A colon-targeted delivery system of torularhodin, and its regulation mechanism of gut microbiota

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Introduction

- Scientific questions
- Results and discussion
- Conclusion

1.Introduction

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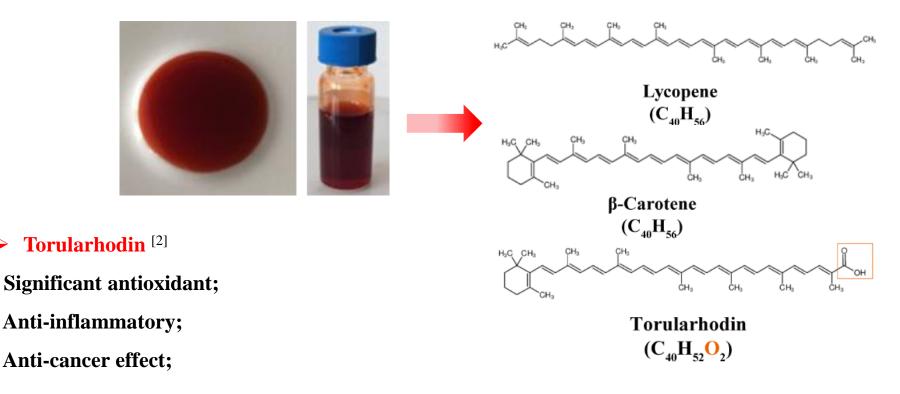


1.1 Torularhodin: One kind of Carotenoids

> Sporidiobolus pararoseus [1]

A facultative aerobic yeast with strong adaptability and wide distribution in nature;

Producing carotenoids, especially torularhodin;

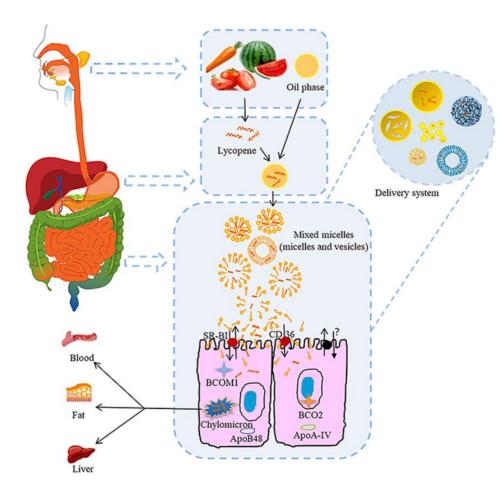


1. Chang Liu, He Qian., Bioresource Technol, 2021. 2. Chang Liu, He Qian., J. Agric. Food Chem, 2019.

1.Introduction



1.2 Gut Health Functions of Carotenoids



Bioaccessibility ^[3.4]

Small intestine:

Lycopene (40%), beta-carotene (27%);

Colon:

Lycopene (40%), beta-carotene (57%);

> Health effects ^[5]

Carotenoids may improve host health by improving gut microbiome.



Isabel Goñi, Journal of Agricultural and Food Chemistry, 2006.
 R. Est évez-Santiago, B, Food & Function, 2015.
 PaulaMapelli-Brahm, Current Opinion in Food Science, 2021.

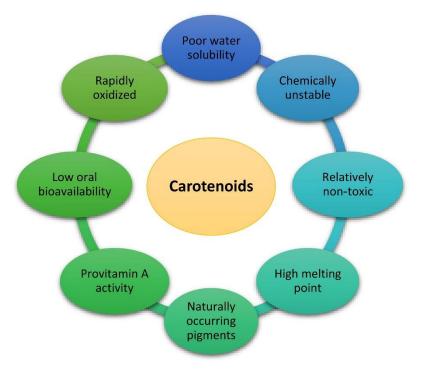
1.Introduction



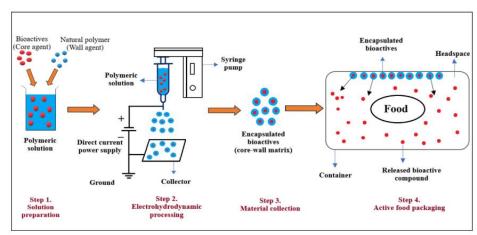
1.3 Carotenoids and colon-targeted delivery systems

