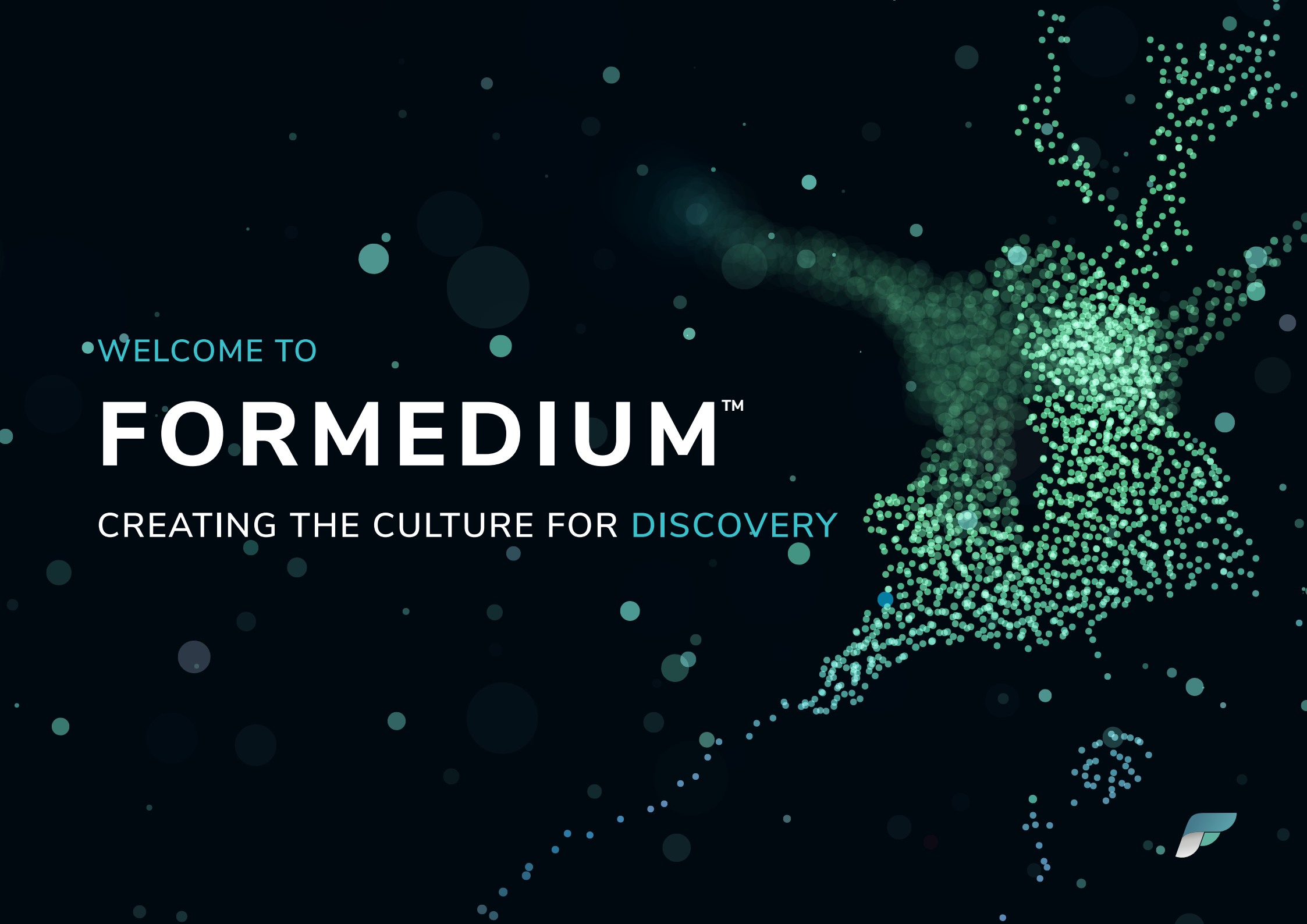
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