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RESEARCH ARTICLE

Typology of farms and spatial patterns on the North China Plain to support crop-livestock integration

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SUPPLEMENTARY MATERIALS

Table S1 Description of farm-structure, farming-practice, and socio-economic variables in the questionnaire

Category	Variable	Practice option	Unit	
Farm-structure variables	Number of field parcels	–	Number	
	Total land area	–	ha	
	Land area with certain types of crops on farm	Grain		ha
		Cash crops		ha
		Others		ha
	Types of livestock on farm	Poultry (Yes/No)		Binary
		Pig (Yes/No)		Binary
		Beef cattle (Yes/No)		Binary
		Others		–
		Number of animals on farm	–	Livestock units
	Land area for grazing	–	ha	
Socio-economic variables	Number of education years	–	Years	
	Family size	–	Number of persons	
	Whether farm income completely depends on farming	Yes/No	Binary	
	Age of household head	–	Years	
	Mineral fertilizer management			
	The quantity of mineral fertilizer applied	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	
	The quantity of mineral urea applied	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	
Organic fertilizer management				
Farming-practice variables	The amount of manure applied on croplands	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	
	The proportion of manure exported	Yes/No	%	
	The amount of manure imported from neighboring farms	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	
	Feed management			
	The amount of purchased feed	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	
	The amount of feed imported from neighboring farms	Yes/No	kg·ha ⁻¹ ·yr ⁻¹	

S1 The selection of clustering algorithms

In this study, we used the *cValid* package to compare five clustering algorithms: hierarchical cluster analysis, partition around the medoids (PAM), divisive analysis (DIANA), K-means and model-based clustering (MODEL). The R package provides functions to evaluate the results of a clustering analysis^[1], allowing users to evaluate multiple algorithms simultaneously and choose the most suitable method. There are three validation measures in this package, “internal”, “stability” and “biological”. We selected “internal” measures to do cluster validation as “stability” is more suitable for high-throughput genomic data and biological validation mainly evaluates biological data. Internal validation assesses cluster quality in terms of compactness, separation, and connectedness. The compactness measures the similarity of clusters, while separation evaluates the differences between clusters, which are measured by the Dunn index^[2] and silhouette^[3]. Connectedness refers to how closely observations are grouped with their nearest neighbors, measured by connectivity^[4]. A good clustering algorithm is indicated by a minimum connectivity, and maximum silhouette index and Dunn index. The comparison between the performance of clustering algorithms is shown in Figure S1, indicating that the hierarchical cluster analysis was the most appropriate choice for our data.

