

The Chinese Barley Malt Filterability-Related Proteins Explored by the Proteomic Strategy

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The filterability defect of domestic barley malt is a long term disturbing problem in current Chinese brewing industry. In contrast, beer manufacture using the Canadian and Australian barley malts with superior filterability seldom met this problem. The direct factor of filterability was historically considered to be certain incomplete hydrolyzed macromolecules, such as β -glucan, arabinoxylan (AX) and prolamine, which was attributed to complex reasons. To systematically characterize filterability-related proteins in barley malt, the Canadian Metcalfe barley malt with superior filterability, and the Chinese Dan'er barley malt encountering filterability problem, were chosen for comparative proteomic using 2D-DIGE. The most different proteins, β -amylase and AXAH-I have been verified to be positively related with filterability, while POD (peroxidase) has a negative effect on filterability.

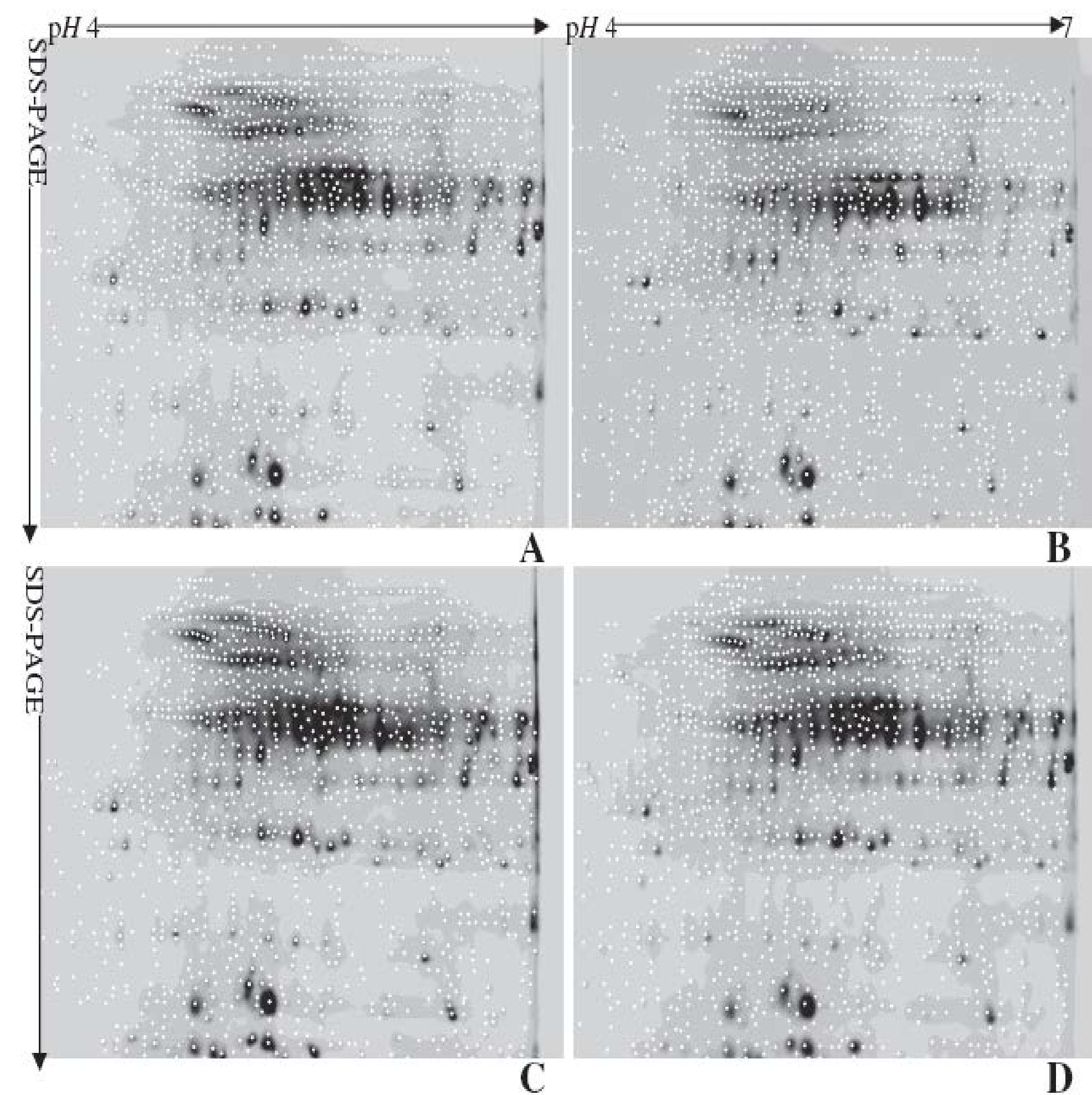


Figure 1. Representative DIGE maps of low-salt soluble proteins (labeled with Cy3) from malts in a pI range of 4-7 and a molecular mass range of 10-60 kDa. A, Metcalfe malt I; B, Metcalfe malt II; C, Dan'er malt I; D, Dan'er malt II.

Table 1 Major quantitative differential proteins between Dan'er and Metcalfe malts

Spot no.	Protein name	Av. ratio (T1, T2)/(C1, C2)	profiles
94	β -amylase	5.55	
68	AXAH-I	1.88	
451	LTP1	-2.51	
115	Peroxidase BP1	-4.28	
262	Serpin Z7	-7.68	
353	Serpin Z4	-5.36	
438	α -amylase/trypsin inhibitor CMb	-2.20	

