I was honoured when asked to curate this collection, but accepted with some trepidation. As the tagline states, Microbiology (Journal of General Microbiology prior to 1994) has been ‘publishing high-quality research since 1947’: capturing the breadth and depth of the journal’s contribution to microbiology in this short opinion piece is nigh impossible. I chose to steer a personal course through the journal archive and highlight some personal favourites here. Such an approach is by its nature highly selective and a function of my own predilections; I apologize upfront for the many outstanding contributions that I could not mention due to space limitations. I hope, however, to remind readers of the seminal work published in Microbiology over the years and perhaps to shine a light on some forgotten gems.

The early years of the journal saw a number of significant publications on improved methods for the isolation and characterization of microbes. In the journal’s first year, Derrick Edward reported a new selective media for the cultivation of mycoplasmas, or pleuropneumonia-like organisms (PPLO) as they were called at the time (Edward, 1947). Key innovations were his inclusion of thallium acetate to suppress the growth of contaminants and yeast extract to achieve greater consistency in growth. Supplementing with yeast extract was based on his observation of improved growth of the organisms in basal media near contaminating staphylococci or after addition of staphylococci culture filtrates. Although subsequently modified, notably by Leonard Hayflick (Hayflick, 1965), this medium provided a cornerstone for early mycoplasma research. Similarly, Kenneth Butlin and colleagues reported the development of standard media for isolation of sulphate-reducing bacteria (Butlin et al., 1949). The addition of 3% sodium sulphite was used to inhibit contaminants, while immersion of iron rods in the anaerobically incubated mineral salt media generated hydrogen during culture. Their advances allowed pure cultures of sulphur-reducing bacteria to be isolated from environmental samples, laying the foundation for subsequent work on the basic biochemistry of sulphate-reducing bacteria.

Continuing the cultural theme, the growth yield of bacteria in relation to their energy supply was the subject of Thomas Bauchop and Sydney Elsden’s elegant studies (Bauchop & Elsden, 1960). Using anaerobic cultures of Streptococcus faecalis, Saccharomyces cerevisiae and Pseudomonas linderi, they demonstrated that the dry weight growth yield of an organism was proportional to the amount of ATP produced. Their yield coefficient $Y_{ATP}$, sometimes referred to as the Bauchop–Elsden value, was shown to be relatively constant at 10.5 g dry weight of cells per mole of ATP consumed. This paper also described a now common stock salt solution for defined media, often referred to as Bauchop and Elsden solution. In a similar vein, John Beringer’s Tryptone Yeast (TY) media, employed for his analysis of $R$ factor transfer between Rhizobium leguminosarum and Escherichia coli, has since become a standard (Beringer, 1974). The journal’s contribution to improved culture methods even goes beyond the realm of microbiology to touch on botany. In his work on the infection of clover root hairs by Rhizobium, Gosta Fahraeus described a nitrogen-free media for the cultivation of young seedlings (Fahraeus, 1957). Growing root hairs were embedded in agar on glass slides, infected with Rhizobium and then transferred into the medium. This technique permitted the infective process to be observed in striking microscopic detail without disturbing the root system. ‘Fahraeus medium’ has since found wide application for the cultivation of seedlings.

Bacterial classification has been the subject of many major articles over the years. Roger Stanier and colleagues in particular produced two landmark studies on cyanobacteria and pseudomonads (Rippka et al., 1979; Stanier et al., 1966). In ‘Generic assignments, strain histories and properties of pure cultures of cyanobacteria’ (Rippka et al., 1979), Stanier sought to move the classification of cyanobacteria away from its botanical origins to a firmly bacteriological grounding. Five taxonomic sections of cyanobacteria were defined based on physiological properties and structural features (Rippka et al., 1979). Many of the light microscopy images used in the paper to exhibit the structural diversity of cyanobacteria are exquisite, even when compared with modern confocal microscopy images. No doubt the combination of outstanding science and artistry contributed to making this the most cited article published in the journal to date.

