

ผลของดีคาร์บอกซีเลชันของกรดอะมิโนร่วมกันในการปรับปรุงอาหาร
ไฮโดรเจนซัลไฟด์สำหรับการตรวจวิเคราะห์ซัลโมเนลลาในกลุ่มที่สามารถรีดิวซ์
ไทโอซัลเฟตเบื้องต้น

**COMBINED EFFECT OF AMINO ACID DECARBOXYLATION ON THE
IMPROVEMENT OF HYDROGEN SULFIDE ENRICHMENT MEDIA FOR
PRESUMPTIVE SCREENING OF THIOSULFATE – REDUCING SALMONELLA**

พิมพินิภา หิรัณย์สร¹ จูรีพรรณ สารนาค² อาณัติ ดีพัฒนา³ อลักษ์ณท์ ทิพยรัตน์^{4*}
Pimnibha Hirunsorn¹, Jurepan Saranak², Anat Deepatana³, Aluck Thipayarat^{4}*

¹สาขาวิชาเทคโนโลยีการอาหาร คณะเทคโนโลยี มหาวิทยาลัยขอนแก่น

¹Department of Food Technology, Faculty of Technology, Khon Kaen University.

²ภาควิชาฟิสิกส์ มหาวิทยาลัยศรีนครินทรวิโรฒ

²Department of Physics, Syracuse University.

³ภาควิชาวิศวกรรมเคมี คณะวิศวกรรมศาสตร์ มหาวิทยาลัยบูรพา

³Department of Chemical Engineering, Faculty of Engineering, Burapha University.

⁴ภาควิชาวิศวกรรมอาหาร คณะวิศวกรรมศาสตร์ มหาวิทยาลัยเทคโนโลยีพระจอมเกล้าธนบุรี

⁴Department of Food Engineering, Faculty of Engineering, King Mongkut's University of Technology Thonburi.

*Corresponding author, e-mail: athipaya@yahoo.com

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บทคัดย่อ

โรงงานอุตสาหกรรมอาหารต้องการวิธีการวิเคราะห์ที่รวดเร็วและเชื่อถือได้ สามารถทำได้สะดวก และค่าใช้จ่ายไม่สูงเพื่อใช้ในการตรวจสอบการปนเปื้อนของ *Salmonella* spp. เบื้องต้น งานวิจัยนี้จึงได้พัฒนาอาหารบ่งชี้การเกิดไฮโดรเจนซัลไฟด์ (H_2S) พร้อมวิธีทดสอบในเพลทระดับไมโครเวล สำหรับการตรวจหาซัลโมเนลลาเบื้องต้นอย่างรวดเร็ว

งานวิจัยนี้ได้ศึกษาผลของการใช้ดีคาร์บอกซีเลชันของกรดอะมิโนร่วมกันต่อการเพิ่มขึ้นของการเกิดตะกอนสีดําในรูปแบบอาหารเหลวบ่งชี้ก๊าซ H_2S (หรือ TFX) ร่วมกับไลซีน-ออร์นิติน (TFXLO) ออร์นิติน-อาร์จินิน (TFXOA) หรือไลซีน-อาร์จินิน (TFXLA) เพื่อปรับปรุงพัฒนาการเกิดไฮโดรเจนซัลไฟด์และการเกิดตะกอนสีดําที่เด่นชัด โดยทดสอบกับซัลโมเนลลาที่สามารถเกิดปฏิกิริยา H_2S^+ จำนวน 7 สายพันธุ์ และซัลโมเนลลาที่ไม่สามารถเกิดปฏิกิริยา H_2S^+ ได้ รวมถึงเชื้อที่ไม่ใช่ซัลโมเนลลาจำนวนรวม 13 สายพันธุ์ อาหารเหลว TFX

ที่ใส่ไลซีน (TFXL) เป็นอาหารควบคุม ปฏิบัติการเกิดตะกอนสีดำเป็นอินดิเคเตอร์สามารถตรวจติดตามจากการวัดค่าการดูดกลืนแสง (OD_{650}) ที่เปลี่ยนแปลงไปและด้วยตาเปล่า