- > Difficulties in the application of carotenoids ^[6]
- Poor water solubility;
- **Poor stability;**

Photo degradability;



Electrospinning technology ^[7]
 Natural polymers for active food packaging;
 Natural, safe;
 Biodegradable;



6. Saeid Maghsoudi, *Critical Reviews in Food Science and Nutrition*, 2022.7. Charles, A, *Compr Rev Food Sci Food*, 2021.

1. Introduction

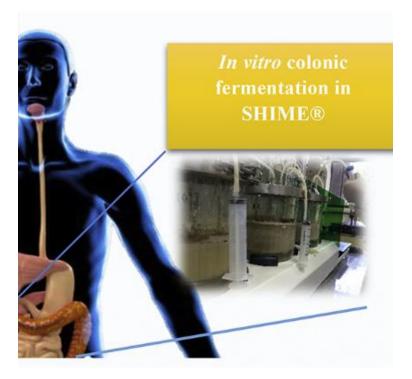


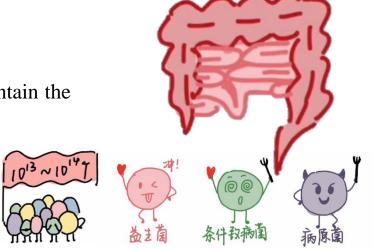
1.4 Gut microbiome and In vitro fermentation

➢ Gut microbiome ^[8]

Exceed 100 trillion;

Multiple functions: energy supply, immune regulation, maintain the integrity of the intestinal barrier, inhibit intestinal pathogens;





> In vitro fermentation ^[9]

Simple and have **no ethical constraints**;

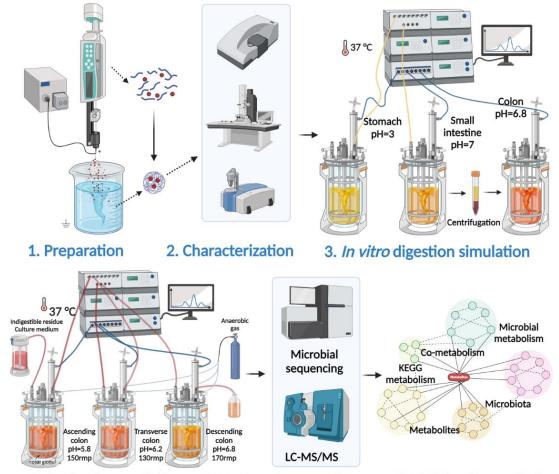
Test the ability of the human gut microbiota to metabolize foods with different structures;

Formulate healthy, functional foods ;

8. Schroeder, *Nature Medicine*, 2016. 9. Sayago-Ayerdi, S. G, Food Research International, 2021.

2. Scientific questions

- > 1. Constructing the colon-targeted delivery system of torularhodin?
- > 2. The effects of torularhodin targeting the colon on the gut microbiome?
- > 3. The interaction mechanisms of gut microbiome-metabolites-host metabolism?

