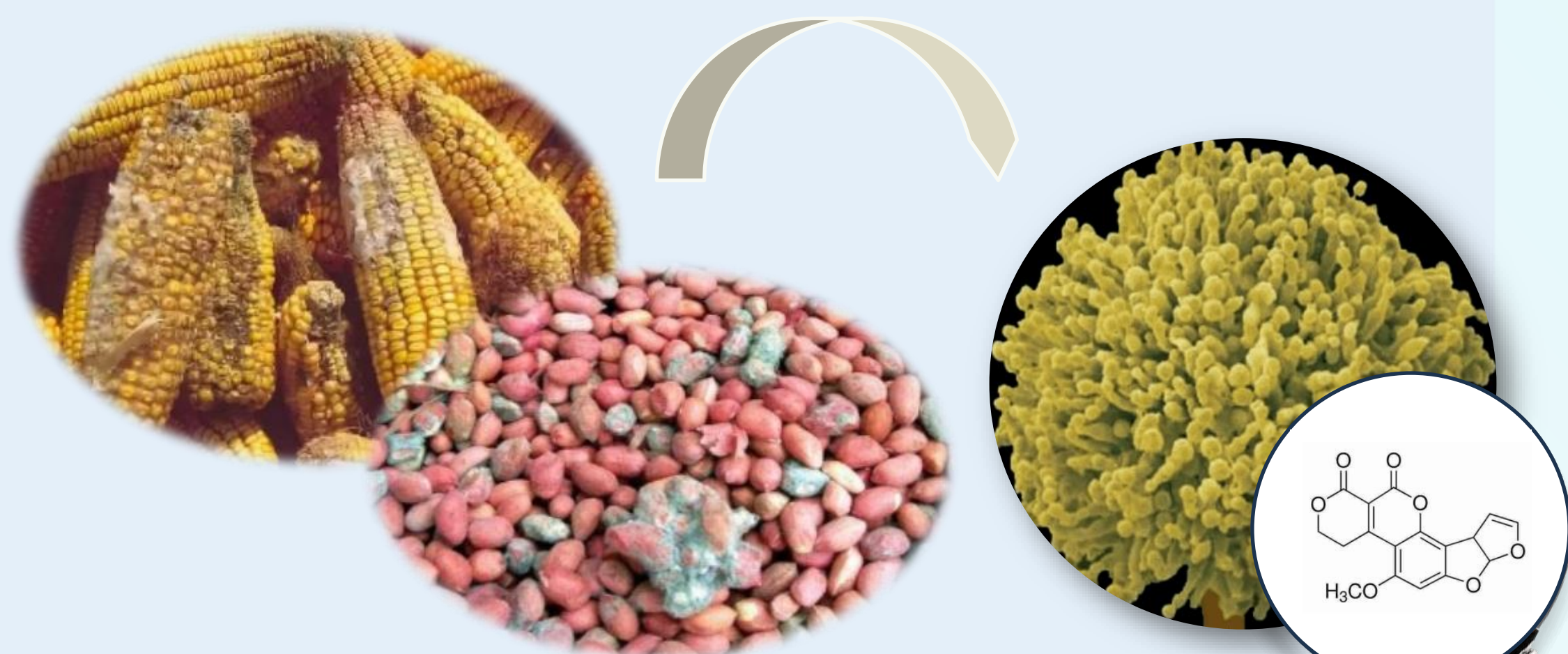


I. Introduction

Aspergillus flavus is a major cause of post-harvest losses in maize and peanuts due to aflatoxin B₁ (AFB₁) contamination. Current detection methods are often slow, invasive, and unsuitable for real-time monitoring, highlighting the urgent need for sensitive and scalable early detection strategies.

