Biofilm formation, structure and function

Grant Kinkead
Independent Researcher, Melbourne, VIC, Australia
grant@kinkead.au

***Abstract*—Biofilm formation is commonly explained as a sequence in which bacteria attach to a surface, accumulate into a structured community and eventually disperse. This account is useful, but it does not encompass every biofilm: bacterial aggregates can form without persistent surface attachment, and their architecture and physiology vary with local conditions. This paper synthesises two peer-reviewed reviews to explain the relationships among community development, extracellular material, bacterial regulation and environmental context. Aggregation or attachment establishes a community; accumulation changes its organisation; and disaggregation or detachment alters its continuity. Matrix composition is relevant to structure, while cyclic di-GMP and quorum sensing are among the mechanisms associated with bacterial biofilm regulation. Nutrients, flow, species composition and local microenvironments further influence architecture and physiology. Together, these findings support a flexible causal account rather than a universal developmental sequence or characteristic shape. The resulting framework clarifies what biofilm formation, structure and function mean, but it cannot predict the behaviour of a particular community without evidence about its organisms and surroundings.**

I. Introduction

Biofilm formation is more than the appearance of bacteria on a surface. Bacteria may organise as attached communities or as aggregates without persistent surface attachment, and their organisation can change through accumulation and separation [1]. These possibilities matter because an explanation limited to surface attachment would exclude some communities before their structure or physiology could be considered. Formation describes how a community comes together and changes over time; structure describes its resulting organisation; function concerns what occurs within that organisation. An account of biofilms must relate these concepts without assuming that one visible form represents every developmental route.

A familiar developmental description moves from attachment through maturation to dispersion [2]. It provides a clear way to discuss changes in an attached community, including the contribution of extracellular material and bacterial regulation. Its explanatory strength becomes a limitation if those stages are treated as a compulsory sequence for every aggregate. A broader description accommodates both attachment and aggregation, followed by accumulation and eventual disaggregation or detachment [1]. The central difficulty is therefore not choosing one vocabulary over the other, but determining which description fits an observed community and what its conditions permit that description to explain.

This paper develops a causal account of biofilm formation, structure and function from those complementary perspectives. It examines developmental descriptions, the relevance of matrix composition and regulatory mechanisms, and the influence of nutrients, flow, species composition and local microenvironments on architecture and physiology [1], [2]. It then distinguishes relationships supported across the reviews from conclusions that depend on a particular organism or setting. This distinction is essential: a general model can guide interpretation, but the structure and activity of a specific biofilm cannot be established solely by assigning it a developmental label.

II. Background and Scope

A staged model makes the changing organisation of a biofilm easier to describe. Attachment identifies one possible beginning; maturation directs attention to continued development; and dispersion acknowledges that an established community is not necessarily permanent [2]. A more inclusive model identifies aggregation or attachment, subsequent growth or accumulation, and disaggregation or detachment [1]. Both accounts recognise change rather than treating a biofilm as a static object. Their difference concerns the starting assumption: the narrower sequence begins with surface association, whereas the broader account does not require it. That difference affects which communities a model can describe without distortion.

The surface-based account remains useful where its starting conditions apply. It helps relate early association to later community organisation and provides terms for discussing how an established biofilm changes [2]. It does not follow, however, that every community must acquire the same shape or remain attached throughout its development. The broader account accommodates aggregates whose organisation cannot be adequately characterised by a fixed surface-bound picture [1]. Used together, the models encourage a distinction between a developmental transition and its physical expression: similar terms for accumulation or separation need not imply identical architecture in different surroundings.

The scope of mechanistic interpretation is also constrained by the organisms represented in the evidence. The review of matrix composition and regulatory mechanisms draws substantially on Pseudomonas, making it informative about possible routes from bacterial behaviour to community organisation without making every observation universal [2]. The broader review emphasises that species composition and local microenvironments affect architecture and physiology [1]. Thus, neither a model organism nor a general lifecycle supplies a complete account of an unidentified community. The

remaining explanatory task is to connect formation, structure and function while keeping the difference between a supported general relationship and a setting-specific outcome explicit.

III. Core Concepts and Mechanisms

Aggregation or attachment establishes the community whose later changes constitute biofilm development. Subsequent accumulation changes its extent and organisation, while disaggregation, detachment or dispersion alters its continuity [1], [2]. These are meaningful transitions, but they need not occur as identical steps under identical conditions. Their causal significance is that each changes the arrangement of cells relative to one another and to their immediate surroundings. Formation is therefore better understood as a continuing reorganisation than as a single act of attaching to a surface. Observing attachment alone does not establish how a community will mature, what structure it will acquire or how long it will remain organised.

Extracellular material is part of the explanation of biofilm structure. The composition of the matrix is relevant to how an organised bacterial community is characterised, alongside its developmental stage [2]. Yet matrix composition cannot be treated as a complete prediction of visible architecture, because nutrients, flow, species composition and local microenvironments also shape the organisation that develops [1]. Structure is consequently neither a purely bacterial property nor simply an imprint of the surroundings. It emerges from community development under particular conditions. This interpretation explains why describing a biofilm's appearance can aid understanding without, by itself, establishing its physiology.

