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THE ROLE OF TEMPERATURE IN MICROBIAL GROWTH: A DISCUSSION AND META-ANALYSIS

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ABSTRACT

Temperature is a fundamental factor influencing microbial growth, affecting metabolism, enzyme activity, and survival. Different microorganisms exhibit varied temperature preferences, classified as psychrophiles, mesophiles, thermophiles, and hyperthermophiles. This paper discusses the impact of temperature on microbial growth, analyzing previous studies on optimal growth conditions, temperature stress responses, and industrial applications. A meta-analysis is conducted to compare growth rates across different temperature ranges. This paper explores the critical role of temperature in microbial growth, examining how it influences metabolism, enzyme activity, and survival across various microorganisms. The classification of microorganisms into psychrophiles, mesophiles, thermophiles, and hyperthermophiles are discussed, along with their optimal growth conditions and responses to temperature stress. A meta-analysis is presented to compare growth rates across different temperature ranges, highlighting the implications for industrial applications.

1. INTRODUCTION

Temperature plays a fundamental role in microbial ecology by directly influencing the growth, survival, and metabolic functions of microorganisms. Microbial species exhibit specific temperature ranges for optimal activity, leading to their classification into psychrophiles, mesophiles, thermophiles, and hyperthermophiles. Each group occupies distinct ecological niches and exhibits specialized biochemical adaptations that allow them to function effectively in their respective thermal environments (Nedwell, 1999). Psychrophiles, for instance, flourish at temperatures below 15°C and exhibit enhanced membrane fluidity and enzyme flexibility,

Enabling survival in polar and deep-sea environments. Conversely, thermophiles and hyperthermophiles thrive in extreme heat, such as in hot springs and hydrothermal vents, where their enzymes remain stable and active under high-temperature stress (Sarmiento et al., 2015; Mairet et al., 2021). These adaptations are crucial for maintaining cellular processes and contribute to the ecological success of microbes across diverse thermal habitats. Temperature also shapes the evolutionary pathways and ecological dynamics of microbial communities. Shifts in thermal conditions, whether due to natural fluctuations or anthropogenic climate change, can disrupt microbial balance, alter nutrient cycling, and impact broader ecosystem functions (Keenleyside, 2019; Engqvist, 2018). Understanding how temperature regulates microbial interactions and community structure is therefore essential in predicting ecological responses to environmental changes.
Microorganisms are further classified based on their temperature preferences. Psychrophiles survive in sub-zero environments, mesophiles thrive in moderate temperatures such as the human body (e.g., *E. coli*, *Salmonella*), thermophiles grow in hot environments like compost piles, and hyperthermophiles inhabit extreme settings like oceanic hydrothermal vents. These distinctions are not only ecologically significant but also relevant for biotechnology, where thermophilic and hyperthermophilic enzymes are utilized in biofuel production, industrial catalysis, and waste treatment (Parker et al., 2016; Libre Texts, 2021).In light of this, the current research aims to explore the relationship between temperature and microbial growth by classifying microorganisms according to their thermal preferences and examining the physiological mechanisms that underlie their adaptability. This study also seeks to assess the implications of temperature-driven microbial changes in ecological and industrial contexts

2. METHOD

This meta-analysis was conducted to synthesize current knowledge on microbial growth rates across different temperature ranges. A comprehensive literature search was performed in major scientific databases, including PubMed, Scopus, and Web of Science, using keywords such as "microbial growth," "temperature," "psychrophiles," "thermophiles," and related terms. Studies published from 2000 to 2024 and written in English were considered. Inclusion criteria encompassed experimental studies reporting microbial growth rates at defined temperature ranges, while reviews, conference abstracts, and studies without quantitative growth data were excluded. Data extraction focused on organism names, optimal growth temperatures, and growth rate measurements.Extracted data were analyzed using statistical techniques described in the original studies, such as Arrhenius plots and the Belehradek model, when available. For studies with sufficient data, growth rate parameters were compared across microbial classifications (psychrophiles, mesophiles, thermophiles, hyperthermophiles) to identify temperature-related patterns. Quality assessment of included studies was performed following standard guidelines to evaluate the reliability of reported growth rates. When applicable, findings were integrated with genomic and proteomic insights reported in the literature to discuss microbial thermal adaptations and their biotechnological implications.

3. ETHIC APPROVAL

This study constitutes a meta-analysis of data derived exclusively from previously published sources. As no original data involving human participants or animals were collected or analyzed, ethical approval from an institutional review board was not required.