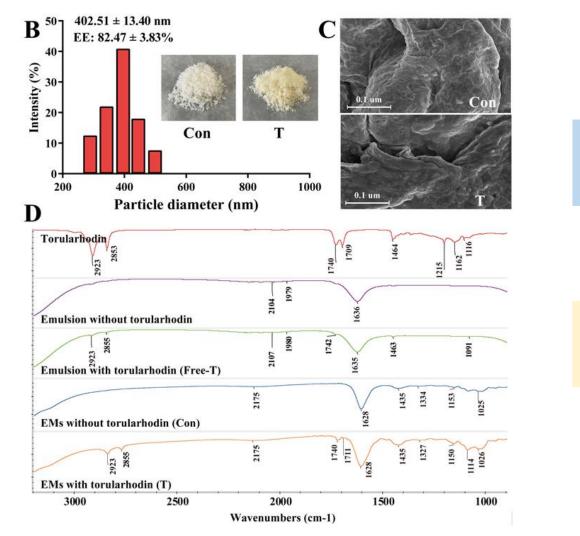


4. In vitro fermentation 5. Muti-omics experiments 6. Multi-omics analysis





3.1 Electrospinning microspheres

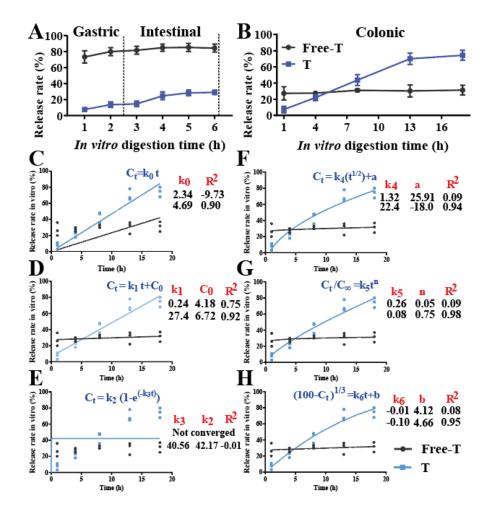


Torularhodin helps to relieve the microspheres and maintain structure.

Electrospinning microspheres could wrap torularhodin to form a stable system.



3.2 In vitro digestion

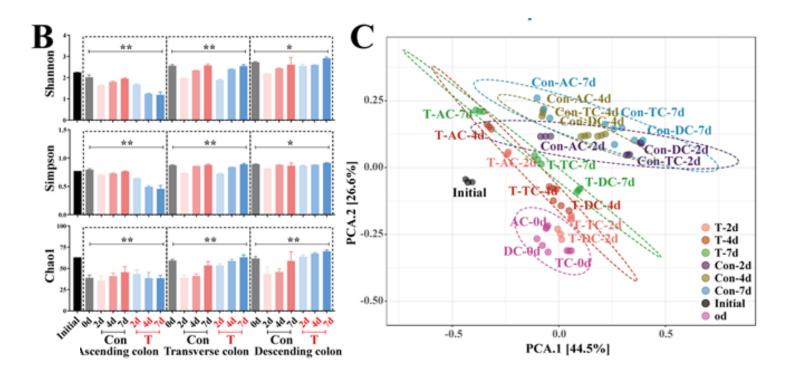


The release of torularhodin is a Korsmeyer-Peppas model owing to non-Fickian transport (n = 0.75).

Electrospinning microspheres can be used as carriers for torularhodin in the food industry.



3.3 Gut Microbiome



- 1. The addition of torularhodin can regulate the diversity and abundance of gut microbiota.
- 2. The change of the gut microbiota in the transverse colon and descending colon is not obvious, and the diversity composition is more stable.