In the current world where genome data are transforming microbiology, evidenced by the launch of the Microbiology Society’s new Microbial Genomics journal, one can’t but...
help be drawn to Peter Sneath’s back-to-back publications on numerical taxonomy (Sneath, 1957a, b). Sneath first set out his case for a system of bacterial classification based on overall similarity across a range of measured ‘characters’ (Sneath, 1957b). Crucially, he suggested that all such characters be given equal weighting when deriving the ultimate groupings. He developed these ideas further in the following paper ‘The application of computers to taxonomy’, where he described how multiple phenotypic features could be numerically coded to facilitate computational analysis (Sneath, 1957a). The need for such approaches was stated in the first sentence: ‘The classification of bacteria has reached a point at which there is a need for some mechanical aid to sorting the data’. Clearly Sneath was ahead of his time in using computational approaches to address ‘big data’ problems in microbiology.

The emerging field of bacterial genetics was showcased in 1953 with back-to-back publications by Hayes (1953) and Cavalli et al. (1953) on the nature of bacterial transformation – an area of some controversy at the time. In the first of these papers, William Hayes described spontaneous mutants of ‘Bacterium coli K12’ that had lost the ability to undergo genetic recombination (Hayes, 1953). He hypothesized that these mutants had lost some ‘gene carrier’ that they might reacquire via a process akin to phage infection. In detailed crosses he showed that ‘fertility depends on the presence of a gene carrier in F+ cells and its absence from F– cells’, using the F+/F– nomenclature introduced by Joshua Lederberg, Luca Cavalli-Sforza and Esther Lederberg (Lederberg et al., 1952). The following paper from Cavalli-Sforza, Lederberg and Lederberg corroborated Hayes’ findings and extended their own observations on ‘infective inheritance’ and its control through sex compatibility (Cavalli et al., 1953). Later research would show that the F+ factor was in fact a plasmid, but these papers provided significant clues to deciphering the mechanistic puzzle of bacterial transformation.

Insights into the mechanisms of microbial pathogenesis have also been covered in depth by many authors. Harry Smith published notable contributions to the study of bacterial pathogenesis in the journal, with studies on Bacillus anthracis, Brucella, and Neisseria gonorrhoeae (Smith, 1990). These included several papers on the purification and characterization of the tripartite anthrax toxin and the use of in vivo grown bacilli to facilitate toxin purification (Smith & Stanley, 1962; Stanley & Smith, 1961, 1963; Stanley et al., 1960). Smith was already convinced in 1947 that ‘to learn more about bacterial pathogenicity we should examine organisms grown in vivo’ (Smith, 1990) – a concept that has truly come to fruition with modern tools in cellular and molecular biology.

Microbiology has seen the first descriptions of important microbes over the years. In his paper on genetic recombination in Pseudomonas aeruginosa, Bruce Holloway described four P. aeruginosa strains that formed the basis of his analyses (Holloway, 1955). One of these, ‘strain 1, isolated from a wound in Melbourne’, was subsequently designated PAO1 and generously distributed to other laboratories. PAO1 is now the most widely used P. aeruginosa strain in the world and the first to have its genome sequenced. The search for a strong coagulase producing strain of Staphylococcus aureus led Edward Duthie and Lisa Lorenz to isolate S. aureus ‘Newman’ from a case of secondarily infected tubercular osteomyelitis (Duthie & Lorenz, 1952); the high virulence of this strain made it a staple of the staphylococcal research community. Another first was the description Candida dubliniensis by Derek Sullivan and David Coleman (Sullivan et al., 1995), identified from cases of oral candidosis as distinct from the other pathogenic Candida species and an emerging pathogen, particularly in human immunodeficiency virus-positive individuals.

My own favourite bacterial phylum, the Actinobacteria, has been well served by the journal. The publications of David Hopwood and colleagues charted the rise of actinobacterial genetics, including the first definitive plasmid localization of antibiotic synthesis genes shown for methylenomycin encoded by the SCP1 linear plasmid (Kirby & Hopwood, 1977; Kirby et al., 1975). Michael Goodfellow, David Minnikin and colleagues contributed influential works on taxonomy and lipid analysis of Actinobacteria, including a simple and widely adopted method for extraction and analysis of quinones (Collins et al., 1977). Significant publications on mycobacteria have encompassed antigen discovery (Berthet et al., 1998), genetic markers for molecular epidemiology (Frothingham & Meeker-O’Connell, 1998), genome annotation (Camus et al., 2002) and tools for mutant generation (Bardarov et al., 2002; Parish & Stoker, 2000).