4. RESULT

This section presents a synthesis of findings from previous studies concerning microbial growth rates across diverse temperature ranges. Visual aids such as tables and graphs may be used to illustrate these results, derived either directly from published raw data or through the application of analytical methods described in the Methods section. Several studies have reported notable variability in microbial growth parameters relative to temperature. Rosso (1996) introduced a model characterizing microbial growth using three cardinal temperatures—minimum, optimum, and maximum—demonstrating that these parameters are independent of the optimum growth rate. This model, supported by a dataset comprising 217 observations, is widely accepted for its biological significance and simplicity. In a meta-analysis focused on yeast growth, Chen et al. (2021) employed Gaussian process modeling to estimate growth rates over time under varying raffinose concentrations. Their analysis revealed that sugar concentration significantly influenced peak growth rates, enabling reliable comparisons among replicates and identifying trends in microbial nutrient response. Engqvist (2020) analyzed a large dataset of over 160,000 microbial records from culture collections to correlate enzyme function annotations with growth temperatures.

This extensive study highlighted metabolic adaptations associated with temperature variation, integrating empirical data with mechanistic modeling to elucidate temperature effects on enzymatic activity and microbial community dynamics. Furthermore, Huang (2019) adapted the Arrhenius equation to model bacterial growth responses beyond optimal temperatures, providing enhanced predictive capacity for thermal adaptation patterns. These results contribute to a deeper understanding of microbial ecology and have practical implications for industrial temperature regulation.

5. DISCUSSION

The results of this meta-analysis underscore the complexity and variability of microbial growth responses to temperature. Comparisons between modeled and observed growth rates demonstrate the utility of various mathematical approaches, such as Arrhenius and Belehradek models, in capturing these dynamics. The integration of large datasets from diverse species enables a more robust understanding of thermal adaptations. Notably, this analysis reveals how microbial metabolic strategies and enzyme functionalities evolve to optimize growth within specific temperature ranges. These findings have practical significance for industrial processes that depend on microbial efficiency, such as fermentation and waste treatment.

Further research should focus on refining predictive models and exploring the genetic basis of thermal tolerance. Additionally, understanding the impact of rapid environmental changes on microbial communities will be vital for mitigating risks in natural and engineered ecosystems.

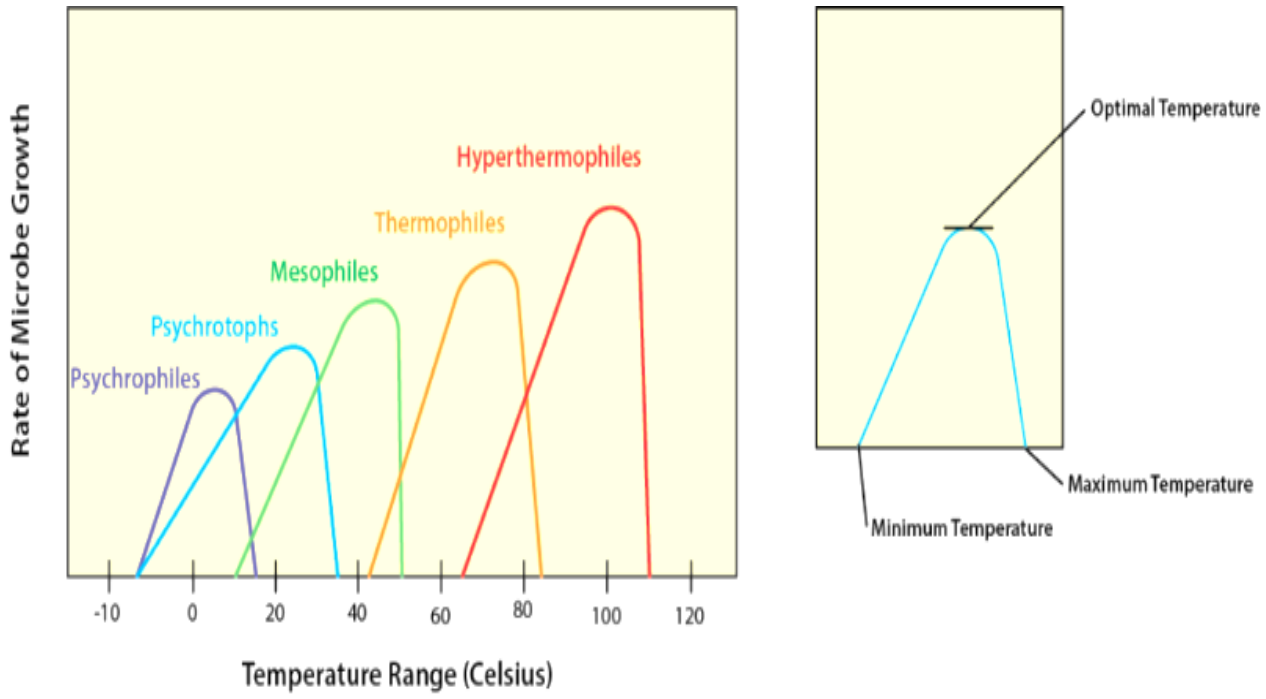

Figure 1. Graph showing bacterial growth rate as a function of temperature. The curve skews toward the optimum temperature, which is thought to reflect rapid protein denaturation occurring as temperatures exceed the optimal range for microbial growth (Keenleyside, 2019).