ผลการวิจัยพบว่า ส่วนเสริมที่ใส่ลงไปร่วมกับกรดอะมิโนให้ผลการตกตะกอนของเฟอรัสซัลไฟด์ที่แตกต่างกัน และให้ค่าการดูดกลืนแสง OD_{650} ขึ้นอยู่กับซีโรวาร์ของซัลโมเนลลา การเกิดตะกอนสีดำของซัลโมเนลลามีความเข้มและคมชัดมากขึ้นเมื่อมีการปรับปรุงสูตรกรดอะมิโน โดยเฉพาะอาหารเหลวที่มีการใช้อาร์จินีน-ไทโรซีนร่วมกัน ซึ่งจะให้ค่าการดูดกลืนแสงที่ 650 นาโนเมตร ($OD_{650} = 1.7 - 2.5$) เปรียบเทียบกับการใช้ไลซีนเพียงตัวเดียว ($OD_{650} = 1.4 - 2.1$) ปกติแล้วระบบไทโอซัลเฟต-เฟอร์ริกแอมโมเนียมซิเตรทนี้มักพบการเกิดตะกอนสีดำในซัลโมเนลลากลุ่มพิเศษ (*Salmonella Anatum* และ *Salmonella Typhi*) ค่อนข้างน้อย แต่เมื่อใช้ไลซีน-อาร์จินีนร่วมกัน มีผลช่วยเพิ่มความเข้มของอาหารเหลวไฮโดรเจนซัลไฟด์ จากที่ให้ค่า OD_{650} ที่ต่ำที่ 0.9 เพิ่มขึ้นเป็น 1.6 ใน *S. Anatum* ได้ อย่างไรก็ตาม สำหรับ *S. Typhi* ยังไม่มีการใช้กรดอะมิโนร่วมกันสูตรใดที่สามารถปรับปรุงการเกิดไฮโดรเจนซัลไฟด์ได้ อาหารเหลวบ่งชี้ไฮโดรเจนซัลไฟด์ทุกสูตรสามารถแยกซัลโมเนลลาที่ไม่สามารถเกิดไทโอซัลเฟตรีดิวซ์ซึ่งออกจากซัลโมเนลลสายพันธุ์ปกติได้ แต่ยังไม่สามารถแยกเชื้อแข่งขันของซัลโมเนลลาได้ ยกเว้น *Citrobacter freundii* สามารถแยกได้ในอาหารเหลวสูตร TFXL

โดยสรุปการใช้อาร์จินีนและไทโรซีนเป็นสารอาหารพื้นฐานนั้น สามารถปรับปรุงระบบการเกิดปฏิกิริยาไฮโดรเจนซัลไฟด์ให้ชัดเจนขึ้น อาหารเหลวบ่งชี้การเกิดปฏิกิริยาการเกิดไฮโดรเจนซัลไฟด์นั้นนับเป็นอาหารเหลวทางเลือกโดยเวลาที่ใช้ในการตรวจวิเคราะห์ทั้งหมดสำหรับผลการตรวจวิเคราะห์เบื้องต้นสั้นลงและรวดเร็วกว่าวิธีวิเคราะห์แบบทั่วไปที่ใช้เวลาถึง 48 ชั่วโมง

คำสำคัญ: ดีคาร์บอกซีเลชันของกรดอะมิโน การสร้างไฮโดรเจนซัลไฟด์ วิธีการไมโครเพลท การตรวจหาซัลโมเนลลาเบื้องต้น

Abstract

The food industry needs rapid and reliable methods that are convenient and cost-effective as primary screens for routine inspections of *Salmonella* spp. contamination. To fulfil *Salmonella* screening step, hydrogen sulfide (H_2S) indicator medium was proposed and tested in a microwell plate.

Method: The combined effect of amino acid decarboxylation on the increase of black precipitation, H_2S indicator broth (TFX) plus with lysine-ornithine (TFXLO), ornithine-arginine (TFXOA), or lysine-arginine (TFXLA) were studied in seven H_2S^+ *Salmonella* serovars and thirteen non-salmonellae *Salmonella* and non-salmonellae to improve hydrogen sulfide production and black precipitation contrast. The TFX broth containing lysine (TFXL) was compared as control. The black precipitates, as indicator of the reaction were followed by optical density (OD_{650}) changes and visualization.