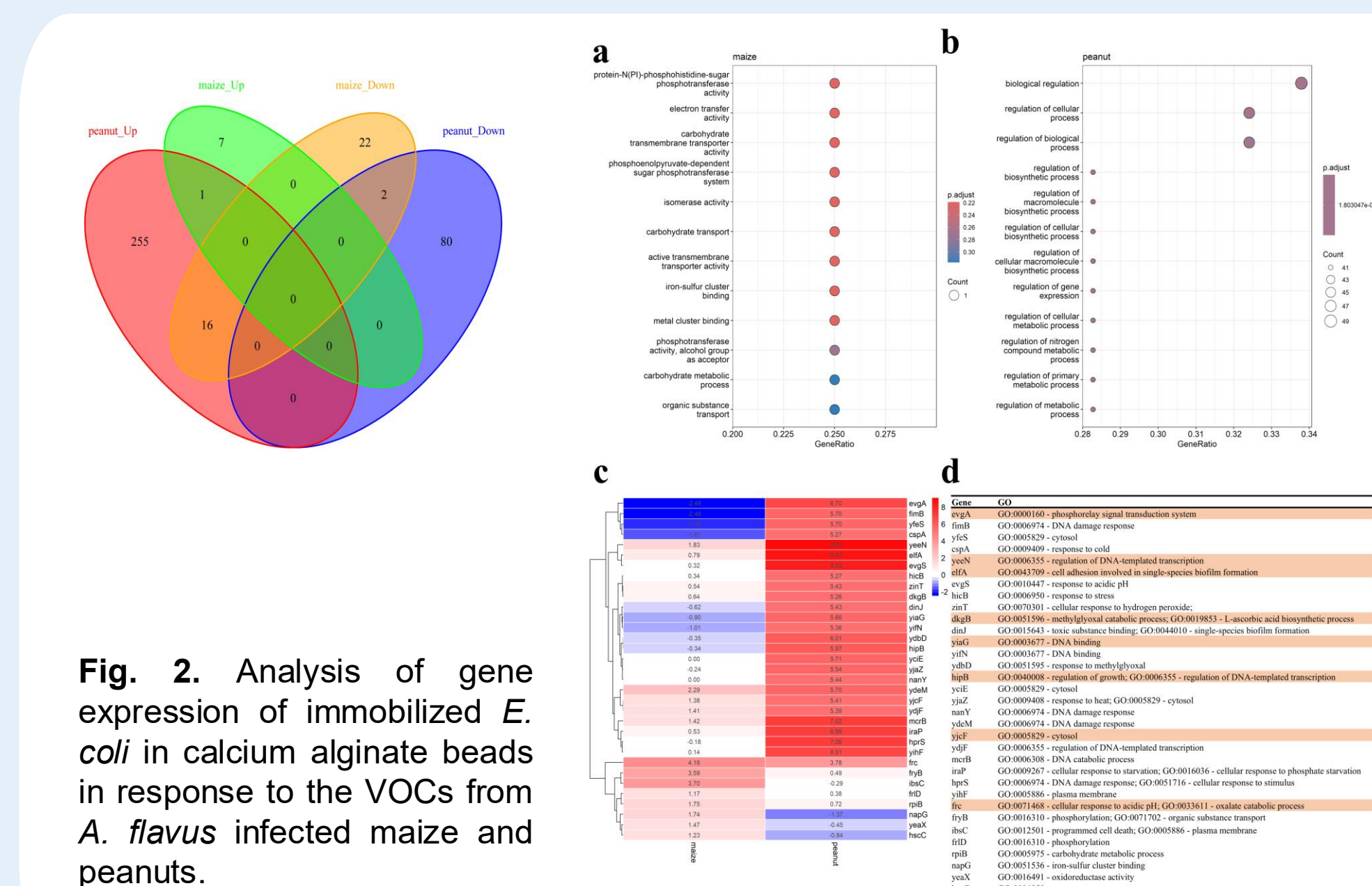
II. Objectives

This study aims to develop a non-invasive, transcriptome-guided whole-cell biosensor array integrated with machine learning models for early and quantitative prediction of *A. flavus* infection stages and AFB₁ levels in maize and peanut kernels.



IV. Results and Expectation

Eight infection-induced promoters were identified from *E. coli* transcriptomic responses to VOCs.



Feature importance analysis revealed that early host responses, including transcriptional regulation and biofilm formation, served as key predictive features, thereby providing mechanistic interpretability not attainable with conventional optical or chemical assays.