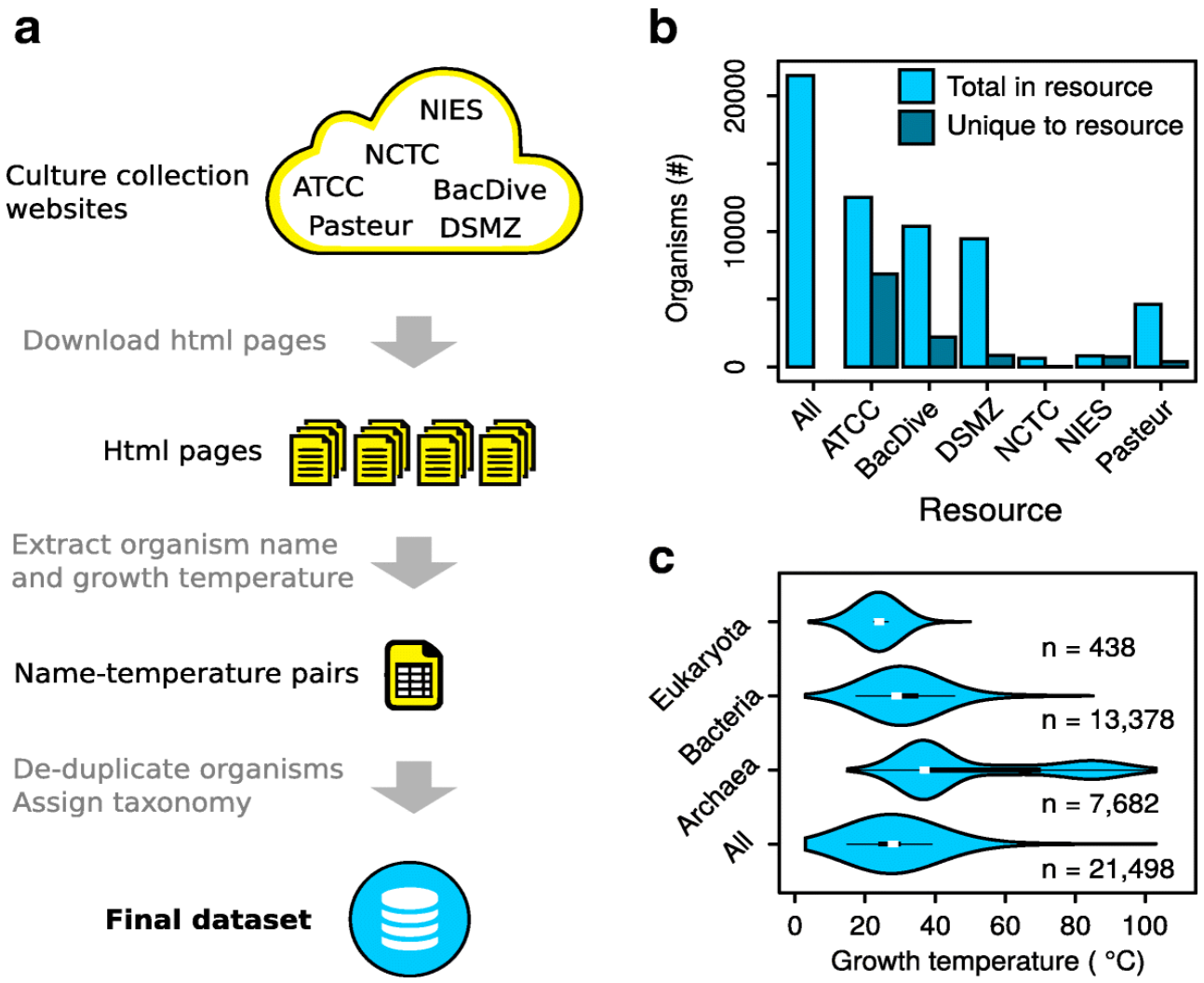

Figure 2. Culture collection centers provide a rich source of microbial growth temperature data.
(a) Overview of the methodology for collecting the growth temperature dataset.
(b) Comparison of databases highlighting the number of unique organisms each contributes.
(c) Violin plot showing the distribution of growth temperatures across organisms from the three domains of life. The white dot indicates the median, the thick black bar represents the interquartile range, and the outer shape shows kernel density estimates. (Adapted from Engqvist, 2018).