3. Results and discussion



3.3 Gut Microbiome

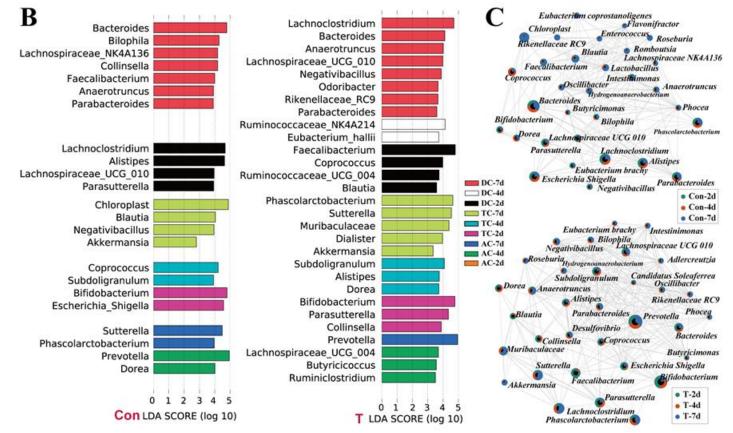
Phylum	Class	Order	Family	Genus		Con T scending co	- N	Con vs T (4d)	Con vs T (7d)	1	Con	T	ST	vs T	Con vs T (7d)	G	n	T colo	Con vs T (2d)	vs T	Con vs T (7d)
erracomicrobia	Ferrucomicrobiae	Verracomicrobiales	Akkermansiaceae	Akkermansia	Top14									*					. 8	٠	8
Proteobacteria	Gammaproteobacteria	Enterobacteriales	Burkholderiaceae Enterobacteriaceae	Escherichia-Shigella	Top09					1			**	**							
		Betaproteobacteriales		Parasutterella Sutterella	Top08 Top03					. –			**	**					**	**	** 1
	Deltaproteobacteria	Desulfovibrionales	Desulforibrionaceae	Desulfovibrio	Top24					+				++	++				٠	**	**
	22 10 10 10 10 10 10 10 10 10 10 10 10 10			Bilophila	Top31					1				**	**	-				**	
	Clostridia Negativicutes	Clostridiales Selenomonadales	Ruminococcaceae Acidaminococcaceae Veillonellaceae	Dialister	Topl9					+		100	**	**				100	11		1
Firmicates				Phascolarctobacterium	Top06		14									-	-				
				Subdoligranulum	Top12					-			**			-	+++		**	**	**
				Ruminococcaceae_NK4A214 Ruminococcaceae_UCG	Top20 Top07					1 -						-					
				Ruminiclostridium	Top35					1				**	8 4			12	44		
				Oscillibacter	Top32		1	1 **	-				1	1			100	100	**		-
				Negativibacillus	Top26		1	в	**				8	**					**	**	**
				Intestinimonas	Top28			**		+			**	*	** ;			1.15	**	*	*
				Hydrogenoanaerobacterium			8	**	88					8	**					*	8
				Faecalibacterium	Top11					+			**	**	** 1					**	*
				Anaerotruncus	Top21		**	п	**			14	**	**	** (**	**	**
			Lachnospiraceae	Roseburia	Top34				**			20	8	**	8			12	2	**	
				Lachnospiraceae_UCG	Top16		**	٠		+			**	**	**				**	**	**
				Lachnoclostridium	Top05		**	п	**			201	**	**	**				**	п	**
				Dorea	Top22		**		88				**	**	* (.88	**	
				Coprococcus	Top18		**	**	44	4 🗌				**	n				**	**	
				Blautia	Top23			**	**	+				**				12.00		**	**
			Family XIII	Family XIII AD3011	Top30								**	**					41	**	48
			Christensenellaceae	Christensenellaceae R-7	Top25		8		8								n			**	
	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Top27												100	100			
Bacteroidetes	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides	Top13				10	4 E				11	÷.,						-
			Rikenellaceae	Alistipes Rikenellaceae RC9	Top10 Top33					•							٠.				
			Muribaculaceae Prevotellaceae	Prevotella	Top01					5 –									44		
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			Bacteroidaceae	Bacteroides	Top04			**	**	<u>+</u>	100 11			**	** 4		20		.88	**	**
The second second second	Coriobacteriia	Coriobacteriales	Coriobacteriaceae	Collinsella	Top15				**	+				**	** 4					**	*
ctinobacteria	Actinobacteria	Bifidobacteriales	Bifidobacteriaceae	Bifidobacterium	Top02			**		•			**	**			120	100	**	**	

- 1. There were more gut microbiome with significantly increased abundance in the descending colon than transverse colon.
- 2. Significantly increased in *Prevotella* (Top01), *Phascolarctobacterium* (Top06), *Ruminococcaceae UCG* (Top07),
- Faecalibacterium (Top11), Lachnospiraceae UCG (Top16), Muribaculaceae (Top17).
 Significantly decreased included Sutterella (Top03), Bacteroides (Top04), Escherichia-Shigella (Top09), Alistipes (Top10),
 - Parabacteroides (Top13), Collinsella (Top15), and Intestinimonas (Top28).

