Michel, F., and B. Dujon. 1983. Conservation of RNA secondary structures in two intron families including mitochondrial-, chloroplast-, and nuclear-encoded members. *EMBO (Eur. Mol. Biol. Organ.) J.*, 2:33-38.

Michot, B., and J.-P. Bachellerie. 1987. Comparisons of large subunit rRNAs reveal some eukaryote-specific elements of secondary structure. *Biochimie*, 69:11-23.

Michot, B., N. Hassouna, and J.-P. Bachellerie. 1984. Secondary structure of mouse 28S rRNA and general model for the folding of the large rRNA in eukaryotes. *Nucleic Acids Res.*, 12: 4259-4279.

Mindell, D. P., and R. L. Honeycutt. 1989. Variability in transcribed regions of ribosomal DNA and early divergences in birds. *Auk*, 106: 539-548.

———, and ———. 1990. Ribosomal RNA in vertebrates: evolution and phylogenetic applications. *Annu. Rev. Ecol. Syst.*, 21:541-566.

Miyamoto, M. M., and S. M. Boyle. 1989. The potential importance of mitochondrial DNA sequence data to eutherian mammal phylogeny.

In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 437-450. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Miyamoto, M. M., F. Kraus, and O. A. Ryder. 1990. Phylogeny and evolution of antlered deer determined from mitochondrial DNA sequences. *Proc. Natl. Acad. Sci. USA*, 87:6127-6131.

Miyamoto, M. M., S. M. Tanhauser, and P. J. Laipis. 1989. Systematic relationships in the artiodactyl tribe Bovini (family Bovidae) as determined from mitochondrial DNA sequences. *Syst. Zool.*, 38:342-349.

Montgomery, L., B. Flesher, and D. Stahl. 1988. Transfer of *Bacteroides succinogenes* (Hungate) to *Fibrobacter* gen. nov. as *Fibrobacter succinogenes* comb. nov. and description of *Fibrobacter intestinalis* sp. nov. *Int. J. Syst. Bacteriol.*, 38:430-435.

Moore, R. L. 1977. Ribosomal ribonucleic acid cistron homologies among *Hyphomicrobium* and various other bacteria. *Can. J. Microbiol.*, 23: 478-481.

Mordarski, M., M. Goodfellow, A. Tkacz, G. Pulverer, and K. P. Schaal. 1980. Ribosomal ribonucleic acid similarities in the classification of *Rhodococcus* and related taxa. *J. Gen. Microbiol.*, 118:313-319.

Morgan, E. A. 1982. Ribosomal RNA genes in *Escherichia coli*. In H. Busch and L. Rothblum (eds.), *The Cell Nucleus: rDNA*, Vol. X, Part A, pp. 1-29. Academic Press, New York.

Nagylaki, T. 1984. Evolution of multigene families under interchromosomal gene conversion. *Proc. Natl. Acad. Sci. USA*, 81:3796-3800.

Nagylaki, T., and T. D. Petes. 1982. Intrachromosomal gene conversion and the maintenance of sequence homogeneity among repeated genes. *Genetics*, 100:315-337.

Nairn, C. J., and R. J. Ferl. 1988. The complete nucleotide sequence of the small-subunit ribosomal RNA coding region for the cycad *Zamia pumila*: phylogenetic implications. *J. Mol. Evol.*, 27:133-141.

Nazar, R. N., T. O. Sitz, and H. Busch. 1976. Sequence homologies in mammalian 5.8S ribosomal RNA. *Biochemistry*, 15:505-508.

Neefs, J.-M., Y. Van de Peer, L. Hendriks, and R. de Wachter. 1990. Compilation of small ribosomal subunit RNA sequences. *Nucleic Acids Res.*, 18s:2237-2318.

Nelkin, B., D. Strayer, and B. Vogelstein. 1980. Divergence of primate ribosomal RNA genes as assayed by restriction enzyme analysis. *Gene*, 11:89-96.

Nelles, L., B.-L. Fang, G. Volckaert, A. Vandenberghe, and R. de Wachter. 1984. Nucleotide sequence of a crustacean 18S ribosomal RNA gene and secondary structure of eukaryotic small subunit ribosomal RNAs. *Nucleic Acids Res.*, 12:8749-8768.

Nelson, D. W., and B. M. Honda. 1985. Genes coding for 5S ribosomal RNA of the nematode *Caenorhabditis elegans*. *Gene*, 38:245-251.

Nevo, E., and A. Beiles. 1988. Ribosomal DNA non-transcribed spacer polymorphism in subterranean mole rats: genetic differentiation, environmental correlates and phylogenetic relationships. *Evol. Ecol.*, 2:139-156.

Nickrent, D. L., and C. R. Franchina. 1990. Phylogenetic relationships of the Santalales and relatives. *J. Mol. Evol.*, 31:294-301

Nishikawa, K., and S. Takemura. 1974. Nucleotide sequence of 5 S RNA from *Torulopsis utilis*. *FEBS Lett.*, 40:106-109.

Noller, H. F. 1984. Structure of ribosomal RNA. *Annu. Rev. Biochem.*, 53:119-162.

Noller, H. F., and C. R. Woese. 1981. Secondary structure of 16S ribosomal RNA. *Science*, 212: 403-411.

Noller, H. F., J. Kop, V. Wheaton, J. Brosius, R. R. Gutell, A. M. Kopylov, F. Dohme, W. Herr, D. A. Stahl, R. Gupta, and C. R. Woese. 1981. Secondary structure model for 23S ribosomal RNA. *Nucleic Acids Res.*, 9:6167-6189.

Ohama, T., H. Hori, and S. Osawa. 1983. The nucleotide sequence of 5S rRNAs from a sea-cucumber, a starfish and a sea-urchin. *Nucleic Acids Res.*, 11:5181-5184.

Ohama, T., T. Kumazaki, H. Hori, and S. Osawa. 1984. Evolution of multicellular animals as deduced from 5S rRNA sequences: a possible early emergence of the Mesozoa. *Nucleic Acids Res.*, 12:5101-5108.

Ohama, T., T. Kumazaki, H. Hori, S. Osawa, and M. Takai. 1983. Fresh-water planarias and a marine planaria are relatively dissimilar in the 5S rRNA sequences. *Nucleic Acids Res.*, 11: 473-476.

Ohkubo, S., H. Iwasaki, H. Hori, and S. Osawa. 1986. Evolutionary relationship of denitrifying bacteria as deduced from 5S rRNA sequences. *J. Biochem.*, 100:1261-1267.

Olsen, G. J. 1987. Earliest phylogenetic branchings: comparing rRNA-based evolutionary trees inferred with various techniques. *Cold Spring Harbor Symp. Quant. Biol.*, 52:825-837.

Olsen, G. J., and M. L. Sogin. 1982. Nucleotide sequence of *Dictyostelium discoideum* 5.8S ribosomal ribonucleic acid: evolutionary and secondary structural implications. *Biochemistry*, 21:2335-2343.

Olsen, G. J., N. R. Pace, M. Nuell, B. P. Kaine, R. Gupta, and C. R. Woese. 1985. Sequence of the 16S rRNA gene from the thermoacidophilic

archaebacterium *Sulfolobus solfataricus* and its evolutionary implications. *J. Mol. Evol.*, 22: 301-307.

Østergaard, L., N. Larsen, H. Leffers, J. Kjems, and R. Garrett. 1987. A ribosomal RNA operon and its flanking region from the archaebacterium *Methanobacterium thermoautotrophicum*, Marburg strain: transcription signals, RNA structure and evolutionary implications. *Syst. Appl. Microbiol.*, 9:199-209.

Oyaizu, H., and C. R. Woese. 1985. Phylogenetic relationships among the sulfate-reducing bacteria, myxobacteria and purple bacteria. *Syst. Appl. Microbiol.*, 6:257-263.

Oyaizu, H., B. Debrunner-Vossbrinck, L. Mandelco, J. A. Studier, and C. R. Woese. 1987. The green non-sulfur bacteria: a deep branching in the eubacterial line of descent. *Syst. Appl. Microbiol.*, 9:47-53.

Pace, B., and L. L. Campbell. 1971a. Homology of ribosomal ribonucleic acid of *Desulfovibrio* species with *Desulfovibrio vulgaris*. *J. Bacteriol.*, 106:717-719.

———, and ———. 1971b. Homology of ribosomal ribonucleic acid of diverse bacterial species with *Escherichia coli* and *Bacillus stearothermophilus*. *J. Bacteriol.*, 107:543-547.

Pace, N. R., G. J. Olsen, and C. R. Woese. 1986. Ribosomal RNA phylogeny and the primary lines of evolutionary descent. *Cell*, 45:325-326.

Palleroni, N. J., R. Kunisawa, R. Contopoulou, and M. Doudoroff. 1973. Nucleic acid homologies in the genus *Pseudomonas*. *Int. J. Syst. Bacteriol.*, 23:333-339.

Palmer, J. D. 1985a. Evolution of chloroplast and mitochondrial DNA in plants and algae. In R. J. MacIntyre (ed.), *Molecular Evolutionary Genetics*, pp. 131-240. Plenum Press, New York.

———. 1985b. Comparative organization of chloroplast genomes. *Annu. Rev. Genet.*, 19:325-354.

Park, Y.-H., H. Hori, K.-I. Suzuki, S. Osawa, and K. Komagata. 1987. Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences. *J. Bacteriol.*, 169:1801-1806.

Paster, B. J., E. Stackebrandt, R. B. Hespell, C. M. Hahn, and C. R. Woese. 1984. The phylogeny of the spirochetes. *Syst. Appl. Microbiol.*, 5:337-351.

Paster, B. J., W. Ludwig, W. G. Weisburg, E. Stackebrandt, R. B. Hespell, C. M. H. Reichenbach, K. O. Stetter, and C. R. Woese. 1985. A phylogenetic grouping of the *Bacteroides, Cytophagas*, and certain *Flavobacteria*. *Syst. Appl. Microbiol.*, 6:34-42.