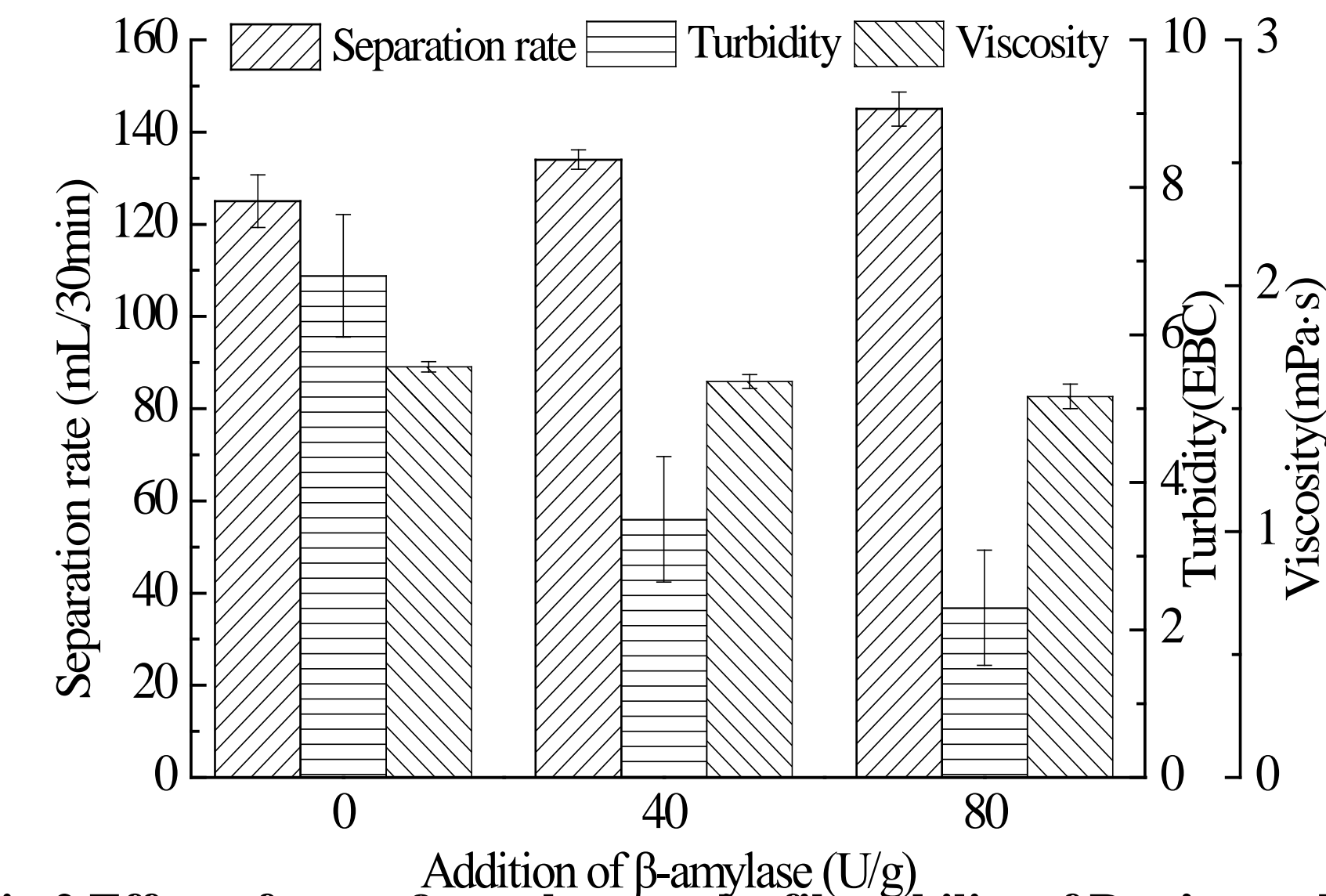


Fig.2 Effect of extra β -amylase on the filterability of Dan'er malt.