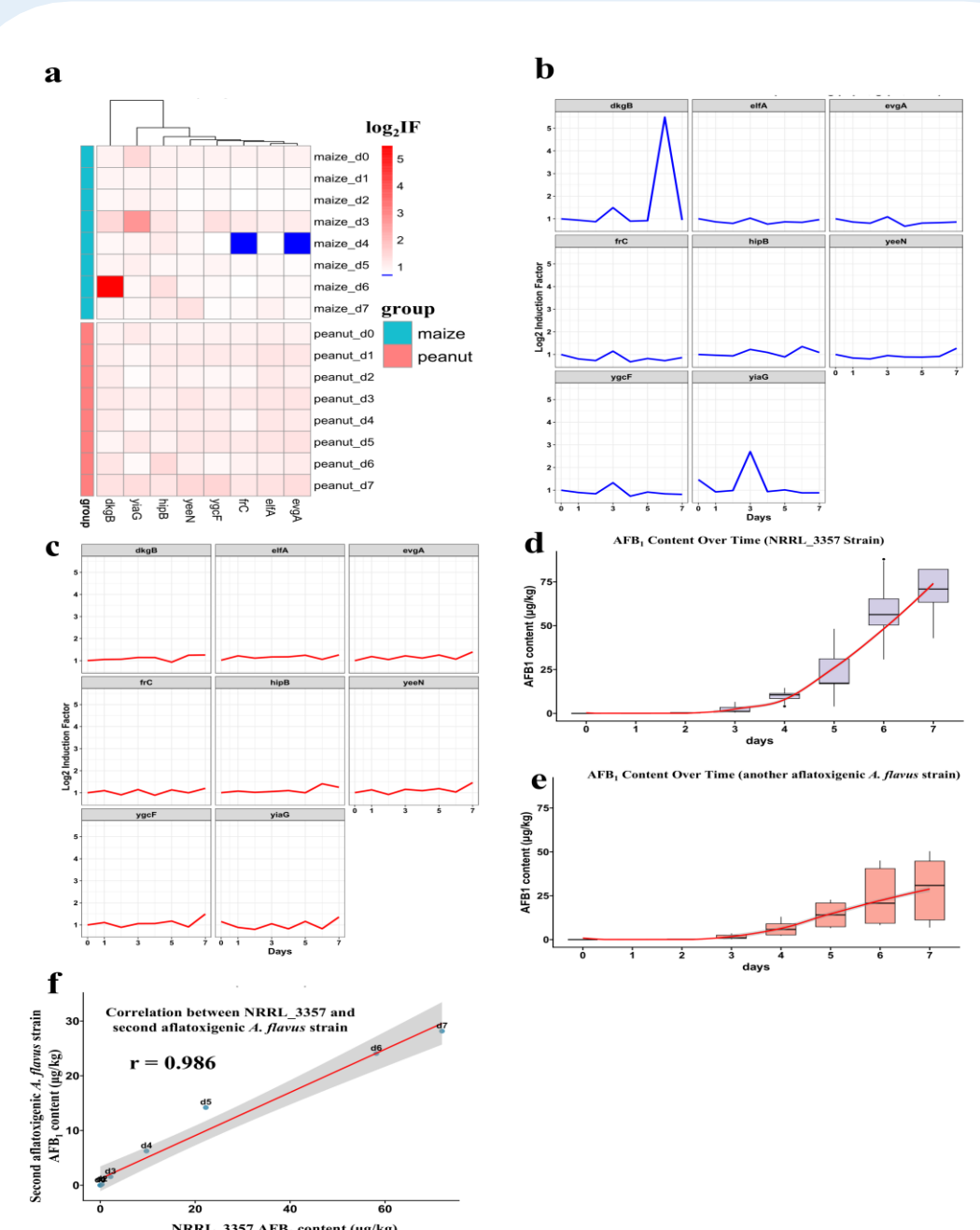


Fig. 3. Temporal dynamics and clustering of whole-cell bioreporter responses to *A. flavus*-induced VOCs in maize and peanut. (a) Hierarchical clustering.