Paster, B. J., A. Lee, J. G. Fox, F. E. Dewhirst, L. A. Tordoff, G. J. Fraser, J. L. O'Rourke, N. S. Taylor, and R. Ferrero. 1991. Phylogeny of *Helicobacter felis* sp. nov., *Helicobacter mustelae*, and related bacteria. *Int. J. Syst. Bacteriol.*, 41: 31-38.

Patterson, C. (ed.) 1987. *Molecules and Morphology in Evolution: Conflict or Compromise?* Cambridge University Press, Cambridge.

———. 1989. Phylogenetic relations of major groups: conclusions and prospects. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 471-488. Elsevier Science Publishers (Biomedical Division), Amsterdam.

———. 1990. Reassessing relationships. *Nature*, 344:199-200.

Pavlakis, G. N., B. R. Jordan, R. M. Wurst, and J. N. Vournakis. 1979. Sequence and secondary structure of *Drosophila melanogaster* 5.8S and 2S rRNAs and of the processing site between them. *Nucleic Acids Res.*, 7:2213-2338.

Pechman, K. J., B. J. Lewis, and C. R. Woese. 1976. Phylogenetic status of *Sporosarcina ureae*. *Int. J. Syst. Bacteriol.*, 26:305-310.

Perasso, R., A. Baroin, L. H. Qu, J.-P. Bachellerie, and A. Adoutte. 1989. Origin of the algae. *Nature*, 339:142-144.

Perelson, A. S., and G. I. Bell. 1977. Mathematical models for the evolution of multigene families by unequal crossing over. *Nature*, 265:304-310.

Peterson, R. C., J. L. Doering, and D. D. Brown. 1980. Characterization of two *Xenopus* somatic 5S DNAs and one minor oocyte-specific 5S DNA. *Cell*, 20:131-141.

Petes, T. D. 1980. Unequal meiotic recombination within tandem arrays of yeast ribosomal DNA genes. *Cell*, 19:765-774.

Qi, G.-R., G.-J. Cao, P. Jiang, X.-L. Feng, and X.-R. Gu. 1988. Studies on the sites expressing evolutionary changes in the structure of eukaryotic 5S ribosomal RNA. *J. Mol. Evol.*, 27:336-340.

Qu, L.-H., M. Nicoloso, and J.-P. Bachellerie. 1988. Phylogenetic calibration of the 5′ terminal domain of large rRNA achieved by determining twenty eucaryotic sequences. *J. Mol. Evol.*, 28:113-124.

Qu, L.-H., N. Hardman, L. Gill, L. Chappell, M. Nicoloso, and J.-P. Bachellerie. 1986. Phylogeny of helminths determined by rRNA sequence comparison. *Mol. Biochem. Parasitol.*, 20:93-99.

Qu, L.-H., R. Perasso, A. Baroin, G. Brugerolle, J.-P. Bachellerie, and A. Adoutte. 1988. Molecular evolution of the 5′-terminal domain of large-subunit rRNA from lower eukaryotes. A broad phylogeny covering photosynthetic and non-photosynthetic protists. *BioSystems*, 21: 203-208.

Raff, R. A., K. G. Field, G. J. Olsen, S. J. Gio-

vannoni, D. J. Lane, M. T. Ghiselin, N. R. Pace, and E. C. Raff. 1989. Metazoan phylogeny based on analysis of 18S ribosomal RNA. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 247–260. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Raff, R. A., K. G. Field, M. T. Ghiselin, D. J. Lane, G. J. Olsen, A. L. Parks, B. A. Parr, N. R. Pace, and E. C. Raff. 1988. Molecular analysis of distant phylogenetic relationships in echinoderms. In C. R. C. Paul and A. B. Smith (eds.), *Echinoderm Phylogeny and Evolutionary Biology*, pp. 29–41. Oxford University Press, Oxford.

Ragan, M. A. 1988. Ribosomal RNA and the major lines of evolution: a perspective. *BioSystems*, 21:177–188.

Rausch, H., N. Larsen, and R. Schmitt. 1989. Phylogenetic relationships of the green alga *Volvox carteri* deduced from small-subunit ribosomal RNA comparisons. *J. Mol. Evol.*, 29: 255–265.

Raynal, F., B. Michot, and J.-P. Bachellerie. 1984. Complete nucleotide sequence of mouse 18S rRNA gene: comparison with other available homologs. *FEBS Lett.*, 167:263–268.

Reddy, P., R. Appels, and B. R. Baum. 1990. Ribosomal DNA spacer-length variation in *Secale* spp. (*Poaceae*). *Plant Syst. Evol.*, 171:205–220.

Reeder, R. H. 1984. Enhancers and ribosomal gene spacers. *Cell*, 38:349–351.

Reeder, R. H., J. G. Roan, and M. Dunaway. 1983. Spacer regulation of *Xenopus* ribosomal gene transcription: competition in oocytes. *Cell*, 35:449–456.

Roe, B. A., D.-P. Ma, R. K. Wilson, and J. F.-H. Wong. 1985. The complete nucleotide sequence of the *Xenopus laevis* mitochondrial genome. *J. Biol. Chem.*, 260:9759–9774.

Rogall, T., J. Wolters, T. Flohr, and E. Böttger. 1990. Towards a phylogeny and definition of species at the molecular level within the genus *Mycobacterium*. *Int. J. Syst. Bacteriol.*, 40:323–330.

Rogers, S. O., S. Honda, and A. J. Bendich. 1986. Variation in the ribosomal RNA genes among individuals of *Vicia faba*. *Plant Mol. Biol.*, 6:339–345.

Rogers, M. J., J. Simmons, R. T. Walker, W. G. Weisburg, C. R. Woese, R. S. Tanner, I. M. Robinson, D. A. Stahl, G. Olsen, R. H. Leach, and J. Maniloff. 1985. Construction of the mycoplasma evolutionary tree from 5S rRNA sequence data. *Proc. Natl. Acad. Sci. USA*, 82: 1160–1164.

Roggentin, T., and P. Hirsch. 1989. Ribosomal RNA cistron similarities among *Hyphomicrobium* species and several other hyphal, budding bacteria. *Syst. Appl. Microbiol.*, 11:140–147.

Romaniuk, P. J., B. Zoltowska, T. J. Trust, D. J. Lane, G. J. Olsen, N. R. Pace, and D. A. Stahl. 1987. *Campylobacter pylori*, the spiral bacterium associated with human gastritis, is not a true *Campylobacter* sp. *J. Bacteriol.*, 169:2137–2141.

Rossau, R., A. Van Landschoot, M. Gillis, and J. De Ley. 1991. Taxonomy of *Moraxellaceae* fam. nov., a new bacterial family to accommodate the genera *Moraxella, Acinetobacter*, and *Psychrobacter* and related organisms. *Int. J. Syst. Bacteriol.*, 41:310–319.

Rothschild, L. J., M. A. Ragan, A. W. Coleman, P. Heywood, and S. A. Gerbi. 1986. Are rRNA sequence comparisons the Rosetta Stone of phylogenetics? *Cell*, 47:640.

Rowan, R., and D. A. Powers. 1991. A molecular genetic classification of zooxanthellae and the evolution of animal-algal symbioses. *Science*, 251:1348–1351.

Rubstov, P. M., M. M. Musakhanov, V. M. Zakharyev, A. S. Krayev, K. G. Skryabin, and A. A. Bayev. 1980. The structure of the yeast ribosomal RNA genes. I. The complete nucleotide sequence of the 18S ribosomal RNA gene from *Saccharomyces cerevisiae*. *Nucleic Acids Res.*, 8:5779–5794.

Saccone, C., P. Cantatore, G. Gadaleta, R. Gallerani, C. Lanave, G. Pepe, and A. M. Kroon. 1981. The nucleotide sequence of the large ribosomal RNA gene and the adjacent tRNA genes from rat mitochondria. *Nucleic Acids Res.*, 9:4139–4147.

Saghai-Maroof, M. A., K. M. Soliman, R. A. Jorgensen, and R. W. Allard. 1984. Ribosomal DNA spacer length polymorphisms in barley: Mendelian inheritance, chromosomal location, and population dynamics. *Proc. Natl. Acad. Sci. USA*, 81:8014–8018.

Salim, M., and B. E. H. Maden. 1981. Nucleotide sequence of *Xenopus laevis* 18S ribosomal RNA inferred from gene sequence. *Nature*, 291:205–208.

Sankoff, D., C. Morel, and R. J. Cedergren. 1973. Evolution of 5S RNA and the nonrandomness of base replacement. *Nature New Biology*, 245:232–234.

Sasaki, T., T. Okazaki, M. Muramatsu, and R. Kominami. 1987. Variation among mouse ribosomal RNA genes within and between chromosomes. *Mol. Biol. Evol.*, 4:594–601.

Schaal, B. A., W. J. Leverich, and J. Nieto-Sotelo. 1987. Ribosomal DNA variation in the native plant *Phlox divaricata*. *Mol. Biol. Evol.*, 4:611–621.

Schlegel, M., H. J. Elwood, and M. L. Sogin. 1991. Molecular evolution in hypotrichous ciliates: sequence of the small subunit ribosomal RNA genes from *Onychodromus quadricornutus* and *Oxytricha graulifera* (Oxytrichidae, Hypotrichida, Ciliophora). *J. Mol. Evol.*, 32:64-69.

Schleifer, K. H., and W. Ludwig. 1989. Phylogenetic relationships among bacteria. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 103-117. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Schnare, M. N., J. C. Collings, and M. W. Gray. 1986. Structure and evolution of the small subunit ribosomal RNA gene of *Crithidia fasciculata*. *Curr. Genet.*, 10:405-410.

Schwartz, R. M., and M. O. Dayhoff. 1978. Origins of prokaryotes, eukaryotes, mitochondria and chloroplasts. *Science*, 199:395-403.

Schwarz, Z., and H. Kössel. 1980. The primary structure of 16S rDNA from *Zea mays* chloroplast is homologous to *E. coli* 16S rRNA. *Nature*, 283:739-742.

