Characterizing the binding interaction between ultrafine carbon black (UFCB) and catalase: electron microscopy and spectroscopic analysis

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Paper Summary

Word count: 4525 Number of figures: 8 Number of tables: 3 1. The dispersion effect of FW200 in tween 80



Figure S1. The image of FW200 dispersed in tween 80. C_{FW200} (1-6) = 0, 10, 20, 30, 40, 50 µg mL⁻¹.



2. The Phase Plot of the zeta-potential measurement of FW200-tween 80 mixture.

Figure S2. Phase plot of FW200-tween 80.

3. Inner-filter effect of FW200-CAT system



Fig. S3 The inner-filter effect of FW200-CAT system. Conditions: C_{CAT} : 2 μ M, $C_{FW200} = 0, 5, 15, 20, 25, 30, 35, 40, 45, 50 \ \mu g \ mL^{-1}$. pH = 7.4, T = 300K

4. Inner-filter effect of T80-CAT system



Fig. S4 The inner-filter effect of T80-CAT system. Conditions: C_{CAT} : 2 μ M, $C_{T80} = 0$, 1, 5, 10, 20, 30, 40, 50 μ g mL⁻¹. pH = 7.4, T= 300K

5. RLS spectra measurement

As shown in Figure S 1A and B, with FW200 (tween 80 as dispersant) being titrated into the catalase (CAT) solution and the Milli-Q water, the RLS intensity of these two solutions increased dose-dependently. The changing extent of the FW200-CAT solution was larger than that of the Milli-Q water with FW200 alone, suggesting that the increase of RLS intensity of the FW200-CAT system was caused by the binding between FW200 nanoparticles and CAT.



Fig. S5 RLS spectra: A: FW200-CAT system, B: FW200 alone, C: tween 80-CAT system, D: maximum RLS intensity of tween 80-CAT derived from C. Conditions: $C_{FW200} = 0, 10, 20, 30, 40, 50 \ \mu g \ mL^{-1}, C_{tween 80} = 0, 1, 5, 10, 20, 30, 40, 50 \ \mu g \ mL^{-1}, C_{CAT} = 2 \ \mu M.$

6. Homologous identity of bovine catalase and mouse catalase

Bovine catalase has a 91% homologous identity with homo catalase, so it is profound to use bovine liver catalase in the molecule level toxicity.

Sequences producing significant alignments:

Select: All None Selected:0

# Alignments #Download ~ GenPept Graphics Multiple alignment												
Description	Max	Total	Query	Е	e Ident	Accession						
Description	score	score	cover	value								
catalase [Bos taurus]	1028	1028	100%	0.0	91%	NP_001030463.1						

	Range 1: 1 to 527 GenPept Graphics							🔻 Next Match 🔺 Previous Match				
	Score		Expect	Method	1ethod			Positives		Gaps		
	1028 8	oits(26	59) 0.0	Composition	al matrix	adjust.	482/527(91%)	505/527(95	5%)	0/527(0%)		
Catalase [Homo] →	Query	1	MADSRDPASD	QMQHWKEQRAAG	KADVLTTG	AGNPVGDI GNPVGDI	KLNVITVGPRGPLL KLN +TVGPRGPLL	VQDVVFTDE	60	identical part —— of these two		
Catalase [Bos] 	Sbjct	1	MADNRDPASD	QMKHWKEQRAAG	KPDVLTTG	GGNPVGDI	KLNSLTVGPRGPLL	VQDVVFTDE	60	sequences		
	Query	61	MAHFDRERIP	ERVVHAKGAGAF ERVVHAKGAGAF	GYFEVTHD	TKYSKA	KVFEHIGKKTPIAV	RFSTVAGES	120			
	Sbjct	61	MAHFDRERIP	ERVVHAKGAGAF	FGYFEVTHD	TRYSKA	VFEHIGKRTPIAV	RFSTVAGES	120			
	Query	121	GSADTVRDPR GSADTVRDPR	GFAVKFYTEDGN GFAVKFYTEDGN	WDLVGNNTI	PIFFIRD	PILFPSFIHSQKRN +LFPSFIHSQKRN	PQTHLKDPD PQTHLKDPD	180			
	Sbjct	121	GSADTVRDPR	GFAVKFYTEDGN	WDLVGNNT	PIFFIRD	ALLFPSFIHSQKRN	PQTHLKDPD	180			
	Query	181	MVWDFWSLRP MVWDFWSLRP	ESLHQVSFLFSI ESLHQVSFLFSI	ORGIPDGHR		HTFKLVNANGEAVY(HTFKLVNANGEAVY)	CKFHYKTDQ CKFHYKTDQ	240			
	Sbjct	181	MVWDFWSLRP	ESLHQVSFLFSI	ORGIPDGHR	MNGYGSI	HTFKLVNANGEAVY	CKFHYKTDQ	240			
	Query	241	GIKNLSVEDA	ARLSQEDPDYGI	RDLFNAIA	CAN THE SECOND	TFYIQVMTFNQAET	FPFNPFDLT	300			
	Sbjct	241	GIKNLSVEDA	ARLAHEDPDYGL	RDLFNAIA	GNYPSW	TLYIQVMTFSEAEI	FPFNPFDLT	300			
	Query	301	KVWPHKDYPL KVWPH DYPL	IPVGKLVLNRNF IPVGKLVLNRNF	PVNYFAEVE	QIAFDPS:	MPPGIEASPDKML	QGRLFAYPD QGRLFAYPD	360			
	Sbjct	301	KVWPHGDYPL	IPVGKLVLNRNF	VNYFAEVE	LAFDPS	MPPGIEPSPDKML	QGRLFAYPD	360			
	Query	361	THRHRLGPNY THRHRLGPNY	LHIPVNCPYRAF	RVANYQRDG	PMCMQDNO	QGGAPNYYPNSFGAI	PEQQPSALE	420			
	Sbjct	361	THRHRLGPNY	LQIPVNCPYRAF	RVANYQRDG	PMCMMDN	QGGAPNYYPNSFSA	PEHQPSALE	420			
	Query	421	HSIQYSGEVR	RFNTANDDNVTG RFN+ANDDNVTG	QVRAFYVNV	NEEQRKI	RLCENIAGHLKDAQ	IFIQKKAVK +FIQKKAVK	480			
	Sbjct	421	HRTHFSGDVQ	RFNSANDDNVTG	VRTFYLKV	NEEQRKI	RLCENIAGHLKDAQ	LFIQKKAVK	480			
	Query	481	NFTEVHPDYG	SHIQALLDKYNA	AEKPKNAIH FKPKNA+H		HLAAREKANL 52	7				
	Sbjct	481	NFSDVHPEYG	SRIQALLDKYNE	EKPKNAVH	TYVQHGSI	LSAREKANL 52	7				

Fig. S6 homologous identity of bovine catalase and homo catalase. The data was obtained from the NCBI (National Center for Biotechnology Information) and contrast between these two sequences was conducted by using BLAST (Basic Local Alignment Search Tool).