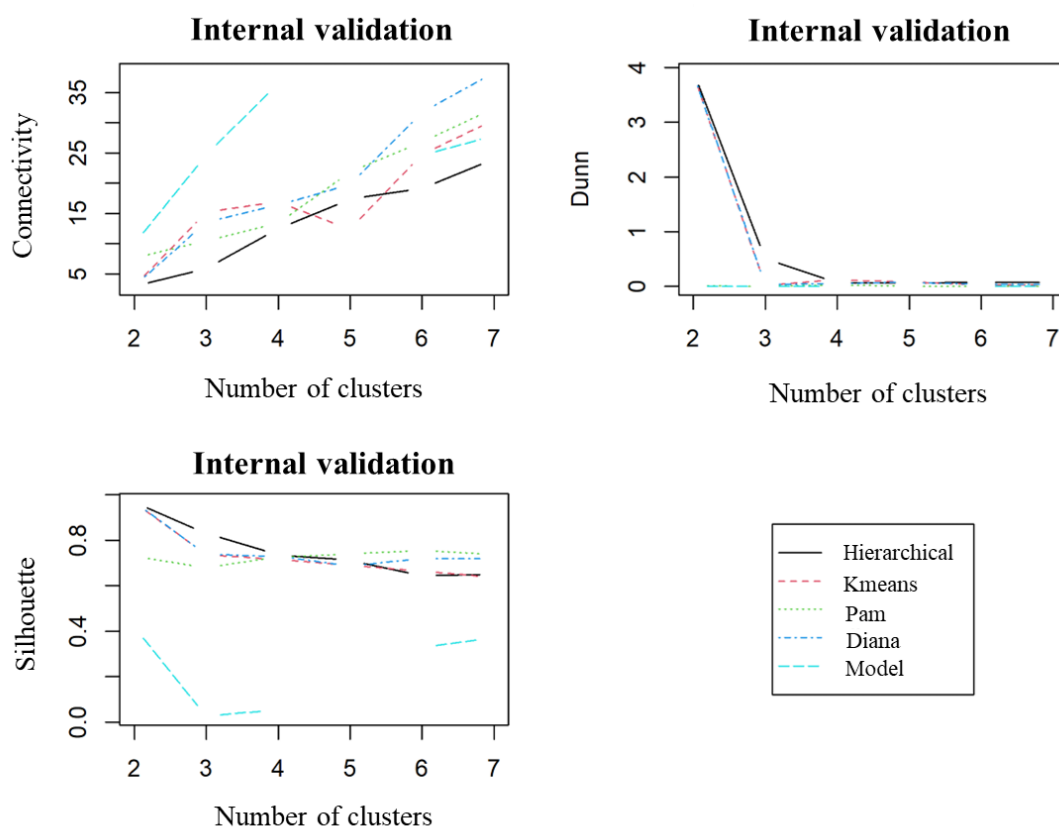


Fig. S1 The outcomes of comparison among the five clustering algorithms using connectivity, Dunn index, and silhouette scores to determine the optimal clustering method.

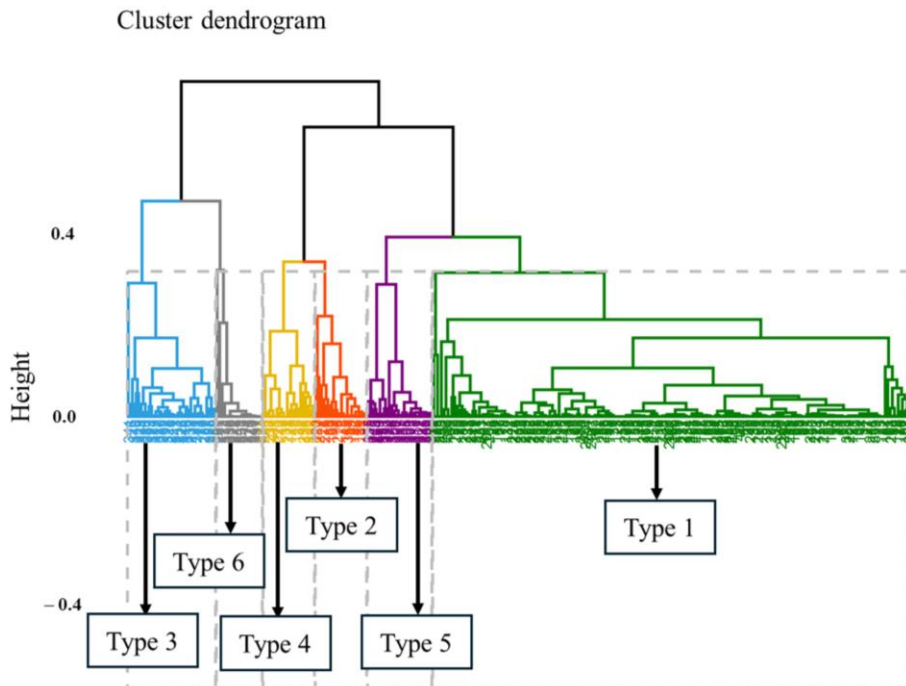


Fig. S2 The dendrogram was cut and six farm typologies were identified. Type 1, grain farm; Type 2, cash crop farm; Type 3, mixed farm; Type 4, commercial farm; Type 5, small mixed farm; Type 6, landless farm.

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