Scoles, G. J., B. S. Gill, Z.-Y. Xin, B. C. Clarke, C. L. McIntyre, C. Chapman, and R. Appels. 1988. Frequent duplication and deletion events in the 5S RNA genes and the associated spacer regions of the *Triticeae*. *Plant Syst. Evol.*, 160: 105-122.

Seewaldt, E., and E. Stackenbrandt. 1982. Partial sequence of 16S ribosomal RNA and the phylogeny of *Prochloron*. *Nature*, 295:618-620.

Seperack, P., M. Slatkin, and N. Arnheim. 1988. Linkage disequilibrium in human ribosomal genes: implications for multigene family evolution. *Genetics*, 119:943-949.

Simon, C., A. Franke, and A. Martin. 1991. The polymerase chain reaction: DNA extraction and amplification. In G. M. Hewitt, A. W. B. Johnston, and J. P. W. Young (eds.), *Molecular Techniques in Taxonomy*, pp. 329-355. Springer-Verlag, Berlin.

Simon, C., S. Pääbo, T. D. Kocher, and A. C. Wilson. 1990. Evolution of mitochondrial ribosomal RNA in insects as shown by the polymerase chain reaction. In M. Clegg and S. O'Brien (eds.), *Molecular Evolution*, UCLA Symposia on Molecular and Cellular Biology, New Series, Vol. 122, pp. 235-244. Wiley-Liss, New York.

Simpson, R. T., and D. W. Stafford. 1983. Structural features of a phased nucleosome core particle. *Proc. Natl. Acad. Sci. USA*, 80:51-55.

Sites, J. W., and S. K. Davis. 1989. Phylogenetic relationships and molecular variability within and among six chromosome races of *Sceloporus grammicus* (Sauria, Iguanidae), based on nuclear and mitochondrial markers. *Evolution*, 43: 296-317.

Smith, A. B. 1989. RNA sequence data in phylogenetic reconstruction: testing the limits of its resolution. *Cladistics*, 5:321-344.

Smith, G. P. 1973. Unequal crossover and the evolution of multigene families. *Cold Spring Harbor Symp. Quant. Biol.*, 38:507-513.

———. 1976. Evolution of repeated DNA sequences by unequal cross overs. *Science*, 191: 528-534.

Sogin, M. L. 1989. Evolution of eukaryotic microorganisms and their small subunit ribosomal RNAs. *Am. Zool.*, 29:487-499.

———. 1990. Amplification of ribosomal RNA genes for molecular evolution studies. In M. A. Innis, D. H. Gelfand, J. J. Sninsky, and T. J. White (eds.), *PCR Protocols: A Guide to Methods and Applications*, pp. 307-314. Academic Press, San Diego.

Sogin, M. L., and H. J. Elwood. 1986. Primary structure of the *Paramecium tetraurelia* small-subunit rRNA coding region: phylogenetic relationships within the ciliophora. *J. Mol. Evol.*, 23:53-60.

Sogin, M. L., and J. H. Gunderson. 1987. Structural diversity of eukaryotic small subunit ribosomal RNAs: evolutionary implications. *Ann. NY Acad. Sci.*, 503:125-139.

Sogin, M. L., U. Edman, and H. Elwood. 1989. A single kingdom of eukaryotes. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 133-143. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Sogin, M. L., H. J. Elwood, and J. H. Gunderson. 1986. Evolutionary diversity of eukaryotic small-subunit rRNA genes. *Proc. Natl. Acad. Sci. USA*, 83:1383-1387.

Sogin, M. L., M. T. Swanton, J. H. Gunderson, and H. J. Elwood. 1986. Sequence of the small subunit ribosomal RNA gene from the hypotrichous ciliate *Euplotes aediculatus*. *J. Protozool.*, 33:26-29.

Sogin, M. L., J. H. Gunderson, H. J. Elwood, R. A. Alonso, and D. A. Peattie. 1989. Phylogenetic meaning of the kingdom concept: an unusual ribosomal RNA from *Giardia lamblia*. *Science*, 243:75-77.

Sogin, M. L., A. Ingold, M. Karlok, H. Nielsen, J. Enberg. 1986. Phylogenetic evidence for the acquisition of ribosomal RNA introns subsequent to the divergence of some of the major *Tetrahymena* groups. *EMBO (Eur. Mol. Biol. Organ.) J.*, 5:3625-3630.

Sogin, S. J., M. L. Sogin, and C. R. Woese. 1972. Phylogenetic measurement in procaryotes by primary structural characterization. *J. Mol. Evol.*, 1:173-184.

Spencer, D. F., L. Bonen, and M. W. Gray. 1981. Primary sequence of wheat mitochodrial 5S ribosomal ribonucleic acid: functional and evolu-

tionary implications. *Biochemistry*, 20:4022-4029.

Spencer, D. F., M. N. Schnare, and M. W. Gray. 1984. Pronounced structural similarities between the small ribosomal RNA genes of wheat mitochondria and *Escherichia coli*. *Proc. Natl. Acad. Sci. USA*, 81:493-497.

Spencer, D. F., J. C. Collings, M. N. Schnare, and M. W. Gray. 1987. Multiple spacer sequences in the nuclear large subunit ribosomal RNA gene of *Crithidia fasciculata*. *EMBO (Eur. Mol. Biol. Organ.) J.*, 6:1063-1071.

Stackebrandt, E., and O. Charfreitag. 1990. Partial 16S rRNA primary structure of five Actinomyces species: phylogenetic implications and development of an *Actinomyces israelii*-specific oligonucleotide probe. *J. Gen. Microbiol.*, 136: 37-43.

Stackebrandt, E., and C. R. Woese. 1981. The evolution of prokaryotes. In M. J. Carlile, J. R. Collins, and B. E. B. Mosely (eds.), *Molecular and Cellular Aspects of Microbial Evolution*, pp. 1-31. Cambridge University Press, Cambridge.

Stackebrandt, E., U. Wehmeyer, and B. Schink. 1989. The phylogenetic status of *Pelobacter acidigallici, Pelobacter venetianus*, and *Pelobacter carbinolicus*. *Syst. Appl. Microbiol.*, 11:257-260.

Stackebrandt, E., V. J. Fowler, F. Fiedler, and H. Seiler. 1983. Taxonomic studies on *Arthrobacter nicotianae* and related taxa: description of *Arthrobacter uratoxydans* sp. nov. and *Arthrobacter sulfureus* sp. nov. and reclassification of *Brevibacterium protophormiae* as *Arthrobacter protophormiae* comb. nov. *Syst. Appl. Microbiol.*, 4:470-486.

Stackebrandt, E., B. Wunner-Füssl, V. J. Fowler, and K.-H. Schleifer. 1981. Deoxyribonucleic acid homologies and ribosomal ribonucleic acid similarities among sporeforming members of the order *Actinomycetales*. *Int. J. Syst. Bacteriol.*, 31:420-431.

Stackebrandt, E., H. Pohla, R. Kroppenstedt, H. Hippe, and C. R. Woese. 1985. 16S rRNA analysis of *Sporomusa, Selenomonas*, and *Megasphaera*: on the phylogenetic origin of gram-positive eubacteria. *Arch. Microbiol.*, 143:270-276.

Stackebrandt, E., W. Ludwig, W. Schubert, F. Klink, H. Schlensner, T. Roggentin, and P. Hirsch. 1984. Molecular genetic evidence for early evolutionary origin of budding peptidoglycan-less eubacteria. *Nature*, 307:735-737.

Stahl, D. A., and J. W. Urbance. 1990. The division between fast- and slow-growing species corresponds to natural relationships among mycobacteria. *J. Bacteriol.*, 172:116-124.

Stahl, D. A., D. J. Lane, G. J. Olsen, D. J. Heller, T. M. Schmidt, and N. R. Pace. 1985. A phylogenetic analysis of certain sulfur-oxidizing and related morphologically conspicuous bacteria by 5S ribosomal RNA sequences. *Int. J. Syst. Bacteriol.*, 37:116-122.

Stambrook, P. J. 1978. Heterogeneity in Chinese hamster ribosomal DNA. *Chromosoma*, 65:153-159.

Stanton, T. B., N. S. Jenson, T. A. Casey, L. A. Tordoff, F. E. Dewhirst, and B. J. Paster. 1991. Reclassification of *Treponema hyodysenteriae* and *Treponema innocens* in a new genus, *Serpula* gen. nov., as *Serpula hyodysenteriae* comb. nov. and *Serpula innocens* comb. nov. *Int. J. Syst. Bacteriol.*, 41:50-58.

Steele, K. P., K. E. Holsinger, R. K. Jansen, and D. W. Taylor. 1991. Assessing the reliability of 5S rRNA sequence data for phylogenetic analysis in green plants. *Mol. Biol. Evol.*, 8: 240-248.

Stock, D. W., K. D. Moberg, G. S. Whitt, and L. R. Maxson. 1991. Phylogenetic implications of the 18S ribosomal RNA sequence of the coelacanth *Latimeria chalumnae* (Smith), *Envir. Biol. Fishes*, 32:99-117.

Stöcklein, L., W. Ludwig, K. H. Schleifer, and E. Stackebrandt. 1983. Comparative oligonucleotide cataloguing of 18S ribosomal RNA in phylogenetic studies of eukaryotes. In U. Jensen and D. E. Fairbrothers (eds.), *Protein and Nucleic Acids in Plant Systematics*, pp. 58-62. Springer-Verlag, Berlin.

Subrahmanyam, C. S., B. Cassidy, H. Busch, and L. I. Rothblum. 1982. Nucleotide sequence of the region between the 18S rRNA sequence and the 28S rRNA sequence of rat ribosomal DNA. *Nucleic Acids Res.*, 10:3667-3680.

Suzuki, H., K. Moriwaki, and E. Nevo. 1987. Ribosomal DNA (rDNA) spacer polymorphism in mole rats. *Mol. Biol. Evol.*, 4:602-610.