Result: Different supplement with combined amino acids provided different ferrous sulfide precipitates and OD_{650} signals depending on *Salmonella* serovars. The black precipitates of all typical *Salmonella* had improved with more contrast in all combined amino acids, especially ornithine-arginine based broth ($OD_{650} = 1.7-2.5$), compared to single lysine usage ($OD_{650} = 1.4-2.1$). Thiosulfate-ferric ammonium citrate system commonly provided ineffective results for black precipitates in atypical *Salmonella* (*Salmonella Anatum* and *Salmonella Typhi*). The lysine-arginine combined effect could fix the low H_2S contrast OD_{650} from 0.9 to 1.6 in *S. Anatum*. However, none of combined amino acids was able

to improve hydrogen sulfide production in atypical *S. Typhi*. All H₂S enrichment media could differentiate all non-thiosulfate reducing salmonellae competitors tested out of *Salmonella*. There was no differentiation of three H₂S⁺ *Salmonella* competitors from *Salmonella* in any media, except *Citrobacter freundii* in TFXL broth.

Conclusion: The selected ornithine and arginine as the nutrient base was noted for further improvement in hydrogen sulphide reaction system. With applying H₂S indicator media alternative to conventional selective broths, the total detection time for presumptive results was shortened; more rapid than conventional protocol for up to 48 h.

Keywords: Amino acid decarboxylation, Hydrogen sulfide production, Microplate assay, *Salmonella* presumptive screening

Introduction

Salmonella, an Enterobacteriaceae, has been the leading foodborne illnesses for a century [1]. Consumption of *Salmonella*-contaminated food can cause the gastrointestinal illness, salmonellosis, producing sporadic food-borne outbreaks worldwide [2-5]. Although the most common sources are food products from animals that normally harbor *Salmonella*, many other types of food and beverage can carry *Salmonella* linked to foodborne outbreaks. Ready-to-eat foods are also considered to be serious sources of *Salmonella* contamination [1, 6]. Of several major foodborne pathogens, *Salmonella* has the most critical impact on public health and economic cost [4, 7]. Accordingly, there have been several attempts to improve and develop more efficient, rapid, convenient and reliable *Salmonella* detection methods during past decades [3, 8]. The interest points to the development of biochemical indicator medium, implementation of the miniaturization concept, as well as optical sensor [9-12] to presumptively screen for *Salmonella* contamination in food samples. Among *Salmonella* metabolic activities, reduction of thiosulfate to hydrogen sulfide has been widely used for identification and differentiation of *Salmonella* spp. from other species of Enterobacteriaceae in various conventional selective agars (e.g., xylose lysine decarboxylase agar) [13-15]. This reaction has been coupled with lysine decarboxylation to reduce the strong acid conditions. Strong acids produced by carbohydrate fermentation inhibit hydrogen sulfide production and ferrous sulfide precipitation resulting in low contrast of H₂S⁺ black precipitates [15-16]. Based on this concept, the developed H₂S indicator enrichment media have been successfully developed using lysine, ornithine, or arginine as acid masking preventive system from excessive acidity coupled with optical detection approach [9 - 10]. However, none has been studied the combined effect of double and triple amino acid decarboxylation on hydrogen sulfide production in *Salmonella* and their competitors.

Objectives

This research aimed to study the combined effect of double and triple amino acid decarboxylation on hydrogen sulfide production and ferrous sulfide precipitation of *Salmonella* and non-salmonella in 96-microwell cultivation.

Methods

Bacterial pure cultures and culture preparation

All bacteria were obtained from the Department of Medical Sciences Thailand (DMST, Bangkok, Thailand) and Thailand Institute of Scientific and Technological Research) TISTR, Bangkok, Thailand). The target organisms, *Salmonella* were 5 non-typhoid serovars (*Salmonella* Anatum DMST 19600; *Salmonella* Enteritidis DMST 15673; *Salmonella* Rissen DMST 17365; *Salmonella* Typhimurium TISTR 292; and *Salmonella* Weltevreden DMST 10637) and 2 typhoid and paratyphoid serovars (*Salmonella* Typhi DMST 22842; and *Salmonella* Paratyphi B DMST 28118). The Gram-negative competitive bacteria included *Citrobacter freundii* DMST 16368; *Enterobacter aerogenes* DMST 8216; *Proteus mirabilis*, TISTR 100; *Proteus vulgaris* DMST 557; *Pseudomonas aeruginosa* DMST 4739; *Shigella flexneri* DMST 4423; *Shigella sonnei* DMST 561; *Serratia marcescens* DMST 8845; and *Yersinia enterocolitica* DMST 8012. Few Gram-positive competitive bacteria, *Enterococcus faecalis* DMST4736; *Listeria innocua* DMST 9011; and *Staphylococcus aureus* TISTR 808; were also tested.