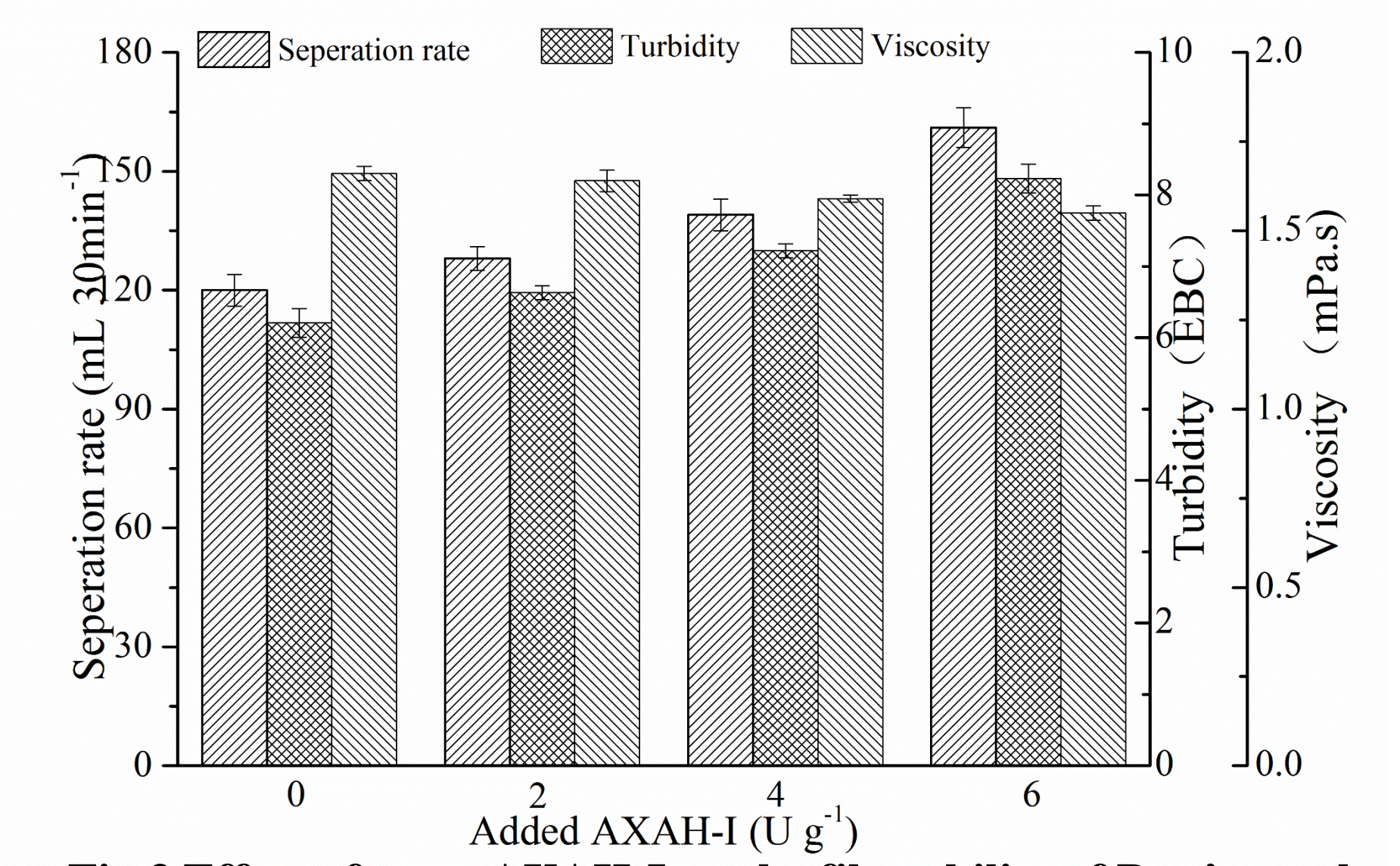


Fig.3 Effect of extra AXAH-I on the filterability of Dan'er malt.