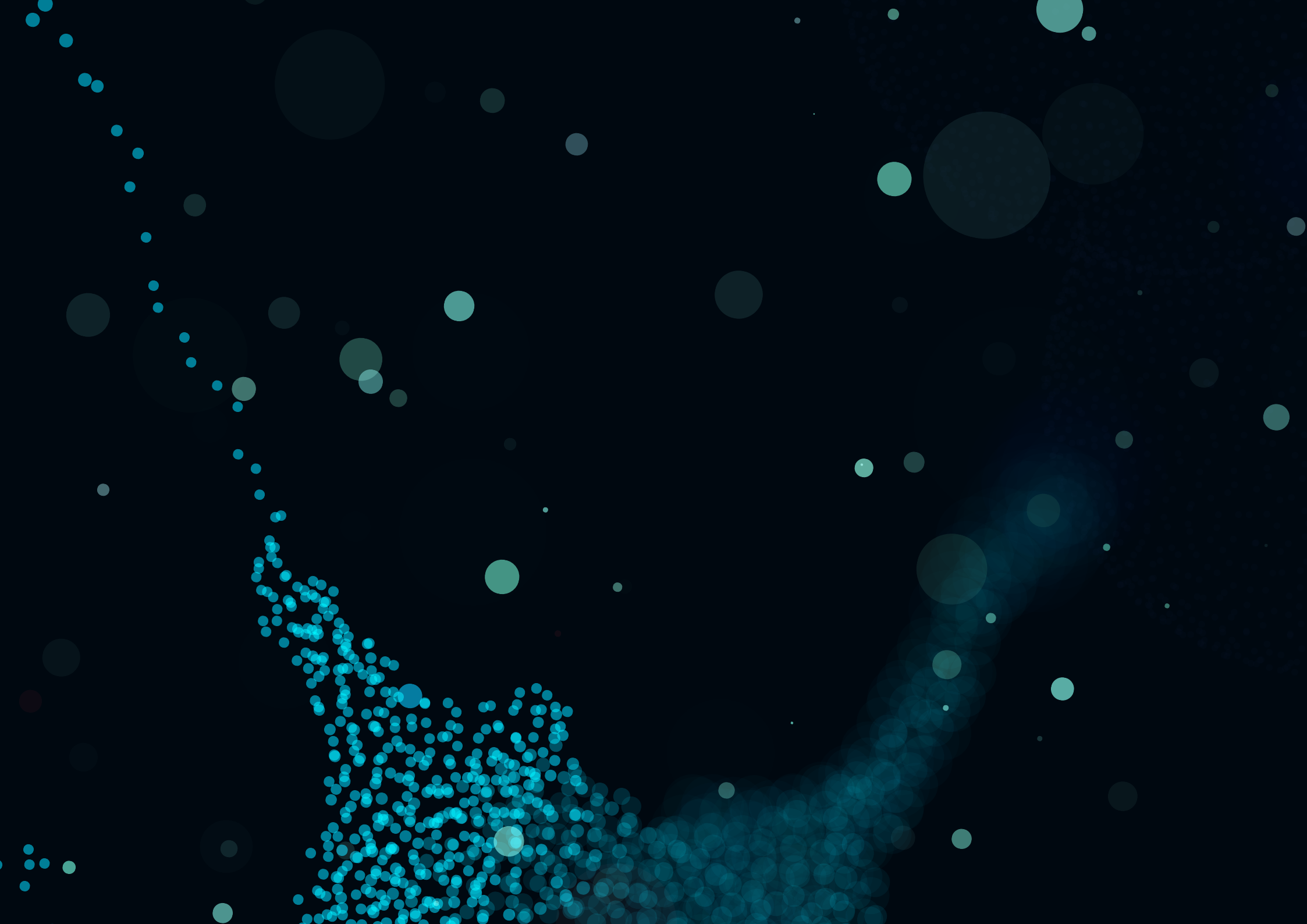