Suzuki, H., N. Miyashita, K. Moriwaki, R. Kominami, M. Muramatsu, T. Kanehisa, F. Bonhomme, M. L. Petras, Z. Yu, and D. Lu. 1986. Evolutionary implication of heterogeneity of the nontranscribed spacer region of ribosomal DNA repeating units in various subspecies of *Mus musculus*. *Mol. Biol. Evol.*, 3:126-137.

Swings, J., M. Gillis, K. Kersters, P. de Vos, F. Gosselé, and J. de Ley. 1980. *Frateuria*, a new genus for "*Acetobacter aurantius*." *Int. J. Syst. Bacteriol.*, 30:547-556.

Swofford, D. L., and G. J. Olsen. 1990. Phylogeny reconstruction. In D. M. Hillis and C. Moritz (eds.), *Molecular Systematics*, pp. 411-501. Sinauer Associates, Sunderland.

Sytsma, K. J., and B. A. Schaal. 1985. Phylogenetics of the *Lisianthius skinneri* (Gentianaceae) species complex in Panama utilizing DNA re-

striction fragment analysis. *Evolution*, 39:594-608.

Szostak, J. W., and R. Wu. 1980. Unequal crossing over in the ribosomal DNA of *Saccharomyces cerevisiae*. *Nature*, 284:426-430.

Takaiwa, F., K. Oono, and M. Sugiura. 1984. The complete nucleotide sequence of a rice 17S rRNA gene. *Nucleic Acids Res.*, 125:5441-5448.

Takaiwa, F., M. Kusuda, N. Saga, and M. Sugiura. 1982. The nucleotide sequence of 5S rRNA from a red alga, *Porphyra yezoensis*. *Nucleic Acids Res.*, 10:6037-6040.

Takaiwa, F., K. Oono, Y. Iida, and M. Sugiura. 1985. The complete nucleotide sequence of a rice 25S·rRNA gene. *Gene*, 37:255-259.

Tanhauser, S. M., W. W. Hauswirth, and P. J. Laipis. 1986. Conserved restriction sites within the ribosomal RNA genes of vertebrates. *Biochim. Biophys. Acta*, 866:19-25.

Tanner, R. S., E. Stackebrandt, G. E. Fox, and C. R. Woese. 1981. A phylogenetic analysis of *Acetobacterium woodii, Clostridium barkeri, Clostridium butyricum, Clostridium lituseburense, Eubacterium limosum*, and *Eubacterium tenue*. *Curr. Microbiol.*, 5:35-38.

Tautz, D., J. M. Hancock, D. A. Webb, C. Tautz, and G. A. Dover. 1988. Complete sequences of the rRNA genes of *Drosophila melanogaster*. *Mol. Biol. Evol.*, 5:366-376.

Thomas, R. H., W. Schaffner, A. C. Wilson, and S. Pääbo. 1989. DNA phylogeny of the extinct marsupial wolf. *Nature*, 340:465-467.

Toivonen, L. A., D. T. Crowe, R. J. Detrick, S. W. Klemann, and J. C. Vaughn. 1983. Ribosomal RNA gene number and sequence divergence in the diploid-tetraploid species pair of North American hylid tree frogs. *Biochem. Genet.*, 21:299-308.

Torczynski, R., A. P. Bollon, and M. Fuke. 1983. The complete nucleotide sequence of the rat 18S ribosomal RNA gene and comparison with the respective yeast and frog genes. *Nucleic Acids Res.*, 11:4879-4890.

Torczynski, R., M. Fuke, and A. P. Bollon. 1985. Cloning and sequencing of a human 18S ribosomal RNA gene. *DNA*, 4:283-291.

Torres, R. A., M. Ganal, and V. Hemleben. 1990. GC balance in the internal transcribed spacers ITS 1 and ITS 2 of nuclear ribosomal RNA genes. *J. Mol. Evol.*, 30:170-181.

Troitsky, A. V., and V. K. Bobrova. 1986. 23S rRNA-derived small ribosomal RNAs: their structure and evolution with references to plant phylogeny. In S. K. Dutta (ed.), *DNA Systematics*, Vol. II, pp. 81-135. CRC Press, Boca Raton.

Tschudi, C., and V. Pirrotta. 1980. Sequence and heterogeneity in the 5S RNA gene cluster of *Drosophila melanogaster*. *Nucleic Acids Res.*, 8:441-451.

Tsuji, K., H. C. Tsien, R. S. Hanson, S. R. DePalma, R. Scholtz, and S. LaRoche. 1989. 16S ribosomal RNA sequence analysis for determination of phylogenetic relationship among methylotrophs. *J. Gen. Microbiol.*, 136:1-10.

Tu, J., D. Prangishvilli, H. Huber, G. Wildgruber, W. Zillig, and K. O. Stetter. 1982. Taxonomic relations between archaebacteria including 6 novel genera examined by cross hybridization of DNAs and 16S rRNAs. *J. Mol. Evol.*, 18:109-114.

Turner, S., T. Burger-Wiersma, S. J. Giovannoni, L. R. Mur, and N. R. Pace. 1989. The relationship of a prochlorophyte *Prochlorothrix hollandica* to green chloroplasts. *Nature*, 337: 380-382.

Ulbrich, N., M. Digweed, and V. A. Erdmann. 1984. The nucleotide sequence of the cytoplasmic 5S rRNA from the horsetail, *Equisetum arvense*. *Nucleic Acids Res.*, 12:1577-1580.

Vandamme, P., E. Falsen, R. Rossau, B. Hoste, P. Segers, R. Tytgat, and J. de Ley. 1991. Revision of *Campylobacter, Helicobacter*, and *Wolinella* taxonomy: emendation of generic descriptions and proposal of *Arcobacter* gen. nov. *Int. J. Syst. Bacteriol.*, 41:88-103.

Vandenberghe, A., A. Wassink, P. Raeymaekers, R. de Baere, E. Huysmans, and R. de Wachter. 1985. Nucleotide sequence, secondary structure and evolution of the 5S ribosomal RNA from five bacterial species. *Eur. J. Biochem.*, 149:537-542.

Vandenberghe, A., M.-W. Chen, E. Dams, R. de Baere, E. de Roeck, E. Huysmans, and R. de Wachter. 1984. The corrected nucleotide sequences of 5S RNAs from six angiosperms with some notes on 5S RNA secondary structure and molecular evolution. *FEBS Lett.*, 171:17-23.

Van Den Bussche. In press. Phylogenetic analysis of restriction site variation in the ribosomal DNA complex of New World leaf-nosed bat genera. *Syst. Zool.*

Van den Eynde, H., Y. Van de Peer, J. Perry, and R. de Wachter. 1990. 5S rRNA sequences of representatives of the genera *Chlorobium, Prosthecochloris, Thermomicrobium, Cytophaga, Flavobacterium, Flexibacter* and *Saprospira* and a discussion of the evolution of eubacteria in general. *J. Gen. Microbiol.*, 136:11-18.

Van den Eynde, H., Y. Van de Peer, H. Vandenabeele, M. Van Bogaert, and R. de Wachter. 1990. 5S rRNA sequences of myxobacteria and radioresistant bacteria and implications for eubacterial evolution. *Int. J. Syst. Bacteriol.*, 40: 399-404.

Van de Peer, Y., J. M. Neefs, and R. de Wachter.

1990. Small ribosomal subunit RNA sequences, evolutionary relationships among different life forms, and mitochondrial origins. *J. Mol. Evol.*, 30:463-476.

Van de Peer, Y., R. de Baere, J. Cauwenberghs, and R. de Wachter. 1990. Evolution of green plants and their relationship with other photosynthetic eukaryotes as deduced from 5S ribosomal RNA sequences. *Plant Syst. Evol.*, 170: 85-96.

Verbeet, M. P., H. van Heerikhuizen, J. Klootwijk, R. D. Fontijn, and R. J. Planta. 1984. Evolution of yeast ribosomal DNA: molecular cloning of the rDNA units of *Kluyveromyces lactis* and *Hansenula wingei* and their comparison with the rDNA units of other Saccharomycetoideae. *Mol. Gen. Genet.*, 195:116-125.

Vossbrinck, C. R., J. V. Maddox, S. Friedman, B. A. Debrunner-Vossbrinck, and C. R. Woese. 1987. Ribosomal RNA sequence suggests microsporidia are extremely ancient eukaryotes. *Nature*, 326:411-414.

Walker, T. A., Y. Endo, W. H. Wheat, I. G. Wool, and N. R. Pace. 1983. Location of 5.8 S rRNA contact sites in 28 S rRNA and the effect of α-sarcin on the association of 5.8 S rRNA with 28 S rRNA. *J. Biol. Chem.*, 258: 333-338.

Walker, W. F. 1981. Proposed sequence homology between the 5'-end regions of prokaryotic 23 S rRNA and eukaryotic 28 S rRNA: relevance to the hypothesis that 5.8S rRNA is homologous to the 5'-end region of 23 S rRNA. *FEBS Lett.*, 126:150-151.

———. 1984a. 5S rRNA sequences from Atractiellales, and basidiomycetous yeasts and fungi imperfecti. *Syst. Appl. Microbiol.*, 5:352-359.

———. 1984b. 5S ribosomal RNA sequences from Zygomycotina and evolutionary implications. *Syst. Appl. Microbiol.*, 5:448-456.

———. 1985. 5S and 5.8S ribosomal RNA sequences and protist phylogenies. *BioSystems*, 18:269-278.

Walker, W. F., and W. F. Doolittle. 1982. Nucleotide sequences of 5S ribosomal RNA from four oomycete and chytrid water molds. *Nucleic Acids Res.*, 10:5717-5721.

———, and ———. 1983a. 5S rRNA sequences from four marine invertebrates and implications for base pairing models of metazoan sequences. *Nucleic Acids Res.*, 11:5159-5164.

———, and ———. 1983b. 5S rRNA sequences from eight basidiomycetes and fungi imperfecti. *Nucleic Acids Res.*, 11:7625-7630.