All pure cultures were sub-cultured on tryptic soy agar (TSA, Lab M, UK) and one loopful of each strain was transferred into 10 ml of tryptic soy broth (TSB, Lab M, UK) in a 10-ml glass tube and incubated under a static condition at 37 ± 1 °C for 24 h. The 10-fold serial dilutions were then done in 0.1 %w/v peptone water (PW, Difco Laboratories, Sparks, MD) to obtain the desired concentration.

Media

The behaviour of the organisms was studied in the following liquid media (pH 7.0 ± 0.1): (1) TFX, adapted from Xylose Lysine Decarboxylase (XLD agar), containing (g/L :soytone (USbiological, Salem, MA), 4.5; xylose (Acros organics, Fair Lawn, N), 1; ferric ammonium citrate (Fisher Scientific, Fair Lawn, NJ), 0.5; sodium thiosulfate, 0.1. The TFX broth was further added with lysine, lysine-ornithine, ornithine-arginine, or lysine-arginine, and lysine-arginine-ornithine (5 g of each amino acid type/L), to derive TFXLO, TFXOA, TFXLA, and TFXLOA broth. L-lysine, L-ornithine, and L-arginine used were from USbiological, Salem, MA. All prepared media was mixed and dissolved with mild heating and cooled to 25 °C before pH adjustment to initial pH 7.0 ± 0.1 by HCl (QR \acute{e} C $^{\circ}$, Malaysia) 1 N and NaOH (Carlo Erba, France) 1 N and then sterilized by filtration through a sterile nylon syringe filter membrane (13 mm diameter, 0.45 μ m pore size, Filtrex, Thailand) before using.

Effect of double and triple amino acid decarboxylation on hydrogen sulfide production in TFX media

To study the effect of amino acid on the increase of black precipitation, each well of the 96-microwell plates was filled with 180 μ L of TFXL, TFXLO, TFXOA, TFXLA, and TFXLOA media. Then each pure culture of salmonellae and non-salmonellae (20 μ L) was individually inoculated into test media. The microplates were incubated under stationary condition at 37 ± 1 °C for 24 h. The optical density (OD) at 650 nm, the optimum wavelength derived from previous study [11], was measured during incubation time using media without inoculum as blank. The control medium was base broth without adding amino acid, TFX.


























Results

The combined effect of lysine, ornithine, or arginine decarboxylation on H₂S production in thiosulfate-reducing *Salmonella* and non-salmonellae

As a consequence of single amino-acid decarboxylation, ornithine produced heavy black precipitates of FeS in most usual *Salmonella*, but modest in *S. Paratyphi B*, and very little in *S. Anatum* and *S. Typhi*. Arginine was great for *S. Anatum*, but worse in the others. Therefore, we assumed that mixing amino acids might achieve the highest H₂S production and black precipitation of iron sulfide. From results of single amino acids, the combination of ornithine and arginine was suggested. However, we further studied double and triple combinations of all three amino acids in the following set of experiments.

The basal medium broth, TFX, was prepared and then added with (1) lysine (L) and ornithine (O), (2) ornithine (O) and arginine (A), (3) lysine (L) and arginine (A), (4) lysine (L), ornithine (O) and arginine (A), to give TFXLO, TFXOA, TFXLA, and TFXLOA broths, respectively. All thiosulfate-reducing *Salmonella* and non-salmonellae (7 log CFU/mL) were tested in the prepared media to study the effect of amino-acid decarboxylation on black precipitation while selecting *Salmonella* competitors out. The control medium for amino acids was TFX with lysine, TFXL broth.