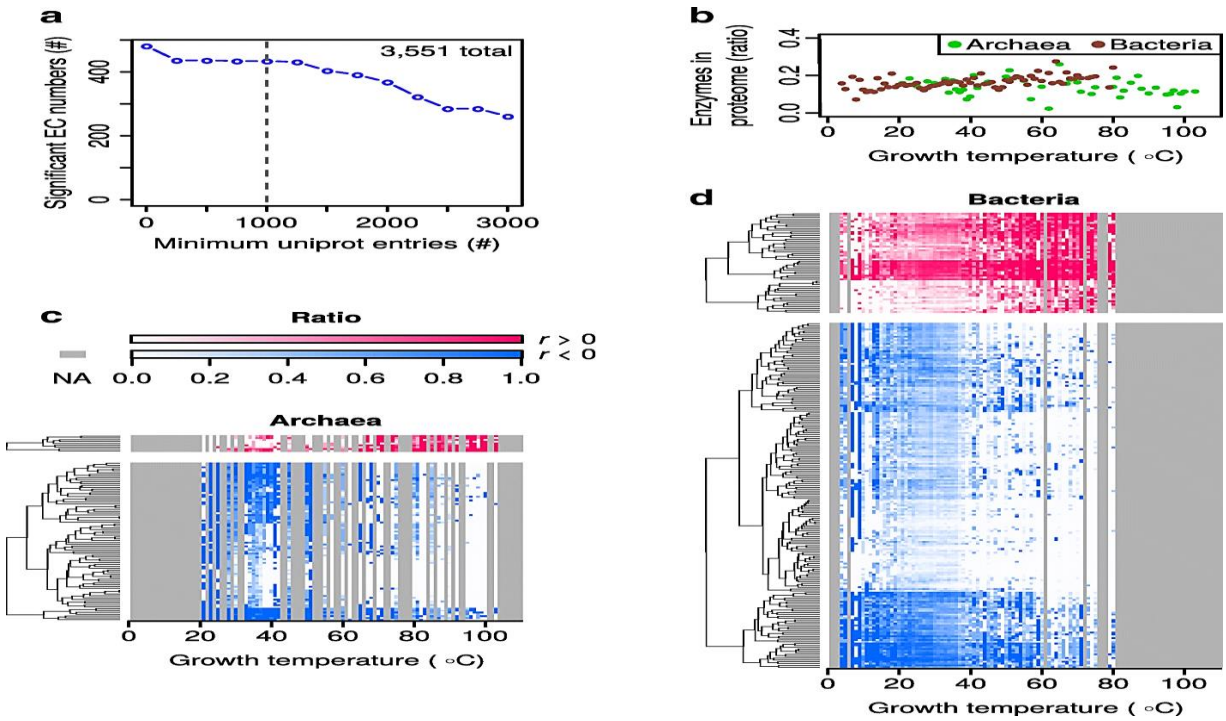

Figure 3. Many enzymes functions correlate with temperature.
(a) Sensitivity plot showing the number of statistically significant EC numbers (corrected p-value < 0.01) detected at various cutoffs for the minimum number of UniProt entries per organism. **(b)** Enzyme annotations as a proportion of the total proteome. Each data point reflects the mean value for organisms growing at a specific temperature, calculated separately for archaea and bacteria. **(c)** Heatmap showing how significant EC number occurrences vary with growth temperatures in archaea. Rows represent EC numbers, columns indicate growth temperatures, and color intensity shows the ratio of organisms containing each EC number.
(d) Same analysis for bacteria. Red indicates positive correlation and blue indicates negative correlation with growth temperature; gray denotes missing data. Spearman's correlation coefficient (r) is used as the metric of association. (Adapted from Engqvist, 2018).

Figure 4. Lactic acid bacteria used in fermenting milk into yogurt or in transforming vegetables into pickles thrive in acidic environments with a pH close to 4.0. Foods such as sauerkraut and pico de gallo have a tangy flavor due to their acidity. Acidic foods have been a staple of the human diet for centuries, in part because most spoilage-causing microbes prefer near-neutral pH levels and do not tolerate acidity well (LibreTexts, 2021). (Image credits: "yogurt" by nina.jsc/Flickr, "pickles" by Noah Sussman, "sauerkraut" by Jesse LaBuff, and "pico de gallo" by regan76/Flickr)