Wallbanks, S., A. J. Martinez-Murcia, J. L. Fryer, B. A. Phillips, and M. D. Collins. 1990. 16S rRNA sequence determination for members of the genus *Carnobacterium* and related lactic acid bacteria and description of *Vagococcus salmoninarum* sp. nov. *Int. J. Syst. Bacteriol.*, 40: 224-230.

Ware, V. C., B. W. Tague, C. G. Clark, R. L. Gourse, R. C. Brand, and S. A. Gerbi. 1983. Sequence analysis of 28S ribosomal DNA from the amphibian *Xenopus laevis*. *Nucleic Acids Res.*, 11:7795-7817.

Watanabe, J.-I., H. Hori, K. Tanabe, and Y. Nakamura. 1989. Phylogenetic association of *Pneumocystis carinii* with the 'Rhizopoda/Myxomycota/Zygomycota group' indicated by comparison of 5S ribosomal RNA sequences. *Mol. Biochem. Parasitol.*, 32:163-167.

Wegnez, M., R. Monier, and H. Denis. 1972. Sequence heterogeneity of 5 S rRNA in *Xenopus laevis*. *FEBS Lett.*, 25:13-20.

Weisburg, W. G., S. J. Giovannoni, and C. R. Woese. 1989. The *Deinococcus-Thermus* phylum and the effect of rRNA composition on phylogenetic tree construction. *Syst. Appl. Microbiol.*, 11:128-134.

Weisburg, W. G., T. P. Hatch, and C. R. Woese. 1986. Eubacterial origin of chlamydiae. *J. Bacteriol.*, 167:570-574.

Weisburg, W. G., S. M. Barns, D. A. Pelletier, and D. J. Lane. 1991. 16S ribosomal DNA amplification for phylogenetic study. *J. Bacteriol.*, 173:697-703.

Weisburg, W. G., Y. Oyaizu, H. Oyaizu, and C. R. Woese. 1985. Natural relationship between Bacteroides and Flavobacteria. *J. Bacteriol.*, 164:230-236.

Weisburg, W. G., C. R. Woese, M. E. Dobson, and E. Weiss. 1985. A common origin of Rickettsiae and certain plant pathogens. *Science*, 230:556-558.

Weisburg, W. G., M. E. Dobson, J. E. Samuel, G. A. Dasch, L. P. Mallavia, L. Mandelco, J. E. Sechrest, E. Weiss, and C. R. Woese. 1989. Phylogenetic diversity of the Rickettsiae. *J. Bacteriol.*, 171:4202-4206.

Weisburg, W. G., J. G. Tully, D. L. Rose, J. P. Petzel, H. Oyaizu, D. Yang, L. Mandelco, J. Sechrest, T. G. Lawrence, J. Van Etten, J. Maniloff, and C. R. Woese. 1989. A phylogenetic analysis of the mycoplasmas: basis for their classification. *J. Bacteriol.*, 171:6455-6467.

Wellauer, P. K., I. B. Dawid, D. D. Brown, and R. Reeder. 1976. The molecular basis for length heterogeneity in ribosomal DNA from *Xenopus laevis*. *J. Mol. Biol.*, 105:461-486.

Wellauer, P. K., R. H. Reeder, I. B. Dawid, and D. D. Brown. 1976. The arrangement of length heterogeneity in repeating units of amplified and chromosomal ribosomal DNA from *Xenopus laevis*. *J. Mol. Biol.*, 105:487-505.

Wells, J. M., B. C. Raju, H.-Y. Hung, W. G. Weisburg, L. Mandelco-Paul, and D. J. Brenner. 1987. *Xylella fastidiosa* gen. nov., sp. nov: gram-negative, xylem-limited, fastidious plant bacteria related to *Xanthomonas* spp. *Int. J. Syst. Bacteriol.*, 37:136-143.

Wheeler, W. C. 1989. The sytematics of insect ribosomal DNA. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 307-321. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Wheeler, W. C., and R. L. Honeycutt. 1988. Paired sequence difference in ribosomal RNAs: evolutionary and phylogenetic implications. *Mol. Biol. Evol.*, 5:90-96.

Willekens, P., E. Huysmans, A. Vandenberghe, and R. de Wachter. 1986. Archaebacterial 5 S ribosomal RNA: nucleotide sequence in two methanogen species, secondary structure models, and molecular evolution. *Syst. Appl. Microbiol.*, 7:151-159.

Willems, A., M. Gillis, and J. de Ley. 1991. Transfer of *Rhodocyclus gelatinosus* to *Rubrivivax gelatinosus* gen. nov., comb. nov., and phylogenetic relationships with *Leptothrix, Sphaerotilus natans, Pseudomonas saccharophila*, and *Alcaligenes latus*. *Int. J. Syst. Bacteriol.*, 41:65-73.

Williams, S. M., and C. Strobeck. 1985. Sister chromatid exchange and the evolution of rDNA spacer length. *J. Theor. Biol.*, 116:625-636.

Williams, S. M., R. W. DeBry, and J. L. Feder. 1988. A commentary on the use of ribosomal DNA in systematic studies. *Syst. Zool.*, 37:60-62.

Williams, S. M., R. DeSalle, and C. Strobeck. 1985. Homogenization of geographical variants at the nontranscribed spacer of rDNA in *Drosophila mercatorum*. *Mol. Biol. Evol.*, 2:338-346.

Wilson, G. N., M. Knoller, R. D. Schmickel, and L. L. Szura. 1984. Individual and evolutionary variation of primate ribosomal DNA transcription initiation regions. *Mol. Biol. Evol.*, 1:221-237.

Woese, C. R. 1987. Bacterial evolution. *Microbiol. Rev.*, 51:221-271.

———. 1989. Archaebacteria and the nature of their evolution. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 119-130. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Woese, C. R., and G. E. Fox. 1977. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. *Proc. Natl. Acad. Sci. USA*, 74: 5088-5090.

Woese, C. R., and G. J. Olsen. 1986. Archaebacterial phylogeny: perspectives on the urkingdoms. *Syst. Appl. Microbiol.*, 7:161-177.

Woese, C. R., P. Blanz, and C. M. Hahn. 1984. What isn't a Pseudomonad: the importance of nomenclature in bacterial classification. *Syst. Appl. Microbiol.*, 5:179-195.

Woese, C. R., J. Maniloff, and L. B. Zablen. 1980. Phylogenetic analysis of the mycoplasmas. *Proc. Natl. Acad. Sci. USA*, 77:494-498.

Woese, C. R., E. Stackebrandt, and W. Ludwig. 1985. What are Mycoplasmas: the relationship of tempo and mode in bacterial evolution. *J. Mol. Evol.*, 21:305-316.

Woese, C. R., P. Blanz, R. B. Hespell, and C. M. Hahn. 1982. Phylogenetic relationships among various helical bacteria. *Curr. Microbiol.*, 7:119-124.

Woese, C. R., E. Stackebrandt, T. J. Macke, and G. E. Fox. 1985. A phylogenetic definition of the major eubacterial taxa. *Syst. Appl. Microbiol.*, 6:143-151.

Woese, C. R., B. A. Debrunner-Vossbrinck, H. Oyaizu, E. Stackebrandt, and W. Ludwig. 1985. Gram-positive bacteria: possible photosynthetic ancestry. *Science*, 229:762-765.

Woese, C. R., R. Gupta, G. M. Hahn, W. Zillig, and J. Tu. 1984. The phylogenetic relationships of three sulfur-dependent Archaebacteria. *Syst. Appl. Microbiol.*, 5:97-105.

Woese, C. R., M. Sogin, D. Stahl, B. J. Lewis, and L. Bonen. 1976. A comparison of the 16S ribosomal RNAs from mesophilic and thermophilic bacilli: some modifications in the Sanger method for RNA sequencing. *J. Mol. Evol.*, 7: 197-213.

Woese, C. R., W. G. Weisburg, C. M. Hahn, B. J. Paster, L. B. Zablen, B. J. Lewis, T. J. Macke, W. Ludwig, and E. Stackebrandt. 1985. The phylogeny of purple bacteria: the gamma subdivision. *Syst. Appl. Microbiol.*, 6:25-33.

Woese, C. R., W. G. Weisburg, B. J. Paster, C. M. Hahn, R. S. Tanner, N. R. Krieg, H.-P. Koops, H. Harms, and E. Stackebrandt. 1984. The phylogeny of purple bacteria: the beta subdivision. *Syst. Appl. Microbiol.*, 5:327-336.

Woese, C. R., L. J. Magrum, R. Gupta, R. B. Siegel, D. A. Stahl, J. Kop, N. Crawford, J. Brosius, R. Gutell, J. J. Hogan, and H. F. Noller. 1980. Secondary structure model for bacterial 16S-like ribosomal RNA: phylogenetic, enzymatic, and chemical evidence. *Nucleic Acids Res.*, 8:2275-2293.

Woese, C. R., E. Stackebrandt, W. G. Weisburg, B. J. Paster, M. T. Madigan, V. J. Fowler, C. M. Hahn, P. Blanz, R. Gupta, K. H. Nealson, and G. E. Fox. 1984. The phylogeny of purple bacteria: the alpha subdivision. *Syst. Appl. Microbiol.*, 5:315-326.

Wolfe, K. H., M. Gouy, Y.-W. Yang, P. M. Sharp, and W.-H. Li. 1989. Date of the monocot-dicot divergence estimated from chloroplast DNA sequence data. *Proc. Natl. Acad. Sci. USA*, 86:6201-6205.

Wolters, J., and V. A. Erdmann. 1986. Cladistic analysis of 5S rRNA and 16S rRNA secondary and primary structure—the evolution of eukaryotes and their relation to Archaebacteria. *J. Mol. Evol.*, 24:152-166.

———, and ———. 1989. Compilation of 5S rRNA and 5S rDNA gene sequences. *Nucleic Acids Res.*, 16:1-74.

Yakura, K., A. Kato, and S. Tanifuji. 1984. Length heterogeneity of the large spacer of *Vicia faba* rDNA is due to the differing number of a 325 bp repetitive sequence elements. *Mol. Gen. Genet.*, 193:400-405.