EXECUTIVE SUMMARY

BRIEF OVERVIEW OF THE COMPANY

- Formedium specialises in manufacturing and supplying high-quality powdered media.
- We offer a wide range of standard industry products and customised formulas.
- Are focused on delivering quality, service, and at very competitive prices.
- Serves the needs of academia, research, and industry.

At Formedium, we specialise in providing blending technology for the manufacturing of industry-standard media and custom nutrient formulations. Our team is highly skilled and agile, enabling us to swiftly respond to the evolving needs of our clients in microbial, cell, and bacterial growth research.

We combine advanced blending techniques with a deep understanding of product development to deliver tailored solutions that support optimal growth conditions for a wide range of scientific applications. Whether you need standard formulations or bespoke blends, we ensure the highest quality, consistency, and precision in every batch.

ABOUT FORMEDIUM

Ian Hodge

Specialised in the chemical and biochemical sectors with a focus on laboratory chemicals, custom synthesis, and research products.

Leadership experience in distributing laboratory chemicals and equipment, as well as managing the sales of specialised biochemical products.

Currently leading a company that manufactures custom bacteriological media for research, with expertise in yeast, E. coli, and fungal systems.

Passionate about science, supporting research projects worldwide.

Suzie Hodge

Extensive experience in field trials, administration, and consultancy.

Early career involved managing field trials in the chemical industry and working as an administrator for a major research and development department.

Later transitioned into consultancy, specialising in policy development for workplace substance abuse.

Since 2002, a key leader at Formedium, where her passion and commitment are unmatched.

MEET OUR TEAM

Senior leadership

Ian

Suzie

Office Team

Anne

Becca

Alex

Laboratory and Manufacturing team

Dave

Tom

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We provide fast responses to custom blend enquiries, allowing researchers to get exactly what they need in minimal time.

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DR SHANE PALMER, MRC MITOCHONDRIAL BIOLOGY UNIT
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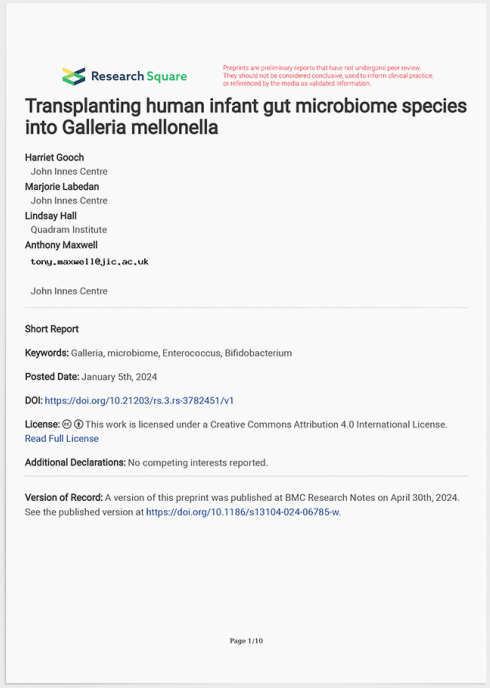

Research Square

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Transplanting human infant gut microbiome species into Galleria mellonella

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John Innes Centre

Short Report

Keywords: Galleria, microbiome, Enterococcus, Bifidobacterium

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Additional Declarations: No competing interests reported.

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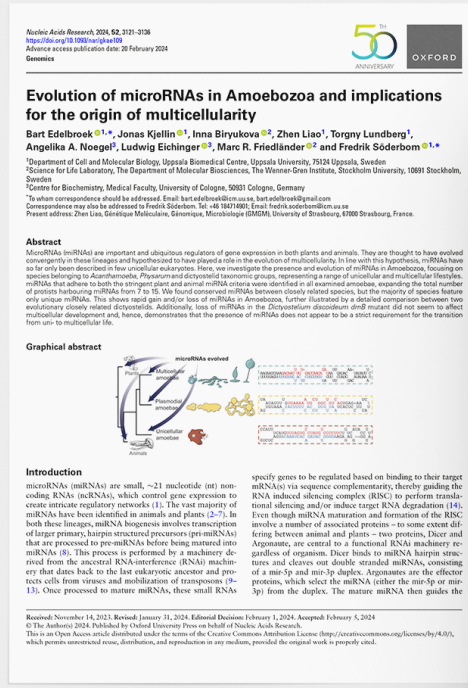

Nucleic Acids Research, 2024, 52, 3121–3136
https://doi.org/10.1093/nar/gkae109
Advance access publication date: 20 February 2024
Genomics

Evolution of microRNAs in Amoebozoa and implications for the origin of multicellularity

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Abstract

MicroRNAs (miRNAs) are important and ubiquitous regulators of gene expression in both plants and animals. They are thought to have evolved convergently in these lineages and hypothesized to have played a role in the evolution of multicellularity. In line with this hypothesis, miRNAs have so far only been described in few unicellular eukaryotes. Here, we investigate the presence and evolution of miRNAs in Amoebozoa, focusing on species belonging to *Acanthamoeba*, *Physarum* and dictyostelid taxonomic groups, representing a range of unicellular and multicellular lifestyles. miRNAs that adhere to both the stringent plant and animal miRNA criteria were identified in all examined amoebae, expanding the total number of protists harbouring miRNAs from 7 to 15. We found conserved miRNAs between closely related species, but the majority of species feature only unique miRNAs. This shows rapid gain and/or loss of miRNAs in Amoebozoa, further illustrated by a detailed comparison between two evolutionary closely related dictyostelids. Additionally, loss of miRNAs in the *Dictyostelium discoideum dmB* mutant did not seem to affect multicellular development and, hence, demonstrates that the presence of miRNAs does not appear to be a strict requirement for the transition from uni- to multicellular life.