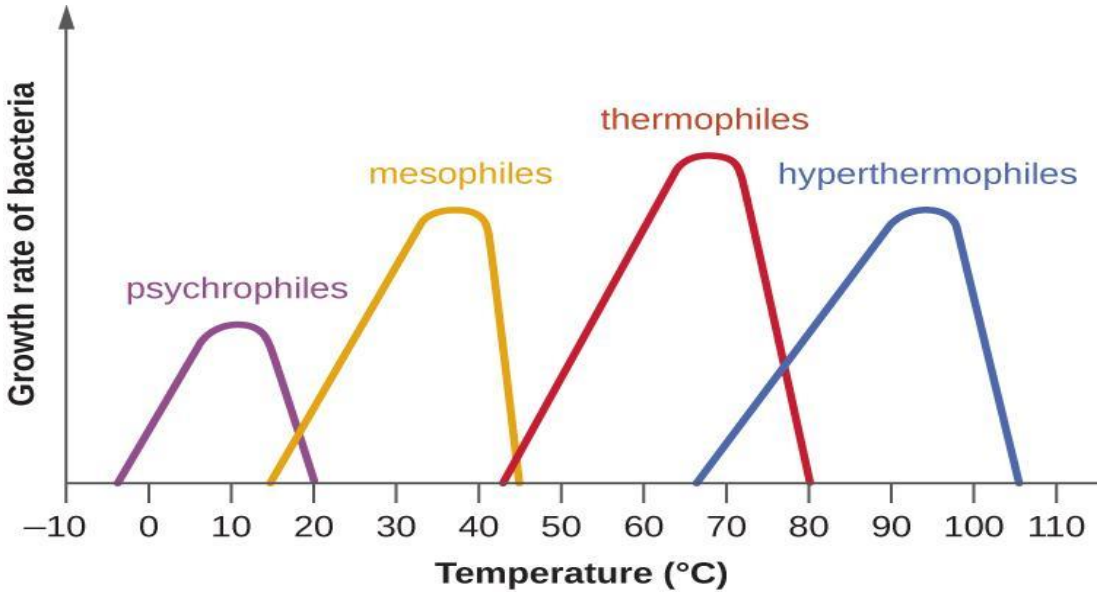

Figure 5. Graph showing bacterial growth rates across different temperature ranges. The X-axis represents temperature in degrees Celsius (°C), and the Y-axis indicates bacterial growth rate.

- The psychrophile curve peaks at 10°C and drops to zero at -5°C and 20°C.
- The mesophile curve peaks at 35°C and drops to zero at 15°C and 45°C.
- The thermophile curve peaks at 65°C, with zero growth below 45°C and above 80°C.
- The hyperthermophile curve peaks at 90°C, tapering off to zero at 65°C and 105°C. (Adapted from LibreTexts, 2021).

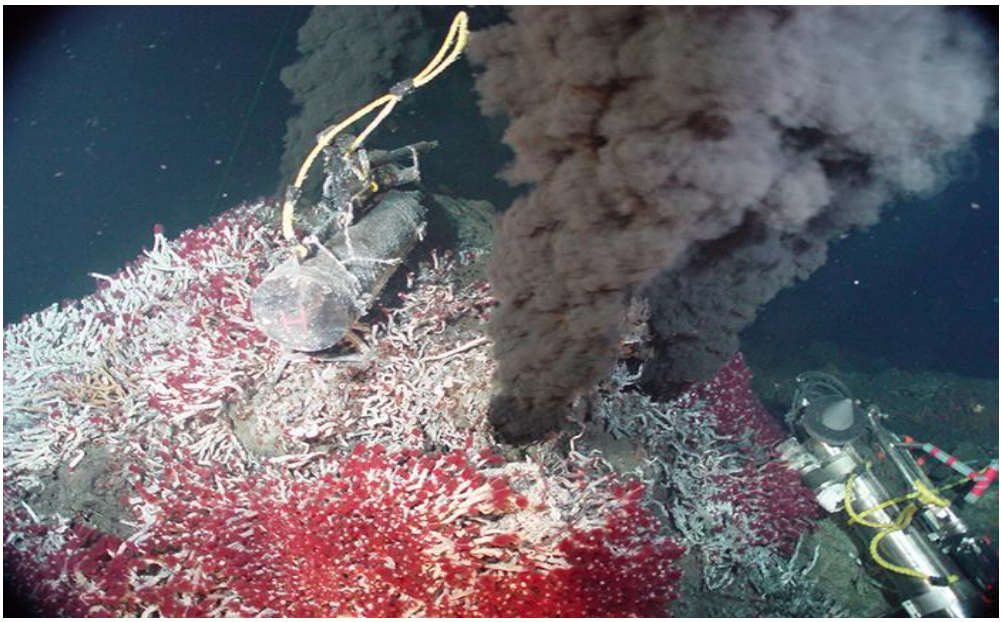

Figure 6. A black smoker at the bottom of the ocean releases hot, chemical-rich water, dramatically increasing the surrounding temperature. These hydrothermal vents create extreme environments that nevertheless support diverse macroscopic life—such as red tubeworms—sustained by a thriving microbial ecosystem (LibreTexts, 2021). (Image credit: NOAA)