Yamano, Y., K. Ohyama, and T. Komano. 1984. Nucleotide sequences of chloroplast 5S ribosomal RNA from cell suspension cultures of the liverworts *Marchantia polymorpha* and *Jungermannia subulata*. *Nucleic Acids Res.*, 12:4621-4624.

Yang, D., and C. R. Woese. 1989. Phylogenetic structure of the "leuconostocs": an interesting case of a rapidly evolving organism. *Syst. Appl. Microbiol.*, 12:145-149.

Yang, D., B. F. Kaine, and C. R. Woese. 1985. The phylogeny of archaebacteria. *Syst. Appl. Microbiol.*, 6:251-256.

Yang, D., Y. Oyaizu, H. Oyaizu, G. J. Olsen, and C. R. Woese. 1985. Mitochondrial origins. *Proc. Natl. Acad. Sci. USA*, 82:4443-4447.

Yao, M.-C., and J. G. Gall. 1977. A single integrated gene for ribosomal RNA in a eucaryote, *Tetrahymena pyriformis*. *Cell*, 12:121-132.

Yokota, Y., T. Kawata, Y. Iida, A. Kato, and S. Tanifuji. 1989. Nucleotide sequences of the 5.8S rRNA gene and internal transcribed spacer regions in carrot and broad bean ribosomal DNA. *J. Mol. Evol.*, 29:294-301.

Zablen, L. B., and C. R. Woese. 1975. Procaryote phylogeny IV: concerning the phylogenetic status of a photosynthetic bacterium. *J. Mol. Evol.*, 5:25-34.

Zablen, L. B., M. S. Kissil, C. R. Woese, and D. E. Buetow. 1975. Phylogenetic origin of the chloroplast and prokaryotic nature of its ribosomal RNA. *Proc. Nat. Acad. Sci. USA*, 72: 2418-2422.

Zellner, G., E. Stackebrandt, H. Kneifel, P. Messner, U. B. Sleytr, E. C. De Macario, H.-P. Zabel, K. O. Stetter, and J. Winter. 1989. Isolation and characterization of a thermophilic, sulfate reducing archaebacterium, *Archaeoglobus fulgidus* Strain Z. *Syst. Appl. Microbiol.*, 11:151-160.

Zhao, H., D. Yang, C. R. Woese, and M. P. Bryant. 1990. Assignment of *Clostridium bryantii* to *Syntrophospora bryantii* gen. nov., comb. nov. on the basis of a 16S rRNA sequence analysis of its crotonate-grown pure culture. *Int. J. Syst. Bacteriol.*, 40:40-44.

Zimmer, E. A., R. K. Hamby, M. L. Arnold, D. A. Leblanc, and E. C. Theriot. 1989. Ribosomal RNA phylogenies and flowering plant evolution. In B. Fernholm, K. Bremer, and H. Jornvall (eds.), *The Hierarchy of Life*, pp. 205-214. Elsevier Science Publishers (Biomedical Division), Amsterdam.

Zweib, C., C. Glotz, and R. Brimacombe. 1981. Secondary structure comparisons between small subunit ribosomal RNA molecules from six different species. *Nucleic Acids Res.*, 9:3621-3640.

APPENDIX

Phylogenetic studies of ribosomal DNA

Abbreviations: nL, nuclear large subunit; nS, nuclear small subunit; mtS, mitochondrial small subunit; mtL, mitochondrial large subunit; cpS, chloroplast small subunit; cpL, chloroplast large subunit; H, hybridization study; O, oligonucleotide catalog; R, restriction enzyme analysis; S, sequence study.

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
Major lineages of life	–	–	–	–	S	–	–	–	–	Kimura and Ohta, 1973
	–	O	–	–	–	–	–	–	–	Woese and Fox, 1977
	–	–	–	–	S	–	–	–	–	Schwartz and Dayhoff, 1978
	–	–	–	–	S	–	–	–	–	Hori and Osawa, 1979
	–	O	–	–	–	–	–	–	–	Fox et al., 1980
	–	–	–	–	S	–	–	–	–	Gray and Spencer, 1981
	–	–	–	–	S	–	–	–	–	Spencer et al., 1981
	–	S	–	–	–	S	–	S	–	McCarroll et al., 1983
	–	–	–	–	S	–	–	–	–	Küntzel et al., 1983
	–	S	–	–	–	S	–	S	–	Gray et al., 1984
	–	–	–	–	S	–	–	–	–	Vandenberghe et al., 1984
	–	S	–	–	–	–	–	–	–	Jarsch and Böck, 1985
	–	S	–	–	–	S	–	S	–	Olsen et al., 1985
	–	S	–	–	–	S	–	S	–	Yang and Oyaizu et al., 1985
	–	–	–	–	S	–	–	–	–	Hori and Osawa, 1986
	–	S	–	–	–	S	–	S	–	Pace et al., 1986
	–	–	–	–	S	–	–	–	–	Willekens et al., 1986
	–	S	–	–	S	–	–	–	–	Wolters and Erdmann, 1986
	–	–	–	–	S	–	–	–	–	Hori and Osawa, 1987
	–	S	–	–	–	–	–	–	–	Lake, 1987
	–	S	–	–	–	–	–	–	–	Olsen, 1987
	–	O,S	–	–	–	–	O,S	–	–	Woese, 1987
	–	S	–	–	–	–	–	–	–	Lake, 1988
	S	S	–	–	–	S	S	S	S	Cedergren et al., 1988
	–	S	–	–	–	–	–	–	–	Ragan, 1988
	–	O	–	–	–	–	–	–	–	Bremer and Bremer, 1989
	S	S	–	–	–	–	–	–	–	Gouy and Li, 1989a
	–	S	–	–	–	–	–	–	–	Lake, 1989a
	S	–	–	–	–	–	–	–	–	Schleifer and Ludwig, 1989
	–	S	–	–	–	–	–	–	–	Woese, 1989
	–	S	–	–	–	–	–	–	–	Van de Peer, Neefs and de Wachter, 1990
	–	S	–	–	–	–	–	–	–	Patterson, 1990
Archaebacteria	–	O	–	–	–	–	–	–	–	Fox and Magram et al., 1977
	–	O	–	–	–	–	–	–	–	Balch et al., 1979
	–	–	–	–	S	–	–	–	–	Fox et al., 1982
	–	H	–	–	–	–	–	–	–	Tu et al., 1982
	–	S	–	–	–	–	–	–	–	Gupta et al., 1983
	–	O	–	–	–	–	–	–	–	Woese and Gupta et al., 1984
	–	S	–	–	–	–	–	–	–	Lechner et al., 1985
	–	S	–	–	–	–	–	–	–	Leinfelder et al., 1985
	–	O	–	–	–	–	–	–	–	Yang, Kaine and Woese, 1985
	H	H	H	–	H	–	–	–	–	Klenk et al., 1986
	–	O	–	–	–	–	–	–	–	McGill et al., 1986
	–	S	–	–	–	–	–	–	–	Woese and Olsen, 1986
	–	S	–	–	–	–	–	–	–	Achenbach-Richter and Gupta et al., 1987
	–	S	–	–	–	–	–	–	–	Kjems et al., 1987
	S	–	–	–	–	–	–	–	–	Leffers et al., 1987
	–	S	–	–	–	–	–	–	–	Østergaard et al., 1987

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
	–	S	–	–	–	–	–	–	–	Achenbach-Richter et al., 1988
	–	O	–	–	–	–	–	–	–	Zellner et al., 1989
	–	–	–	S	–	–	–	–	–	Kjems and Garrett, 1990
Eubacteria	–	–	–	–	O	–	–	–	–	Sogin et al., 1972
	H	H	–	–	–	–	–	–	–	Palleroni et al., 1973
	–	O	–	–	–	–	–	O	–	Bonen and Doolittle, 1975
	–	S	–	–	–	–	–	–	–	Doolittle et al., 1975
	H	–	–	–	–	–	–	–	–	Johnson and Francis, 1975
	–	O	–	–	–	–	–	–	–	Zablen and Woese, 1975
	–	O	–	–	–	–	–	–	–	Zablen et al., 1975
	–	S	–	–	–	–	–	–	–	Bonen and Doolittle, 1976
	–	O	–	–	–	–	–	–	–	Pechman et al., 1976
	–	O	–	–	–	–	–	–	–	Woese et al., 1976
	–	O	–	–	–	–	–	–	–	Balch et al., 1977
	H	H	–	–	–	–	–	–	–	de Smedt and de Ley, 1977
	–	O	–	–	–	–	–	–	–	Fox, Pechman and Woese, 1977
	H	H	–	–	–	–	–	–	–	Moore, 1977
	–	O	–	–	–	–	–	–	–	Bonen and Doolittle, 1978
	H	H	–	–	–	–	–	–	–	de Ley et al., 1978
	–	O	–	–	–	–	–	–	–	Gibson et al., 1979
	H	H	–	–	–	–	–	–	–	de Smedt et al., 1980
	H	H	–	–	–	–	–	–	–	Gillis and de Ley, 1980
	H	H	–	–	–	–	–	–	–	Mordarski et al., 1980
	H	H	–	–	–	–	–	–	–	Swings et al., 1980
	–	O	–	–	–	–	–	–	–	Woese and Magrum et al., 1980
	–	O	–	–	–	–	–	–	–	Woese, Maniloff and Zablen, 1980
	–	O	–	–	–	–	–	–	–	Ludwig et al., 1981
	–	O	–	–	–	–	–	–	–	Stackebrandt and Woese, 1981
	H	H	–	–	–	–	–	–	–	Stackebrandt et al., 1981
	–	O	–	–	–	–	–	–	–	Tanner et al., 1981
	H	H	–	–	–	–	–	–	–	Döpfer et al., 1982
	–	S	–	–	–	–	–	–	–	Seewaldt and Stackebrandt, 1982
	–	O	–	–	–	–	–	–	–	Woese et al., 1982
	–	O	–	–	–	–	–	–	–	Ludwig et al., 1983
	–	O	–	–	–	–	–	–	–	Stackebrandt et al., 1983
	–	–	–	–	S	–	–	–	–	Dekio et al., 1984
	–	–	–	–	S	–	–	–	–	Deming et al., 1984
	–	O	–	–	–	–	–	–	–	Fowler et al., 1984
	–	O	–	–	–	–	–	–	–	Hespell et al., 1984
	–	O	–	–	–	–	–	–	–	Paster et al., 1984
	–	O	–	–	–	–	–	–	–	Stackebrandt et al., 1984
	R	R	R	R,S	–	–	–	–	–	Verbeet et al., 1984
	–	O	–	–	–	–	–	–	–	Woese and Stackebrandt et al., 1984
	–	O	–	–	–	–	–	–	–	Woese and Weisburg et al., 1984
	–	O	–	–	–	–	–	–	–	Woese, Blanz and Hahn, 1984
	–	O	–	–	–	–	–	–	–	Gibson et al., 1985
	–	–	–	–	S	–	–	–	–	Lane and Stahl et al., 1985
	–	–	–	–	S	–	–	–	–	MacDonell and Colwell, 1985a,b
	–	S	–	–	–	–	–	–	–	Oyaizu and Woese, 1985
	–	O	–	–	–	–	–	–	–	Paster et al., 1985
	–	–	–	–	S	–	–	–	–	Rogers et al., 1985
	–	O	–	–	–	–	–	–	–	Stackebrandt et al., 1985
	–	–	–	–	S	–	–	–	–	Stahl et al., 1985
	–	–	–	–	S	–	–	–	–	Vandenberghe et al., 1985