Table 1 Hydrogen sulfide production of salmonellae (7 log CFU/mL) in thiosulfate-ferric ammonium-citrate based broths (TFX) supplemented with different amino acids; (1) lysine (L) and ornithine(O), (2) ornithine (O) and arginine (A), (3) lysine (L) and arginine (A), (4) lysine (L), ornithine (O) and arginine (A), to give TFXLO, TFXOA, TFXLA, and TFXLOA broths under aerobic cultivation at 37 °C after 24 h. The control medium was TFX with lysine, TFXL broth.














































Test strains	H ₂ S indicator broth				
	TFXL	TFXLO	TFXOA	TFXLA	TFXLOA
Salmonellae					
<i>Typical strains</i>					
<i>S. Enteritidis</i>					
<i>S. Rissen</i>					
<i>S. Typhimurium</i>					
<i>S. Weltevreden</i>					
<i>S. Paratyphi B</i>					

Test strains	H ₂ S indicator broth				
	TFXL	TFXLO	TFXOA	TFXLA	TFXLOA
<i>Atypical strains</i>					
<i>S. Anatum</i>					
<i>S. Typhi</i>					

Table 1 and 2 show the black precipitation resulting from *Salmonella* and non-salmonellae, respectively, in TFX broths with double and triple amino acids after 24 h incubation as evaluated by eye. The black precipitates appeared more in LO, OA, LA, and LOA than in L broths with all typical *Salmonella* and *S. Anatum*. The most optimal amino acid combination for *S. Anatum* tended to be LA. No improvement was observed in *S. Typhi* in all media. All broths with two or three amino acids support H₂S production and black precipitation of iron sulfide. Based on eye observation, it was hard to decide which amino acid combinations were most effective; therefore, we used OD₆₅₀ measurement to quantify the black precipitation. We plotted the OD₆₅₀ time course of each organism in each medium to determine the optimum amino acids, which provide the most black precipitation in broth media.

Table 2 Hydrogen sulfide production of non-salmonellae (7 log CFU/mL) in thiosulfate-ferric ammonium-citrate based broths (TFX) supplemented with different amino acids; (1) lysine (L) and ornithine (O), (2) ornithine (O) and arginine (A), (3) lysine (L) and arginine (A), (4) lysine (L), ornithine (O) and arginine (A), to give TFXLO, TFXOA, TFXLA, and TFXLOA broths under aerobic cultivation at 37 °C after 24 h. The control medium was TFX with lysine, TFXL broth.

Test strains	H ₂ S indicator broth				
	TFXL	TFXLO	TFXOA	TFXLA	TFXLOA
Non-salmonellae, Gram-negative					
<i>Citrobacter freundii</i>					
<i>Proteus mirabilis</i>					
<i>Proteus vulgaris</i>					
<i>Enterobacter aerogenes</i>					
<i>Escherichia coli</i>					

Test strains	H ₂ S indicator broth				
	TFXL	TFXLO	TFXOA	TFXLA	TFXLOA
Non-salmonellae, Gram-negative					
<i>Klebsiella pneumoniae</i>					
<i>Serratia marcescens</i>					
<i>Pseudomonas aeruginosa</i>					
<i>Shigella flexneri</i>					
<i>Shigella sonnei</i>					
<i>Yersinia enterocolitica</i>					
Non-salmonellae, Gram-positive					
<i>Enterobacter faecalis</i>					
<i>Staphylococcus aureus</i>					
<i>Listeria innocua</i>					

In Figure 1, we compared the OD₆₅₀ values at 24 h of media with single and double/triple amino acids among different *Salmonella* strains to select the most effective amino acid mixtures for H₂S production. The OD₆₅₀ signals of typical *Salmonella* were significantly improved when changing lysine to other amino acids. The different amino acids promoting the highest OD₆₅₀ values varied depending on the *Salmonella* serovars, for example ornithine (*S. Enteritidis*) and ornithine plus with arginine (*S. Rissen*). None provided the highest OD₆₅₀ in all typical *Salmonella*, the most optimum formula; OA was selected since it gave OD₆₅₀ values above 1.7.