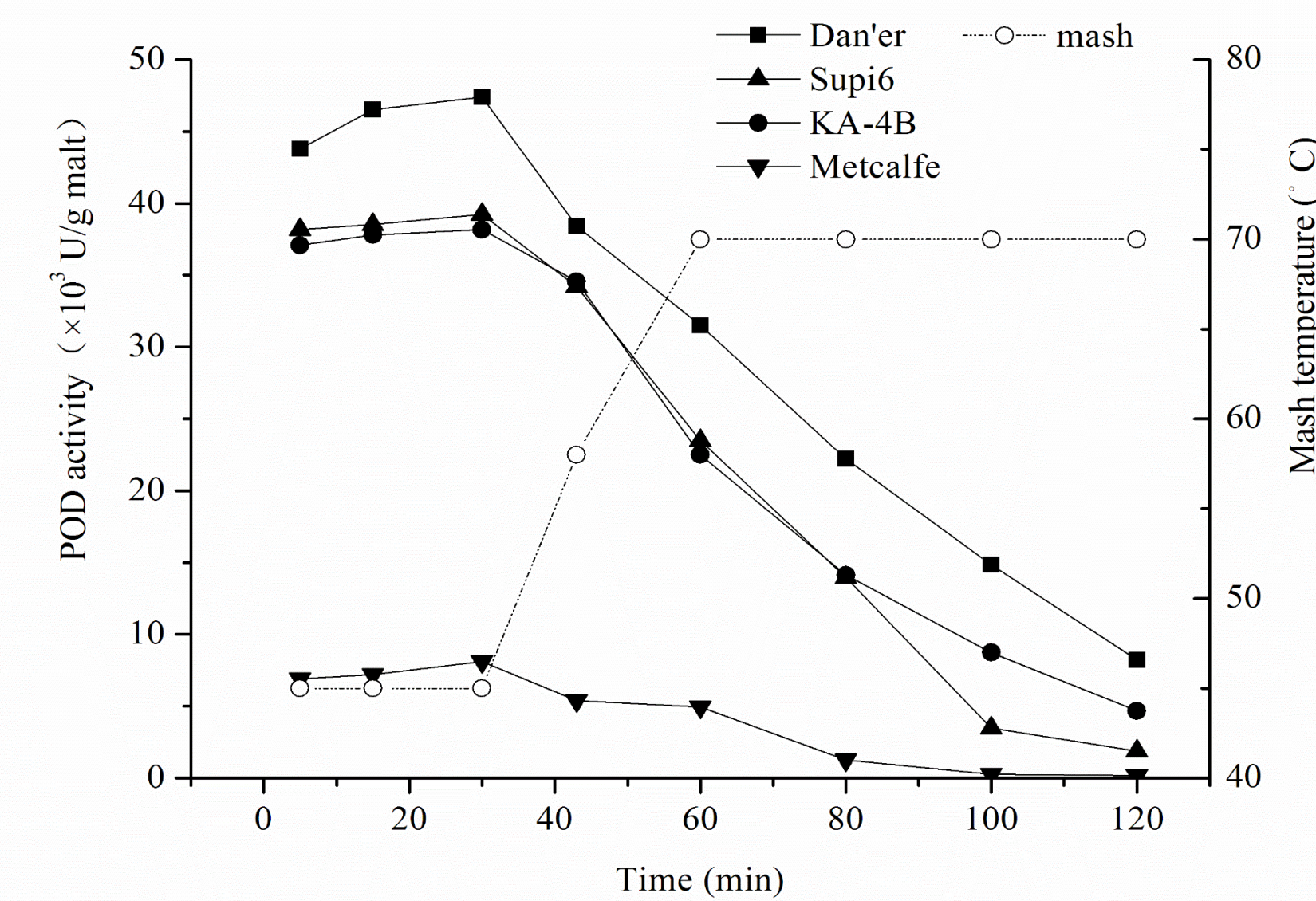


Fig.4 POD activity monitoring during mashing.