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
	–	S	–	–	–	–	–	–	–	Weisburg and Oyaizu et al., 1985
	–	S	–	–	–	–	–	–	–	Weisburg and Woese et al., 1985
	–	S	–	–	–	–	–	–	–	Woese and Debrunner-Vossbrinck et al., 1985
	–	O	–	–	–	–	–	–	–	Woese, Stackebrandt and Ludwig, 1985
	–	O	–	–	–	–	–	–	–	Woese, Stackebrandt, Macke and Fox, 1985
	–	O	–	–	–	–	–	–	–	Woese and Weisburg et al., 1985
	–	–	–	–	S	–	–	–	–	Brayton et al., 1986
	–	–	–	–	S	–	–	–	–	Ohkubo et al., 1986
	–	S	–	–	–	–	–	–	–	Weisburg et al., 1986
	–	S	–	–	–	–	–	–	–	Achenbach-Richter, Stetter and Woese, 1987
	–	O	–	–	–	–	–	–	–	Albrecht et al., 1987
	–	–	–	–	S	–	–	–	–	Dams et al., 1987
	–	S	–	–	–	–	–	–	–	Oyaizu et al., 1987
	–	–	–	–	S	–	–	–	–	Park et al., 1987
	–	S	–	–	–	–	–	–	–	Romaniuk et al., 1987
	–	S	–	–	–	–	–	–	–	Wells et al., 1987
	–	O	–	–	–	–	–	–	–	Auling et al., 1988
	–	–	–	–	S	–	–	–	–	Bomar et al., 1988
	–	S	–	–	–	–	–	–	–	Chuba et al., 1988
	–	–	–	–	S	–	–	–	–	Deming et al., 1988
	–	S	–	–	–	–	–	–	–	Distel et al., 1988
	–	O	–	–	–	–	–	–	–	Ehlers et al., 1988
	–	S	–	–	–	–	–	–	–	Embley et al., 1988a
	–	S	–	–	–	–	–	–	–	Embley et al., 1988b
	–	S	–	–	–	–	–	–	–	Franzmann and Stackebrandt et al., 1988
	–	S	–	–	–	–	–	–	–	Franzmann, Wehmeyer and Stackebrandt, 1988
	–	S	–	–	–	–	–	S	–	Giovannoni et al., 1988
	–	S	–	–	–	–	–	–	–	Montgomery et al., 1988
	–	S	–	–	–	–	–	–	–	Bateson et al., 1989
	–	–	–	–	S	–	–	–	–	Coyne et al., 1989
	–	S	–	–	–	–	–	–	–	Demharter et al., 1989
	–	S	–	–	–	–	–	–	–	Devereux et al., 1989
	–	S	–	–	–	–	–	–	–	Dewhirst et al., 1989
	–	S	–	–	–	–	–	–	–	Fox and Brown, 1989
	–	O	–	–	–	–	–	–	–	Hahn et al., 1989
	–	S	–	–	–	–	–	–	–	Hartmann et al., 1989
	–	S	–	–	–	–	–	–	–	Lim and Sears, 1989
	H	H	–	–	–	–	–	–	–	Roggentin and Hirsch, 1989
	–	O	–	–	–	–	–	–	–	Stackebrandt et al., 1989
	–	S	–	–	–	–	–	–	–	Tsuji et al., 1989
	–	S	–	–	–	–	–	–	–	Turner et al., 1989
	–	S	–	–	–	–	–	–	–	Weisburg and Dobson et al., 1989
	–	S	–	–	–	–	–	–	–	Weisburg, Giovanni and Woese, 1989
	–	S	–	–	–	–	–	–	–	Weisburg and Tully et al., 1989
	–	S	–	–	–	–	–	–	–	Yang and Woese, 1989
	–	S	–	–	–	–	–	–	–	Bateson et al., 1990
	–	–	–	–	S	–	–	–	–	Bulygina et al., 1990

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
	–	S	–	–	–	–	–	–	–	Devereux and He et al., 1990
	–	S	–	–	–	–	–	–	–	Dewhirst et al., 1990
	S	S	–	–	–	–	–	–	–	Guého et al., 1990
	–	S	–	–	–	–	–	–	–	La Fountaine and Rood, 1990
	–	S	–	–	–	–	–	–	–	Rogall et al., 1990
	–	S	–	–	–	–	–	–	–	Stackebrandt and Charfreitag, 1990
	–	S	–	–	–	–	–	–	–	Stahl and Urbance, 1990
	–	–	–	–	S	–	–	–	–	Van den Eynde, Van de Peer, Perry and de Wachter, 1990
	–	–	–	–	S	–	–	–	–	Van den Eynde, Van de Peer, Vandenabeele, Van Bogaert and de Wachter, 1990
	–	S	–	–	–	–	–	–	–	Wallbanks et al., 1990
	–	S	–	–	–	–	–	–	–	Zhao et al., 1990
	H	H	–	–	–	–	–	–	–	Catlin, 1991
	–	S	–	–	–	–	–	–	–	Collins et al., 1991
	–	S	–	–	–	–	–	–	–	Eden et al., 1991
	–	S	–	–	–	–	–	–	–	Fox et al., 1991
	R	R	–	–	–	–	–	–	–	Liebl et al., 1991
	–	S	–	–	–	–	–	–	–	Paster et al., 1991
	H	H	–	–	–	–	–	–	–	Rossau et al., 1991
	–	S	–	–	–	–	–	–	–	Stanton et al., 1991
	S	–	–	–	–	–	–	–	–	Vandamme et al., 1991
	–	S	–	–	–	–	–	–	–	Weisburg et al., 1991
	H	–	–	–	–	–	–	–	–	Willems et al., 1991
Eukaryota	–	–	–	–	S	–	–	–	–	Komiya and Takemura, 1981
	–	–	S	–	–	–	–	–	–	Olsen and Sogin, 1982
	–	–	–	–	S	–	–	–	–	Takaiwa et al., 1982
	–	–	–	–	S	–	–	–	–	Katoh et al., 1983
	–	O	–	–	–	–	–	–	–	Stöcklein et al., 1983
	S	S	–	–	–	–	–	–	–	Hasegawa et al., 1985
	–	–	S	–	–	–	–	–	–	Maroteaux et al., 1985
	–	–	–	–	S	–	–	–	–	Lim et al., 1986
	–	S	–	–	–	–	–	–	–	Medlin et al., 1988
	–	–	–	–	S	–	–	–	–	Qi et al., 1988
	S	–	–	–	–	–	–	–	–	Qu, Nicoloso and Bachellerie, 1988
	S	S	–	–	–	–	–	–	–	Gouy and Li, 1989b
	–	S	–	–	–	–	–	–	–	Sogin, 1989
	–	S	–	–	–	–	–	–	–	Sogin, Edman and Elwood, 1989
	–	S	–	–	S	–	–	–	–	Krishnan et al., 1990
Basal eukaryotes	–	–	–	–	S	–	–	–	–	Delihas et al., 1981
	–	–	S	–	S	–	–	–	–	Hinnebusch et al., 1981
	–	–	S	–	S	–	–	–	–	MacKay and Doolittle, 1981
	–	–	–	–	S	–	–	–	–	Anderson et al., 1982
	–	–	–	–	S	–	–	–	–	Kumazaki, Hori, Osawa, Mita and Higashinakagawa, 1982
	–	–	–	–	S	–	–	–	–	Walker and Doolittle, 1982
	–	–	–	–	S	–	–	–	–	Kumazaki et al., 1983
	–	–	–	–	S	–	–	–	–	Walker and Doolittle, 1983b
	–	S	–	–	–	–	–	–	–	Elwood et al., 1985
	–	–	S	–	S	–	–	–	–	Walker, 1985
	–	S	–	–	–	–	–	–	–	Gunderson et al., 1986
	–	S	–	–	–	–	–	–	–	Herzog and Maroteaux, 1986
	S	–	–	–	–	–	–	–	–	Qu et al., 1986

