Application of spatial analysis to improve the estimation of genetic parameters in Alfalfa (*Medicago sativa* L.)

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Introduction

- Field trials are associated to some form of spatial variation between experimental units in complex and large experimental designs
- spatial analysis can detect the variation patterns

Objectives

Assess the efficiency of spatial analysis and compare with the base model

Materials and Methods

- **Experimental Design-**Row column
- **Breeding population -**145 full-sib and 36 half-sib families
- Herbage accumulation (HA) was collected four times
- Fit two models

Base Model => y = family(checks) + Row + Column + family(regular) +error (id)

Spatial Model => y = family(checks) + Column + Row + family(regular) + error (ar1:Row + ar1:Column)

- Estimate narrow-sense heritability h^2, and selection accuracy
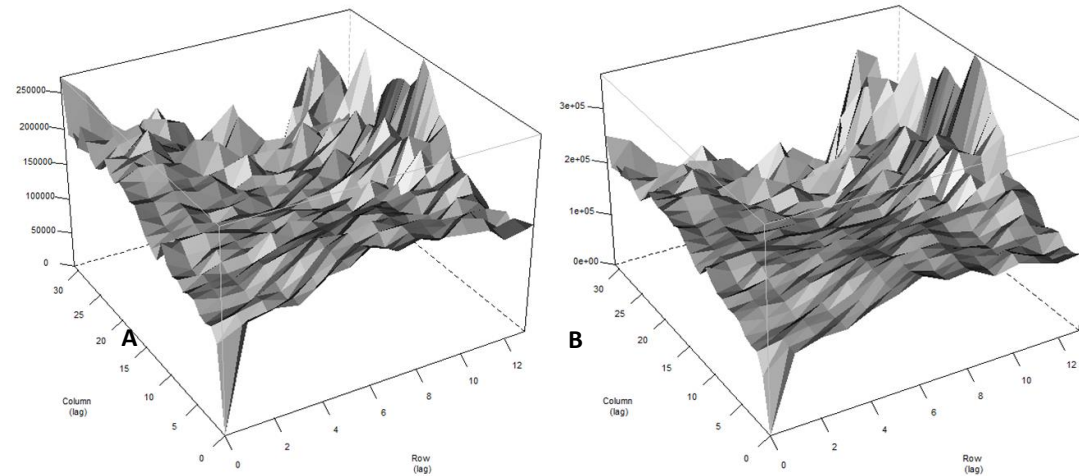
Results and Discussion

Figure . Changes in variograms (A) before (base model) and (B) after (spatial model) inclusion of row and column

Findings

- The autocorrelation had a significant effect in both directions (rows and columns0
- Spatial model has significant effect on all harvests
- Heritability and selection accuracy were increased from base model to spatial model
- Predicted error variance (PEV) was less in spatial model for all harvests except 4th harvest

Table: Genetic parameters from base and spatial model

Harvest	Genetic parameters	Base Model	Spatial Model
1	Heritability	0.28	0.31
	PEV	31145.4	29976.5
	Relative Efficiency	-	103.9
2	Heritability	0.18	0.2
	PEV	15503.4	15048.1
	Relative Efficiency	-	103.1
3	Heritability	0.24	0.27
	PEV	19785.3	19442.6
	Relative Efficiency	-	101.8
4	Heritability	0.19	0.23
	PEV	38223.4	39548.8
	Relative Efficiency	-	97.4

Conclusions

The spatial model can reduce the error and improve the estimation of genetic parameters which can be a great addition in alfalfa breeding program

References

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