Regulatory mechanisms connect bacterial behaviour to changes in community organisation. Cyclic di-GMP and quorum sensing are among the processes considered in the account of biofilm development and regulation [2]. Their relevance is conceptual as well as mechanistic: an attached or aggregated community is not explained solely by the presence of a surface or by external flow conditions. Bacterial responses also matter. However, identifying a regulatory process in studies of particular strains does not show that it governs every biofilm in the same way. A claim about its role in a specific community requires evidence for that community rather than an inference from the general developmental model.

IV. Evidence Synthesis

The reviews converge on a dynamic account of biofilm formation while differing in the breadth of communities their developmental descriptions encompass. Attachment, maturation and dispersion supply a coherent account for relevant attached communities [2]. Aggregation or attachment, accumulation, and disaggregation or detachment retain the idea of change without making a surface essential [1]. The latter does not render the former useless; it clarifies its domain. A stage name is informative when it describes an observed transition, but less informative when it substitutes for evidence about how an aggregate actually developed. Formation should therefore be interpreted through both temporal change and the physical circumstances of the community.

The relationship between structure and function becomes clearer when influences inside and outside the community are considered together. Matrix composition and bacterial regulation help explain aspects of development and organisation [2]. Nutrients, flow, species composition and local microenvironments influence architecture and physiology [1]. These accounts address different parts of the same question: how a community acquires a particular form and what its members experience within it. Neither set of influences should be reduced to the other. A description of extracellular material alone does not identify every environmental condition, while a description of flow alone does not establish the community's regulatory behaviour.

Taken together, the reviews support a causal framework rather than a universal forecast. A community forms through aggregation or attachment, changes as it accumulates, and may later separate; its structure and physiology reflect both its constituents and its local conditions [1], [2]. That synthesis explains why similar developmental terms can apply across settings without implying identical outcomes. It also marks a boundary on inference: the evidence does not establish which influence predominates in every organism or environment. To explain a particular biofilm's function, its observed organisation and circumstances are needed in addition to a general account of how biofilms can develop.

V. Practical Implications and Limitations

Interpretation should begin by determining whether the community is attached, aggregated without persistent attachment, or changing between observed states. A broad account permits these different forms of organisation [1], while a staged account offers terms for development where attachment, maturation and dispersion describe what occurs [2]. The distinction prevents a characteristic image of a surface biofilm from becoming an assumed history for every aggregate. It also makes structural descriptions more precise: an observed form can be reported as such without claiming that it proves a particular sequence of events. Formation and structure remain related, but neither can be read uncritically from the other.

Conditions surrounding a biofilm must be considered when interpreting its function. The reported influence of nutrients, flow, species composition and local microenvironments on architecture and physiology means that a description from one setting cannot automatically determine an outcome in another [1]. Similarly, cyclic di-GMP and quorum sensing are relevant to the reviewed account of development, but their contribution should not be assumed identical across strains or contexts [2]. This is a limit on generalisation, not a rejection of mechanistic explanation. General relationships identify plausible influences; evidence about the actual community is needed to establish their particular roles.

The evidence does not justify predicting a specific biofilm's architecture or activity from its classification alone. The reviews provide an account of developmental transitions, matrix

structure, regulation and environmental influences, while acknowledging variation among communities and settings [1], [2]. A stronger setting-specific explanation would need to establish how the community forms, how its organisation changes, which organisms and local conditions are present, and what physiology is actually observed. Without such information, claims about function should remain conditional. This requirement is especially important when a surface-based developmental picture is being applied to a community that might instead form principally as an aggregate.

VI. Conclusion

Biofilm formation, structure and function are connected aspects of microbial community organisation, but they are not interchangeable descriptions. Aggregation or attachment initiates an organised community; accumulation and separation change it; extracellular material and bacterial regulation contribute to its development [1], [2]. At the same time, nutrients, flow, species composition and local microenvironments help shape architecture and physiology [1]. A staged surface-based account is useful when its assumptions fit the community, while a broader account accommodates forms that it cannot adequately describe. Neither model alone establishes the behaviour of every biofilm.

The most valuable next step in explaining a particular community is to test the fit between the general framework and observations of that community. Its mode of aggregation, changing organisation and surrounding conditions should be established before a proposed regulatory or environmental influence is treated as decisive [1], [2]. This preserves the causal value of the available evidence without turning context-dependent relationships into universal rules. What a reader should understand is not a single obligatory shape or sequence, but a dynamic relationship between community development, physical organisation and locally conditioned physiology.

Acknowledgment

The author used artificial intelligence tools to assist with manuscript drafting and revision, and with LaTeX and bibliography preparation. The author reviewed all AI-assisted output and remains responsible for the final content.

References

[1] K. Sauer, P. Stoodley, D. M. Goeres, L. Hall-Stoodley, M. Burmølle, P. S. Stewart, and T. Bjarnsholt, "The biofilm life cycle: expanding the conceptual model of biofilm formation," *Nature Reviews Microbiology*, 2022.

[2] X. Wang, M. Liu, C. Yu, J. Li, and X. Zhou, "Biofilm formation: mechanistic insights and therapeutic targets," *Molecular Biomedicine*, 2023.