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
	–	S	–	–	–	–	–	–	–	Sogin and Elwood, 1986
	–	S	–	–	–	–	–	–	–	Sogin, Elwood and Gunderson, 1986
	–	S	–	–	–	–	–	–	–	Sogin and Ingold et al., 1986
	–	S	–	–	–	–	–	–	–	Sogin and Swanton et al., 1986
	–	–	S	–	–	–	–	–	–	Troitsky and Bobrova, 1986
	–	S	–	–	–	–	–	–	–	Gunderson and Elwood et al., 1987
	–	S	–	–	–	–	–	–	–	Johnson et al., 1987
	–	S	–	–	–	–	–	–	–	Sogin and Gunderson, 1987
	–	S	–	–	–	–	–	–	–	Vossbrinck et al., 1987
	S	–	–	–	–	–	–	–	–	Baroin et al., 1988
	–	S	–	–	–	–	–	–	–	Clark and Cross, 1988
	–	S	–	–	–	–	–	–	–	Johansen et al., 1988
	–	S	–	–	–	–	–	–	–	Johnson et al., 1988
	–	–	–	–	–	S	S	–	–	Lake et al., 1988
	S	–	–	–	–	–	–	–	–	Lenaers et al., 1988
	–	S	–	–	–	–	–	–	–	Lynn and Sogin, 1988
	S	–	–	–	–	–	–	–	–	Qu and Perasso et al., 1988
	–	S	–	–	–	–	–	–	–	Baverstock et al., 1989
	–	S	–	–	–	–	–	–	–	Johnson et al., 1989
	S	–	–	–	–	–	–	–	–	Lenaers et al., 1989
	S	–	–	–	–	–	–	–	–	Perasso et al., 1989
	–	S	–	–	–	–	–	–	–	Sogin and Gunderson et al., 1989
	–	S	–	–	–	–	–	–	–	Barta et al., 1991
	S	S	S	–	–	–	–	–	–	Gomez et al., 1991
	–	S	–	–	–	–	–	–	–	Hendricks et al., 1991
	S	–	–	–	–	–	–	–	–	Lenaers et al., 1991
	–	S	–	–	–	–	–	–	–	Schlegel et al., 1991
Fungi	S	–	–	–	–	–	S	–	–	Köchel and Küntzel, 1982
	–	–	–	–	S	–	–	–	–	Huysmans et al., 1983
	–	–	–	–	S	–	–	–	–	Chen et al., 1984
	–	–	–	–	S	–	–	–	–	Gottschalk and Blanz, 1984
	–	–	–	–	S	–	–	–	–	Walker, 1984a
	–	–	–	–	S	–	–	–	–	Walker, 1984b
	–	–	–	–	S	–	–	–	–	Gottschalk and Blanz, 1985
	–	–	–	–	S	–	–	–	–	Blanz and Gottschalk, 1986
	R	R	R	R	–	–	–	–	–	Kistler et al., 1987
	–	S	–	–	–	–	–	–	–	Edman et al., 1988
	–	–	–	–	–	S	–	–	–	Cummings, Domenico and Nelson, 1989; Cummings, Domenico, Nelson and Sogin, 1989
	S	–	–	–	–	–	–	–	–	Guadet et al., 1989
	R	R	R	R	–	–	–	–	–	Laaser et al., 1989
	–	S	–	–	–	–	–	–	–	Watanabe et al., 1989
	R	R	R	R	–	–	–	–	–	Lachance, 1990
Plantae	–	–	–	–	S	–	–	–	–	Hori et al., 1984
	–	–	–	–	S	–	–	–	–	Ulbrich et al., 1984
	–	–	–	–	S	–	–	–	–	Yamano et al., 1984
	–	–	–	–	S	–	–	–	–	Hori et al., 1985
	–	S	–	–	–	–	–	–	–	Troitsky and Bobrova, 1986
	–	S	–	–	–	–	–	–	–	Hamby and Zimmer, 1988
	–	–	–	–	S	–	–	–	–	Devereux, Loeblich III and Fox, 1990
	–	–	–	–	S	–	–	–	–	Steele et al., 1991

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
Green algae	–	S	–	–	–	–	–	–	–	Jupe et al., 1988
	–	S	–	–	–	–	–	–	–	Rausch et al., 1989
	–	S	–	–	–	–	–	–	–	Huss and Sogin, 1990
	–	–	–	–	S	–	–	–	–	Van de Peer and de Baere et al., 1990
	–	S	–	–	–	–	–	–	–	Eschbach et al., 1991
	–	R,S	–	–	–	–	–	–	–	Rowan and Powers, 1991
Seed plants	–	S	–	–	–	–	–	–	–	Nairn and Ferl, 1988
	S	S	–	–	–	–	–	–	–	Zimmer et al., 1989
Angiosperms	R	R	R	R	–	–	–	R	R	Sytsma and Schaal, 1985
	–	–	–	–	S	–	–	–	S	Bobrova et al., 1987
	–	–	–	S	–	–	–	–	–	McIntyre et al., 1988
	–	–	–	–	S	–	–	–	–	Scoles et al., 1988
	–	–	–	–	–	–	–	S	S	Wolfe et al., 1989
	–	–	S	S	–	–	–	–	–	Yokota et al., 1989
	R	R	R	R	–	–	–	–	–	Bellarosa et al., 1990
	–	S	–	–	–	–	–	–	–	Nickrent and Franchina, 1990
	R	R	R	R	–	–	–	–	–	Reddy et al., 1990
Animalia	–	–	–	–	S	–	–	–	–	Komiya et al., 1980
	–	–	–	–	S	–	–	–	–	Butler et al., 1981
	–	–	–	–	S	–	–	–	–	Kumazaki, Hori, Osawa, Ishii and Suzuki, 1982
	–	–	–	–	S	–	–	–	–	Komiya et al., 1983
	–	–	–	–	S	–	–	–	–	Ohama and Kumazaki et al., 1983
	–	–	–	–	S	–	–	–	–	Walker and Doolittle, 1983a
	–	–	–	–	S	–	–	–	–	Ohama et al., 1984
	–	–	–	–	S	–	–	–	–	Hendriks et al., 1986
	–	S	–	–	–	–	–	–	–	Field et al., 1988
	–	S	–	–	–	–	–	–	–	Hendriks et al., 1988
	–	S	–	–	–	–	–	–	–	Ghiselin, 1989
	–	S	–	–	–	–	–	–	–	Lake, 1989b
	–	S	–	–	–	–	–	–	–	Patterson, 1989
	–	S	–	–	–	–	–	–	–	Raff et al., 1989
	–	S	–	–	–	–	–	–	–	Lake, 1990
	S	–	–	–	–	–	–	–	–	Christen et al., 1991
	–	S	–	–	–	–	–	–	–	Erwin, 1991
	–	–	–	–	S	–	–	–	–	Halanych, 1991
Platyhelmithes	R	R	R	R	–	–	–	–	–	Blair and McManus, 1989
Mollusca	–	S	–	–	–	–	–	–	–	Ghiselin, 1988
Arthropoda	–	S	–	–	–	–	–	–	–	Abele et al., 1989
Crustacea	–	S	–	–	–	–	–	–	–	Kim and Abele, 1990
Insecta	–	–	–	–	–	–	S	–	–	DeSalle et al., 1987
	–	S	–	–	–	–	–	–	–	Hancock et al., 1988
	–	–	S	–	S	–	–	–	–	Wheeler and Honeycutt, 1988
	R	R,S	R	R	–	–	–	–	–	Wheeler, 1989
Echinoderms	–	–	–	–	S	–	–	–	–	Ohama, Hori and Osawa, 1983
	–	S	–	–	–	–	–	–	–	Raff et al., 1988
	–	S	–	–	–	–	–	–	–	Smith, 1989
Chordata	R	R	R	R	–	–	–	–	–	Tanhauser et al., 1986
	S	–	–	–	–	–	–	–	–	Le et al., 1989
	S	–	–	–	–	–	–	–	–	Hillis, Dixon and Ammerman, 1991
	–	S	–	–	–	–	–	–	–	Stock et al., 1991

APPENDIX *continuation*
Phylogenetic studies of ribosomal DNA

Taxa	nL	nS	5.8S	Spacers	5S	mtS	mtL	cpS	cpL	Reference
Tetrapoda	S	–	–	–	–	–	–	–	–	Hillis and Dixon, 1989
	S	S	–	–	–	–	–	–	–	Hedges et al., 1990
	–	–	–	–	–	S	–	–	–	Meyer and Wilson, 1990
Amphibia	S	–	–	–	–	–	–	–	–	Hillis, 1991
Anura	R	–	–	–	–	–	–	–	–	Hillis and Davis, 1987
	S	–	–	–	–	–	–	–	–	de Sá and Hillis, 1990
	R	R	R	R	–	–	–	–	–	Hillis and Davis, 1986
Caudata	S	–	–	–	–	–	–	–	–	Larson and Wilson, 1989
	S	S	–	–	–	–	–	–	–	Larson, 1991
Amniota										
Mammalia	–	–	–	–	–	S	S	–	–	Miyamoto and Boyle, 1989
Artiodactyls	–	–	–	–	–	S	S	–	–	Miyamoto et al., 1989
	–	–	–	–	–	S	S	–	–	Miyamoto et al., 1990
	–	–	–	–	–	S	S	–	–	Kraus and Miyamoto, 1991
Chiroptera	R	R	R	R	–	–	–	–	–	Baker et al., 1991
	R	R	R	R	–	–	–	–	–	Van Den Bussche, in press
Marsupials	–	–	–	–	–	–	S	–	–	Thomas et al., 1989
Primates	R	R	R	R	–	–	–	–	–	Nelkin et al., 1980
	R	R	R	R	–	–	–	–	–	Wilson et al., 1984
	–	–	–	–	–	S	S	–	–	Hixson and Brown, 1986
	S	–	–	S	–	–	–	–	–	Gonzalez et al., 1990
Rodents	–	–	–	R	–	–	–	–	–	Suzuki et al., 1986
	–	–	–	S	–	–	–	–	–	Sasaki et al., 1987
	–	–	–	R	–	–	–	–	–	Suzuki et al., 1987
	–	–	–	R	–	–	–	–	–	Nevo and Beiles, 1988
	R	R	R	R	–	–	–	–	–	Allard and Honeycutt, 1991
Sauria										
Lepidosauria	R	R	R	R	–	–	–	–	–	Sites and Davis, 1989
Aves	R	R	R	R	–	–	–	–	–	Mindell and Honeycutt, 1989
	R	R	R	R	–	–	–	–	–	Cracraft and Mindell, 1989