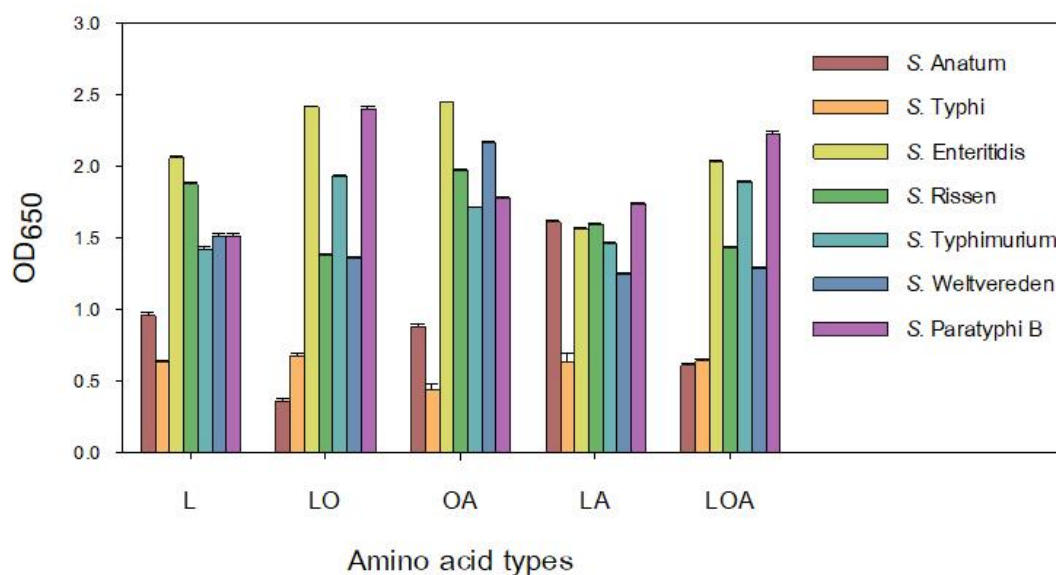


Figure 1. Optical density profiles of hydrogen sulfide broths with different amino acids measured at 650 nm after incubation at 37°C for 24 h.

The major goal for double or triple amino acid optimization was to improve the OD signal in atypical *S. Anatum* and *S. Typhi*. However, no double or triple amino acid combination increased the OD₆₅₀ of *S. Anatum* relative to arginine alone (OD₆₅₀ = 2.147). In addition, all amino acid mixtures resulted in less precipitates and low OD₆₅₀ in *S. Typhi* (OD₆₅₀ = 0.425 – 0.796). The highest OD₆₅₀ of *S. Typhi* was from the formula supplemented with ornithine (OD₆₅₀ = 0.796).

However, combinations of amino acids was not able to improve hydrogen sulfide production in atypical *Salmonella* serovars (*S. Anatum* and *S. Typhi*), but fortunately ornithine and arginine in combination improved the signals in typical strains compared to other amino acids tested. Consequently, the selected ornithine and arginine as the nutrient base was noted for further improvement. Since sugar (type fermentation significantly affects thiosulfate reduction and hydrogen sulfide production in bacteria [17]), the effect of various fermentable sugars supplemented in TFOA broth is interesting for future research.

Conclusions and Discussion

To achieve the rapid *Salmonella* screening for practical use in food industry, the H₂S indicator enrichment media based on the *Salmonella* selective agar formula and coupled with microplate assay was proposed. The TFXL broth was improved by substituting with double and triple amino acid decarboxylation (lysine, ornithine, or arginine). Different supplement with combined amino acids provided different ferrous sulfide precipitates and OD₆₅₀ signals depending on *Salmonella* serovars. It seemed the combination of ornithine and arginine in TFX broth (OD₆₅₀ = 1.7–2.5) was able to enhance optical density change and thiosulfate-reducing metabolism of most *Salmonella* comparing to single lysine usage (OD₆₅₀ = 1.4–2.1) and other amino acid mixtures (OD₆₅₀ = 1.4–2.4). Atypical *Salmonella* (*S. Typhi* and *S. Anatum*) gave low OD₆₅₀

in all media except in TFXLA that *S. Anatum* showed high black precipitations. No differentiation was observed on three common thiosulfate-reducing non-salmonellae (*Citrobacter* and *Proteus* spp.). Only *C. freundii* could be deleted out or showed negative hydrogen sulphide in TFXL media. The further study on fermentable sugar types could possibly increase the sensitivity and selectivity of this H₂S ornithine-arginine based media. The developed H₂S indicator media can be applied for rapid *Salmonella* presumptive screening, alternative to conventional selective enrichment broth with given presumptive result with 48 h from pre-enrichment step (conventional method; 24 h for pre-enrichment and 24 h for selective enrichment followed by agar plating with additional 24 – 48 h for those result).

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