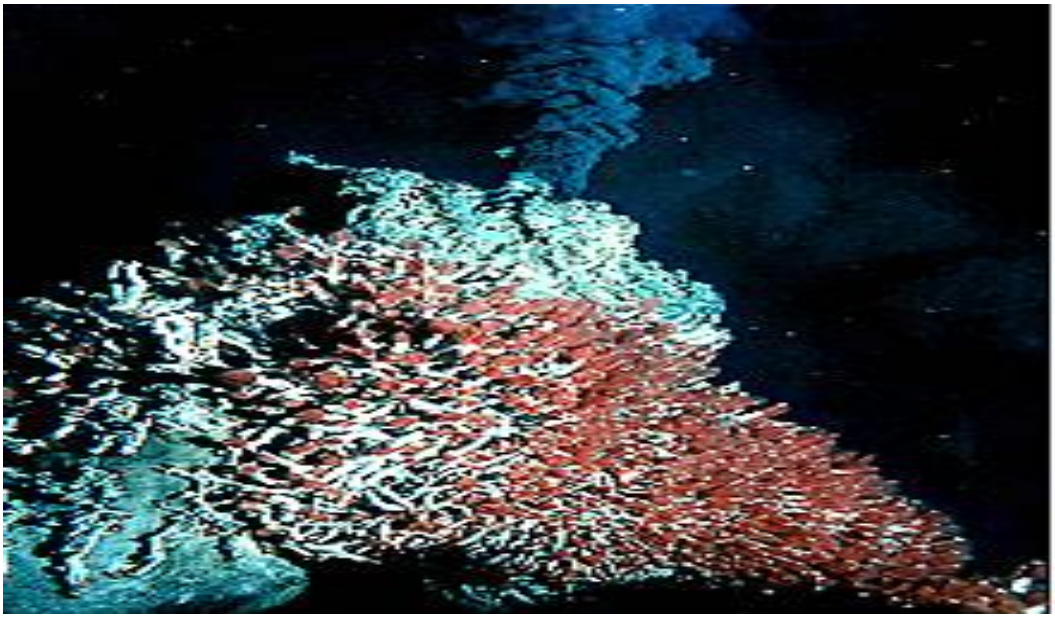

Figure 7. Photograph of a hydrothermal vent showing colonies of tube worms with red gills thriving on the large edifice. These gills host symbiotic hydrogen sulfide (H_2S)-oxidizing lithotrophic bacteria, which provide organic matter to the worms through their symbiotic relationship. Image courtesy of NOAA Ocean Exploration

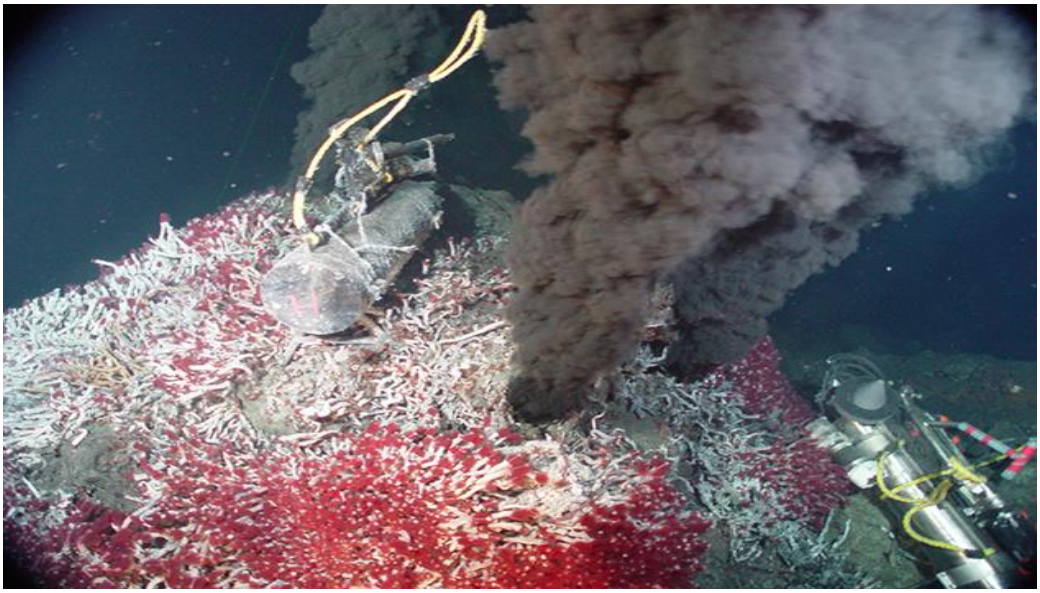

Figure 8. A black smoker at the bottom of the ocean releases hot, chemical-rich water, heating the surrounding environment. These sea vents create an extreme habitat that supports abundant macroscopic life, such as red tubeworms, which rely on a rich microbial ecosystem for sustenance