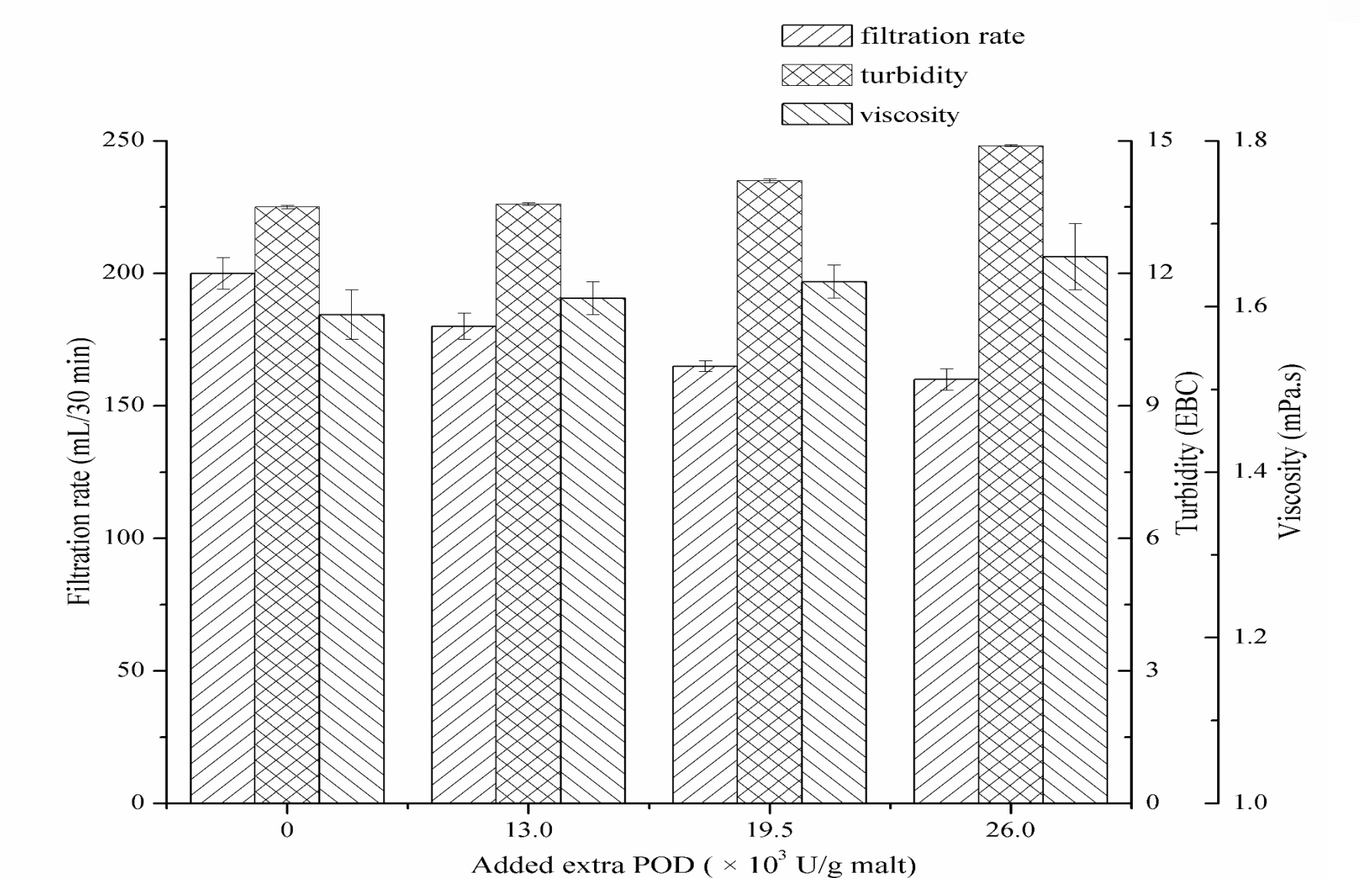


Fig.5 Effect of extra POD on the filterability of Dan'er malt