3. Results and discussion



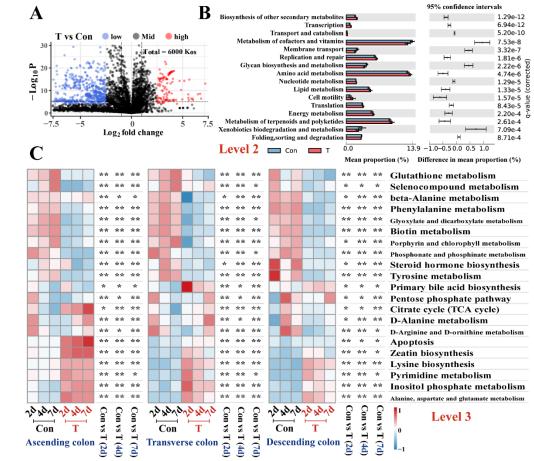
3.3 Gut Microbiome



The key to the gut ecosystem was explained by the LDA and co-occurrence network.
 Microorganisms with greater relevance weights included *Prevotella*, *Bifidobacterium*, *Faecalibacterium*, and *Phascolarctobacterium*.



3.3 Gut Microbiome

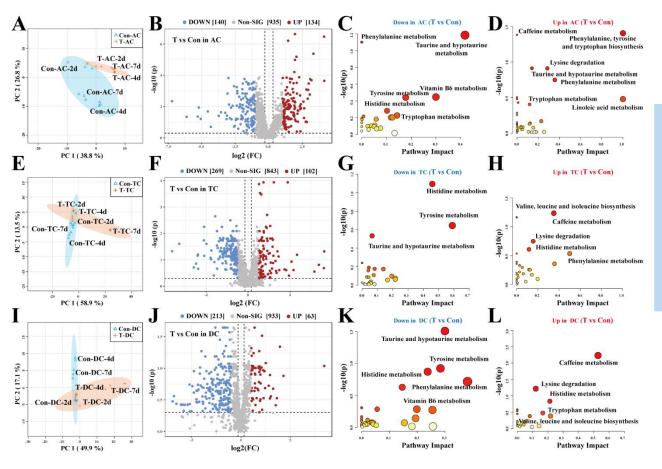


Predictive functional results from KEGG database: Enhanced lysine biosynthesis and inositol phosphate metabolism; Decreased phenylalanine and tyrosine metabolism;

3. Results and discussion



3.4 Metabolome



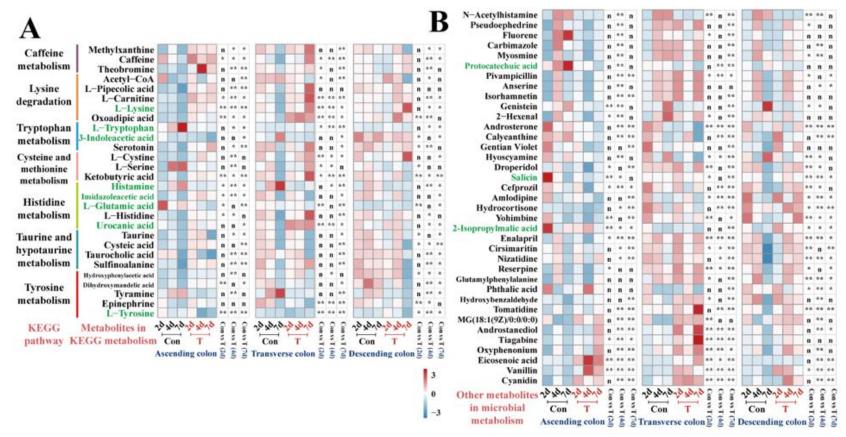
Significantly downregulated: taurine and hypotaurine; histidine and tyrosine metabolism;

Significantly **up-regulated:** lysine degradation, and tryptophan metabolism;

It is relatively consistent with the prediction function of the gut microbiome.