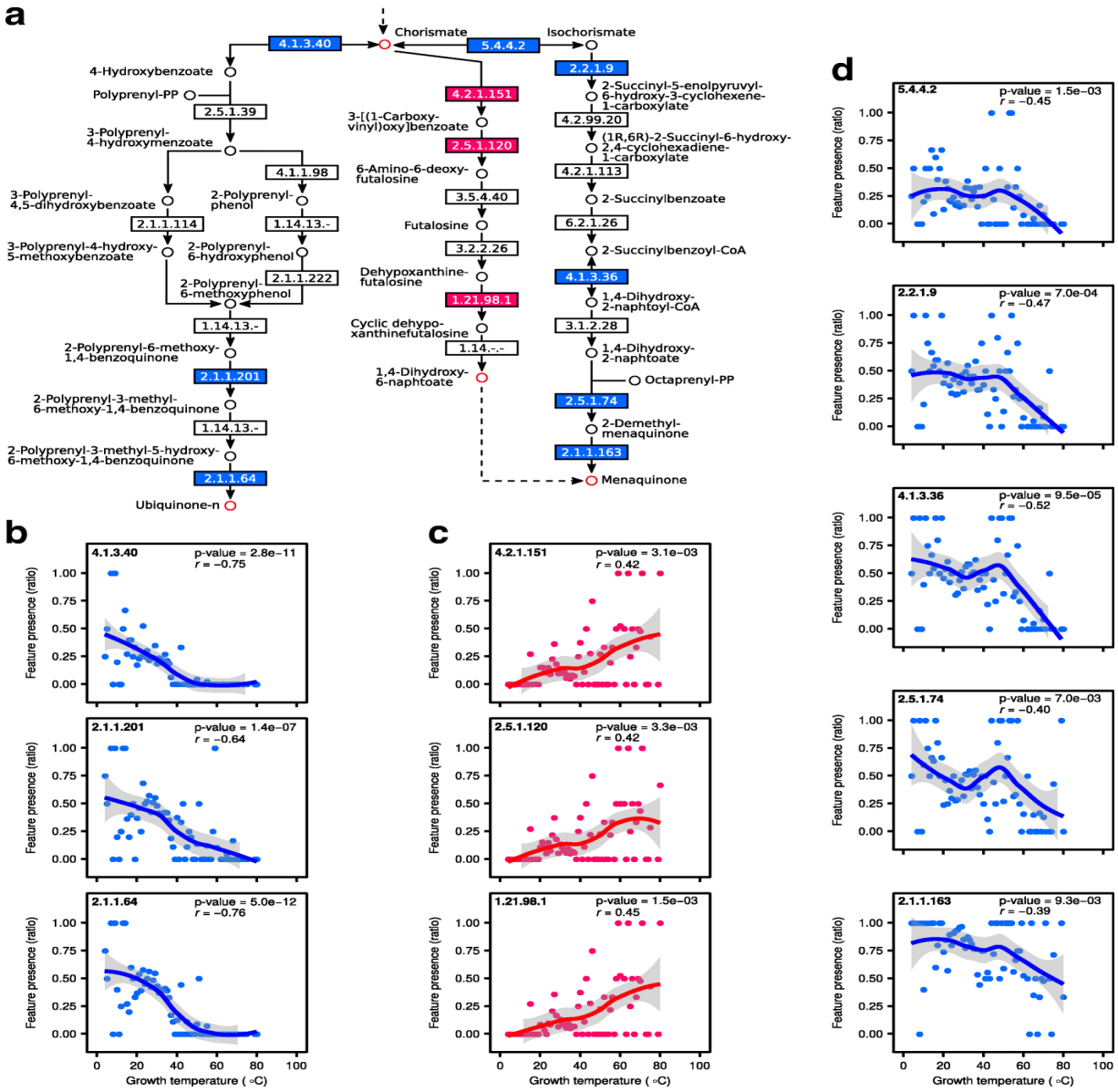

Figure 9. Certain metabolic pathways are enriched for enzyme functions correlated with growth temperature.
(a) A diagram of part of the KEGG pathway "ubiquinone and other terpenoid-quinone biosynthesis" (map00130). Enzymes with occurrence significantly correlated with growth temperature (corrected p-value < 0.01) are shown in red (positive correlation) or blue (negative correlation).
(b) Changes in the presence of enzymes involved in ubiquinone biosynthesis across temperatures. Each point represents the ratio of the EC number's occurrence among organisms growing at a specific temperature. The line shows a locally weighted polynomial regression with a 95% confidence band in gray. Spearman's correlation coefficient (r) is indicated.
(c) Changes in enzyme presence involved in menaquinone biosynthesis via the futalosine pathway with temperature.
(d) Changes in enzyme presence involved in menaquinone biosynthesis via the classical pathway with temperature.
Source: Engqvist (2018).