The rise of molecular methods in the 1990s fundamentally altered approaches to typing and differentiation of bacteria. The development of multilocus sequencing typing (MLST) provided an unambiguous method that greatly facilitated inter-laboratory comparison of typing data, as shown by Mark Enright and Brian Spratt for Streptococcus pneumoniae (Enright & Spratt, 1998). This study identified pneumococcal clones and clonal complexes from a large collection of strains, signalling the power of DNA sequencing to elucidate the global molecular epidemiology and evolution of pathogens. Turning from pure cultures, forays into defining microbial community structure were hugely aided by the development of molecular probes. Karl-Heinz Schleifer and colleagues described 16S rRNA probes and allied fluorescence in situ hybridization protocols for the identification of Bacteroidetes (Manz et al., 1996), Actinobacteria (Roller et al., 1994), and Planctomycetes (Neef et al., 1998) populations in activated sludge and faecal samples. These probes have since gone on to be part of the standard toolbox for characterization of polymicrobial communities.

Moving into the 21st century, the journal published the first reports describing anti-phage features of clustered regularly interspaced short palindromic repeats (CRISPR)
In the first of these, Pourcel et al. (2005) analysed the available genome sequences of *Yersinia pestis* to identify three CRISPR elements, and then amplified and sequenced these loci from multiple *Y. pestis* and *Yersinia pseudotuberculosis* strains (Pourcel et al., 2005). They observed that the majority of new spacers had a homologue in a 46 kb prophage locus, prompting them to propose that new CRISPR spacers arose from phage. Hot on the heels of this work, the subsequent publication by Bolotin et al. (2005) showed a correlation between phage sensitivity of *Streptococcus thermophilus* and the number of spacers in the CRISPR locus. This led the authors to suggest that the CRISPR locus was involved in resistance to phage attack via antisense RNA inhibition of phage gene expression, since clearly confirmed. Furthermore, Bolotin et al. (2005) were the first to detect a short sequence motif adjacent to spacer-matching sequences, suggesting some recognition system at work in selecting sequences for insertion into CRISPR loci. This finding was further extended by Mojica et al. (2009) who defined ‘proto-spacer adjacent motifs’ (PAMs), that were specific to individual CRISPR systems. This led to a model whereby PAMs dictated the acquisition and orientation of new spacers, catalysed by the Cas9 enzyme. As the authors had presciently suggested, the identification of PAMs has become integral to the exploitation of the CRISPR–Cas system as an ‘innovative molecular biology tool’ (Mojica et al., 2009).

I have to make brief mention of the special lectures as they provide a wonderful source of anecdote and historical context. The First Griffith Memorial Lecture, delivered by Hayes (1966), provides insightful and generous biographical details on Fred Griffith and his classic work on pneumococcal transformation. Hayes was struck by Griffith’s failure to mention that transformation led to an ‘inheritable change of character’ and goes on to trace the developments in genetics that led directly from Griffith’s work. This theme is also visited by Allan Downie in the Fourth Griffith Memorial Lecture who focussed on Oswald Avery and colleagues’ work in the ultimate description of DNA as the transforming principle and ‘brought to such a successful conclusion the story which (Griffith) had so dramatically began’ (Downie, 1972). Indeed one can’t help but be struck by the lyrical style of such reviews compared with the standard style of today. One of my favourites in this regard is Andre Lwoff’s Marjory Stephenson Memorial Lecture on ‘The concept of virus’ – an eclectic philosophical discourse on the nature of viruses that merges scientific argument with literary allusion (Lwoff, 1957). It makes many current reviews most dull by comparison.

In the limited space available I have merely managed to skim the journal’s impact on microbiology over the past 70 years. I hope that I have piqued your interest to delve into the archives and explore the rich legacy that lies within. It is a contribution that the Microbiology Society and all associated with *Microbiology* can be hugely proud of, and one that will continue long into the future.

### Highlighted articles


**Fahraeus, G. (1957).** The infection of clover root hairs by nodule bacteria studied by a simple glass slide technique. *J Gen Microbiol* 16, 374–381.


**Sneath, P. H. (1957a).** The application of computers to taxonomy. *J Gen Microbiol* 17, 201–226.


### Further Reading