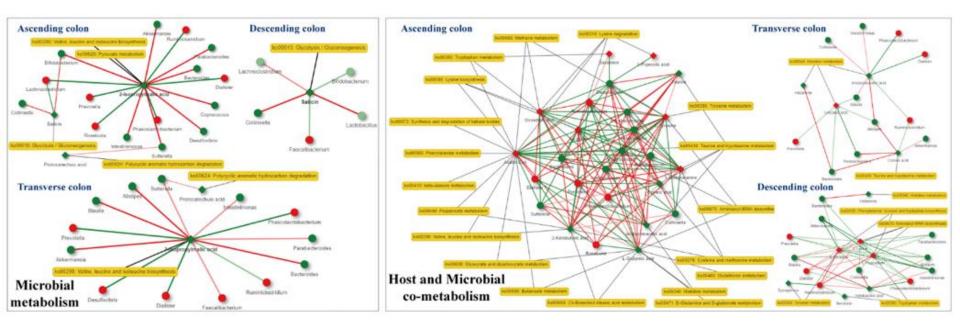
3.4 Metabolome



The marked metabolites were lysine, tyrosine, tryptophan, 3-indoleacetic acid, glutamic acid, and histamine.



3.5 Combined analysis

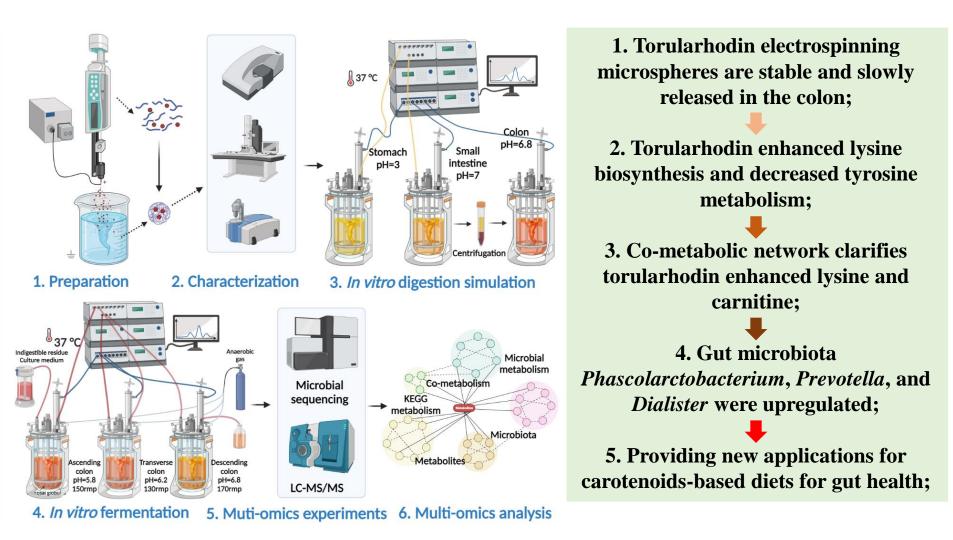


Key metabolites: lysine, tyrosine, tryptophan, 3-indoleacetic acid Key metabolisms: lysine degradation, tyrosine metabolism, tryptophan metabolism, and histidine metabolism. Key microbiome: *Prevotella, Phascolarctobacterium*, and *Dialister*,

The metabolic functions of the gut microbiome are related to human biological functions through the microbiome-host co-metabolic network.

4.Conslusion







Professor Qian's Lab

Postgraduate Research & Practice Innovation Program of Jiangsu Province (2021&2022)

Thanks!

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