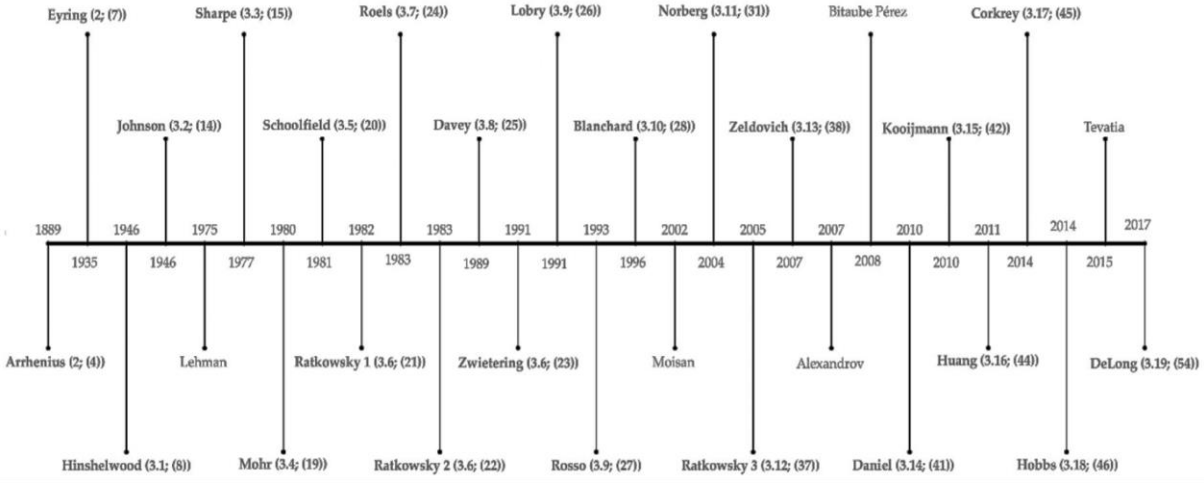

Figure 10. Timeline of temperature models discussed in paragraphs 2–3, beginning with the semi-empirical Arrhenius model from 1889. Each model is identified by the first author's name (paragraph number; equation number). Models highlighted in bold are described in detail within the text, while those in regular font are summarized in Table 1.Source: Huang (2019).

TABLES

Market	Enzyme	Commercially available	Uses
Molecular Biology	Alkaline phosphatases	Antarctic phosphatase (New England Biolabs Inc.)	Dephosphorylation of 5′ end of a linearized fragment of DNA
	Uracil-DNA N-glycosylases (UNGs)	Uracil-DNA *N*-glycosylase (UNG) (ArcticZymes), Antarctic Thermolabile UDG (New England Biolabs Inc.)	Release of free uracil from uracil-containing DNA
	Nucleases	Cryonase (Takara-Clontech)	Digestion of all types of DNA and RNA
Detergent	Lipases	Lipoclean®, Lipex®, Lipolase® Ultra, Kannase, Liquanase®, Polarzyme®, (Novozymes)	Breaking down of lipid stains
	Proteases	Purafect® Prima, Properase®, Excellase (Genencor)	Breaking down of protein stains
	Amylases	Stainzyme® Plus (Novozymes), Preferenz™ S100 (DuPont), Purafect® OxAm (Genencor)	Breakdown starch-based stains
	Cellulases	Rocksoft™ Antarctic, Antarctic LTC (Dyadic), UTA-88 and UTA-90 (Hunan Youtell Biochemical), Retrocell Recop and Retrocell ZircoN (EpyGen Biotech), Celluzyme®, Celluclean® (Novozymes)	Wash of cotton fabrics
	Mannanases	Mannaway® (Novozymes), Effectenz™ (DuPont)	Degradation of mannan or gum
	Pectate lyases	XPect® (Novozymes)	Pectin-stain removal activity
Textile	Amylases	Optisize® COOL and Optisize NEXT (Genencor/DuPont)	Desizing of woven fabrics
	Cellulases	Primafast® GOLD HSL IndiAge® NeutraFlex, PrimaGreen® EcoLight 1 and PrimaGreen® EcoFade LT100 (Genencor/DuPont)	Bio-finishing combined with dyeing of cellulosic fabrics
Food and beverages	Pectinases	Novoshape® (Novozymes), Pectinase 62L (Biocatalysts), Lallzyme® (Lallemand)	Fermentation of beer and wine, breadmaking, and fruit juice processing
Other	Catalase	Catalase (CAT), (Swissaustral)	Textile, research, and cosmetic applications

Table 1. Examples of commercially available cold-active enzymes and their industrial applications. (Hamid, Khan, & Kim (2022).

6. CONCLUSION

Temperature is a pivotal factor influencing microbial growth, with profound implications for both ecological understanding and industrial applications. It governs metabolic activities by modulating enzyme stability and membrane properties, while also shaping microbial community interactions and nutrient cycles (Madigan et al., 2018; Brock & Madigan, 2015). Microorganisms have evolved diverse adaptations to thrive in temperature-specific niches—psychrophiles in cold environments, mesophiles in moderate conditions, thermophiles in hot habitats, and hyperthermophiles in extreme heat—highlighting opportunities for biotechnological exploitation (Cavicchioli et al., 2019; Zhang et al., 2020).

Climate change poses significant challenges to microbial ecosystems, especially in sensitive regions such as the Arctic, where warming disrupts community composition and global biogeochemical processes (Jansson & Hofmockel, 2020; Schimel et al., 2019). Understanding microbial resilience to temperature stress is critical for advancing industrial processes reliant on microbial activity, including food technology, fermentation, and bioremediation (Russell, 2016; Margesin & Miteva, 2011).

Predictive models informed by empirical data provide valuable tools for anticipating microbial responses to thermal fluctuations, thereby optimizing industrial applications and informing climate impact assessments (Baranyi & Roberts, 1994; McKellar & Lu, 2004).

In conclusion, continued research on temperature-dependent microbial growth will not only deepen scientific knowledge but also drive innovations in agriculture, pharmaceuticals, and biotechnology sectors.

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