Graphical abstract

Introduction

microRNAs (miRNAs) are small, ~21 nucleotide (nt) non-coding RNAs (ncRNAs), which control gene expression to create intricate regulatory networks (1). The vast majority of miRNAs have been identified in animals and plants (2–7). In both these lineages, miRNA biogenesis involves transcription of larger primary, hairpin structured precursors (pri-miRNAs) that are processed to pre-miRNAs before being matured into miRNAs (8). This process is performed by a machinery derived from the ancestral RNA-interference (RNAi) machinery that dates back to the last eukaryotic ancestor and protects cells from viruses and mobilization of transposons (9–13). Once processed to mature miRNAs, these small RNAs specify genes to be regulated based on binding to their target mRNA(s) via sequence complementarity, thereby guiding the RNA induced silencing complex (RISC) to perform translational silencing and/or induce target RNA degradation (14). Even though miRNA maturation and formation of the RISC involve a number of associated proteins – to some extent differing between animal and plants – two proteins, Dicer and Argonaute, are central to a functional RNAi machinery regardless of organism. Dicer binds to miRNA hairpin structures and cleaves out double stranded miRNAs, consisting of a mir-5p and mir-3p duplex. Argonautes are the effector proteins, which select the miRNA (either the mir-5p or mir-3p) from the duplex. The mature miRNA then guides the

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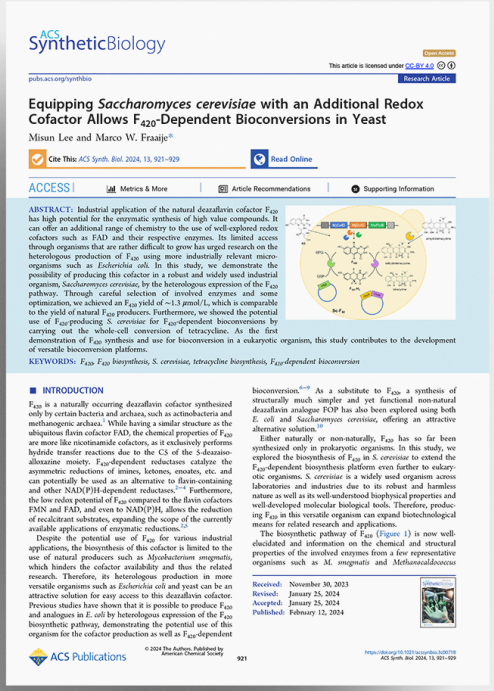

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Research Article

Equipping *Saccharomyces cerevisiae* with an Additional Redox Cofactor Allows F_{420}-Dependent Bioconversions in Yeast

Misun Lee and Marco W. Fraaije*

Cite This: *ACS Synth. Biol.* 2024, 13, 921–929
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ABSTRACT: Industrial application of the natural deazaflavin cofactor F_{420} has high potential for the enzymatic synthesis of high value compounds. It can offer an additional range of chemistry to the use of well-explored redox cofactors such as FAD and their respective enzymes. Its limited access through organisms that are rather difficult to grow has urged research on the heterologous production of F_{420} using more industrially relevant microorganisms such as *Escherichia coli*. In this study, we demonstrate the possibility of producing this cofactor in a robust and widely used industrial organism, *Saccharomyces cerevisiae*, by the heterologous expression of the F_{420} pathway. Through careful selection of involved enzymes and some optimization, we achieved an F_{420} yield of ~1.3 pmol/L, which is comparable to the yield of natural F_{420} producers. Furthermore, we showed the potential use of F_{420}-producing *S. cerevisiae* for F_{420}-dependent bioconversions by carrying out the whole-cell conversion of tetracycline. As the first demonstration of F_{420} synthesis and use for bioconversion in a eukaryotic organism, this study contributes to the development of versatile bioconversion platforms.

KEYWORDS: F_{420}, F_{420} *biosynthesis*, *S. cerevisiae*, *tetracycline biosynthesis*, F_{420}*-dependent bioconversion*

■ INTRODUCTION

F_{420} is a naturally occurring deazaflavin cofactor synthesized only by certain bacteria and archaea, such as actinobacteria and methanogenic archaea.[1] While having a similar structure as the ubiquitous flavin cofactor FAD, the chemical properties of F_{420} are more like nicotinamide cofactors, as it exclusively performs hydride transfer reactions due to the C5 of the 5-deazaisoalloxazine moiety. F_{420}-dependent reductases catalyze the asymmetric reductions of imines, ketones, enoates, etc. and can potentially be used as an alternative to flavin-containing and other NAD(P)H-dependent reductases.[2−5] Furthermore, the low redox potential of F_{420} compared to the flavin cofactors FMN and FAD, and even to NAD(P)H, allows the reduction of recalcitrant substrates, expanding the scope of the currently available applications of enzymatic reductions.[6,7]

Despite the potential use of F_{420} for various industrial applications, the biosynthesis of this cofactor is limited to the use of natural producers such as *Mycobacterium smegmatis*, which hinders the cofactor availability and thus the related research. Therefore, its heterologous production in more versatile organisms such as *Escherichia coli* and yeast can be an attractive solution for easy access to this deazaflavin cofactor. Previous studies have shown that it is possible to produce F_{420} and analogues in *E. coli* by heterologous expression of the F_{420} biosynthetic pathway, demonstrating the potential use of this organism for the cofactor production as well as F_{420}-dependent bioconversions.[4−9] As a substitute to F_{420}, a synthesis of structurally much simpler and yet functional non-natural deazaflavin analogue FOP has also been explored using both *E. coli* and *Saccharomyces cerevisiae*, offering an attractive alternative solution.[10]

Either naturally or non-naturally, F_{420} has so far been synthesized only in prokaryotic organisms. In this study, we explored the biosynthesis of F_{420} in *S. cerevisiae* to extend the F_{420}-dependent biosynthesis platform even further to eukaryotic organisms. *S. cerevisiae* is a widely used organism across laboratories and industries due to its robust and harmless nature as well as its well-understood biophysical properties and well-developed molecular biological tools. Therefore, producing F_{420} in this versatile organism can expand biotechnological means for related research and applications.

The biosynthetic pathway of F_{420} (Figure 1) is now well-elucidated and information on the chemical and structural properties of the involved enzymes from a few representative organisms such as *M. smegmatis* and *Methanoaldoaccus*

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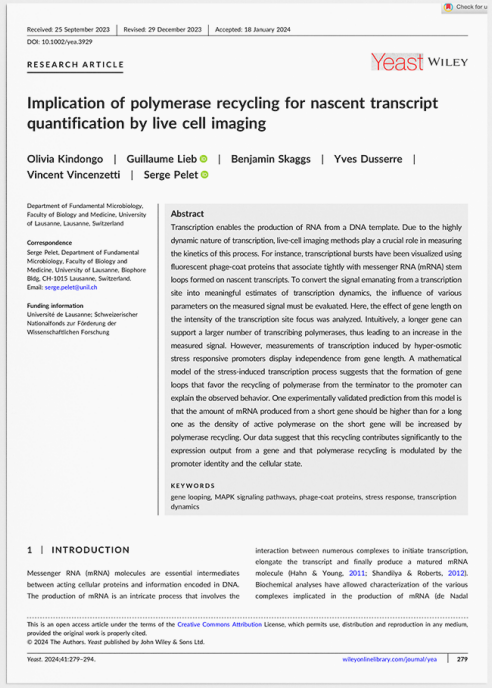

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DOI: 10.1002/yea.3929
RESEARCH ARTICLE
Yeast WILEY

Implication of polymerase recycling for nascent transcript quantification by live cell imaging

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Funding information
Université de Lausanne; Schweizerischer Nationalfonds zur Förderung der Wissenschaftlichen Forschung

Abstract

Transcription enables the production of RNA from a DNA template. Due to the highly dynamic nature of transcription, live-cell imaging methods play a crucial role in measuring the kinetics of this process. For instance, transcriptional bursts have been visualized using fluorescent phage-coat proteins that associate tightly with messenger RNA (mRNA) stem loops formed on nascent transcripts. To convert the signal emanating from a transcription site into meaningful estimates of transcription dynamics, the influence of various parameters on the measured signal must be evaluated. Here, the effect of gene length on the intensity of the transcription site focus was analyzed. Intuitively, a longer gene can support a larger number of transcribing polymerases, thus leading to an increase in the measured signal. However, measurements of transcription induced by hyper-osmotic stress responsive promoters display independence from gene length. A mathematical model of the stress-induced transcription process suggests that the formation of gene loops that favor the recycling of polymerase from the terminator to the promoter can explain the observed behavior. One experimentally validated prediction from this model is that the amount of mRNA produced from a short gene should be higher than for a long one as the density of active polymerase on the short gene will be increased by polymerase recycling. Our data suggest that this recycling contributes significantly to the expression output from a gene and that polymerase recycling is modulated by the promoter identity and the cellular state.

KEYWORDS
gene looping, MAPK signaling pathways, phage-coat proteins, stress response, transcription dynamics

1 | INTRODUCTION

Messenger RNA (mRNA) molecules are essential intermediates between acting cellular proteins and information encoded in DNA. The production of mRNA is an intricate process that involves the interaction between numerous complexes to initiate transcription, elongate the transcript and finally produce a matured mRNA molecule (Hahn & Young, 2011; Shandilya & Roberts, 2012). Biochemical analyses have allowed characterization of the various complexes implicated in the production of mRNA (de Nadal

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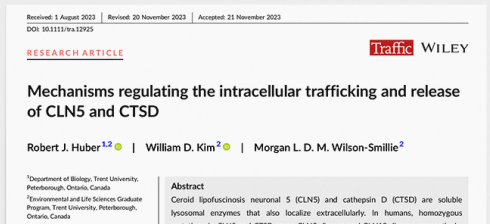

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DOI: 10.1111/tra.12925
RESEARCH ARTICLE
Traffic WILEY

Mechanisms regulating the intracellular trafficking and release of CLN5 and CTSD

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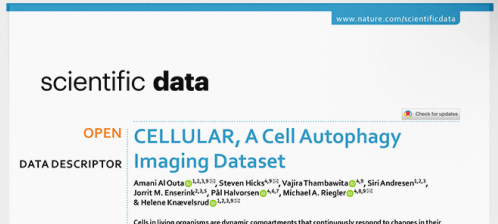
[1]Department of Biology, Trent University, Peterborough, Ontario, Canada
[2]Environmental and Life Sciences Graduate Program, Trent University, Peterborough, Ontario, Canada

Abstract

Ceroid lipofuscinosis neuronal 5 (CLN5) and cathepsin D (CTSD) are soluble lysosomal enzymes that also localize extracellularly. In humans, homozygous



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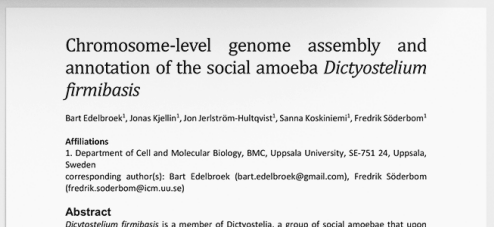
DATA DESCRIPTOR

CELLULAR, A Cell Autophagy Imaging Dataset

Amani Al Outa[1,2,3,5✉], Steven Hicks[4,5✉], Vajira Thambawita[4,5], Siri Andresen[1,2,3], Jorrit M. Enserink[2,3,5], Pål Halvorsen[4,5,7], Michael A. Riegler[4,5,8✉] & Helene Knævelsrud[1,2,3,5✉]

Cells in living organisms are dynamic compartments that continuously respond to changes in their



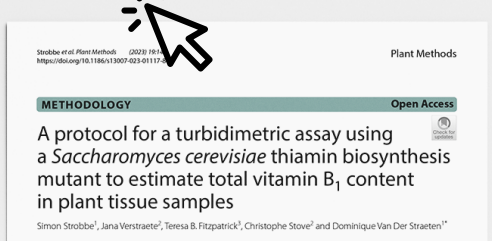
Chromosome-level genome assembly and annotation of the social amoeba *Dictyostelium firmibasis*

Bart Edelbroek[1], Jonas Kjellin[1], Jon Jerlström-Hultqvist[1], Sanna Koskiniemi[1], Fredrik Söderbom[1]

Affiliations
1. Department of Cell and Molecular Biology, BMC, Uppsala University, SE-751 24, Uppsala, Sweden
corresponding author(s): Bart Edelbroek (bart.edelbroek@gmail.com), Fredrik Söderbom (fredrik.soderbom@icm.uu.se)

Abstract

Dictyostelium firmibasis is a member of Dictyostelia, a group of social amoebae that upon



Strobbe *et al. Plant Methods* (2023) 19:1
https://doi.org/10.1186/s13007-023-01117-6
Plant Methods
METHODOLOGY
Open Access

A protocol for a turbidimetric assay using a *Saccharomyces cerevisiae* thiamin biosynthesis mutant to estimate total vitamin B_1 content in plant tissue samples

Simon Strobbe[1], Jana Verstraete[2], Teresa B. Fitzpatrick[3], Christophe Stove[2] and Dominique Van Der Straeten[1*]

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