V. Conclusion

This integrated biosensor-machine learning platform provides a robust, non-invasive approach for real-time monitoring of *A. flavus* contamination, offering significant potential for scalable food safety applications across diverse agroecosystems.

III. Methods

A transcriptome-guided whole-cell biosensor array was developed by integrating eight infection-induced promoters, identified from *E. coli* transcriptomic responses to volatile organic compounds (VOCs), into calcium alginate-immobilized bioreporters coupled with machine learning regression models, as summarized in Figure 1.

Time-resolved bioluminescence signals were used to train ensemble regressors, including XGBoost, CatBoost, and RandomForest, for quantitative prediction of infection stages and AFB₁ levels.

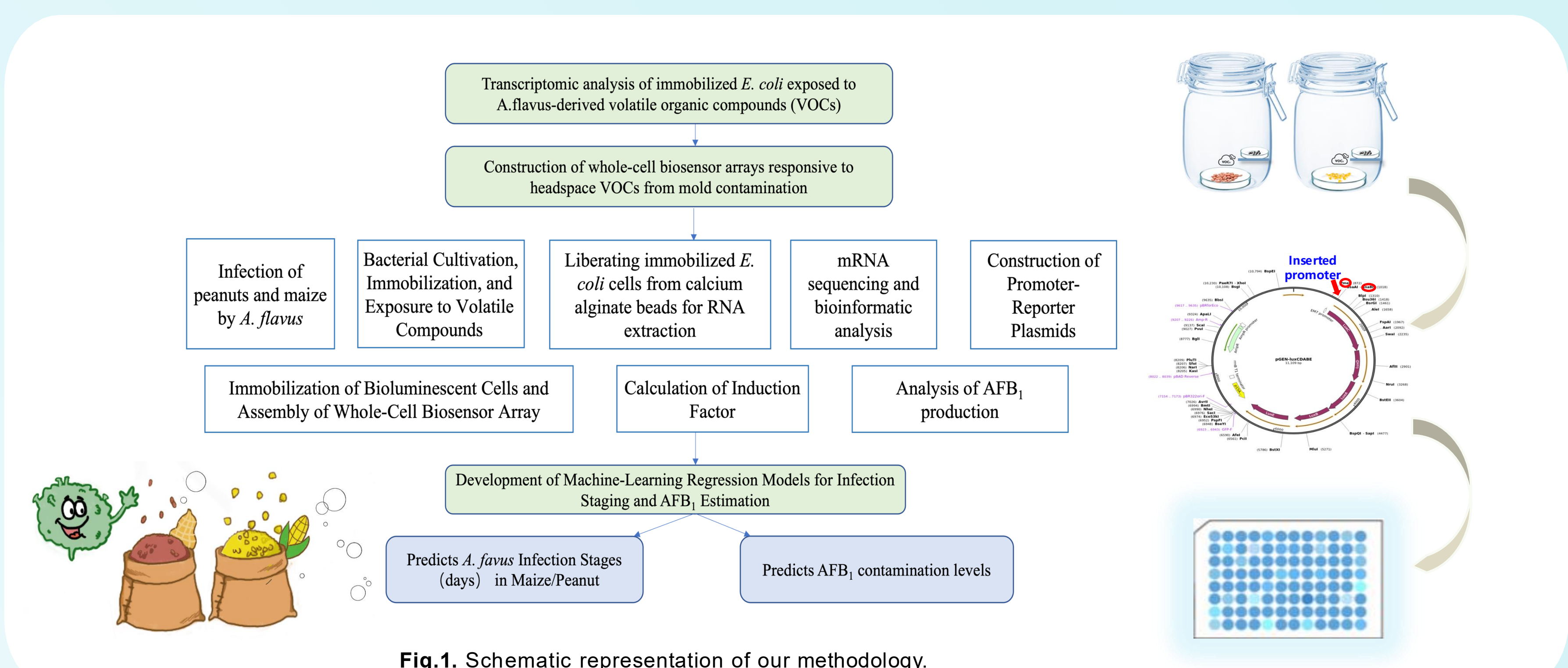
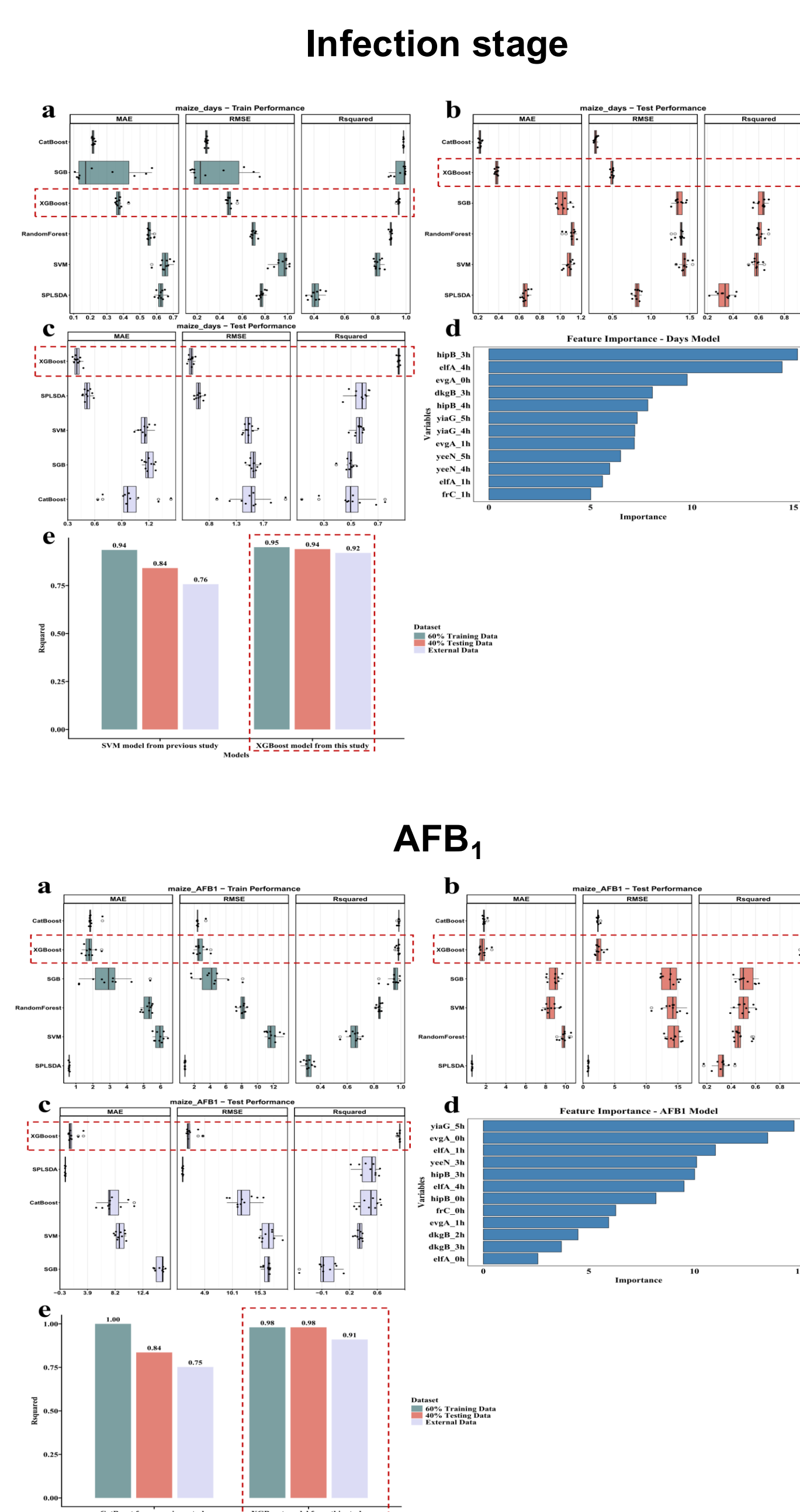


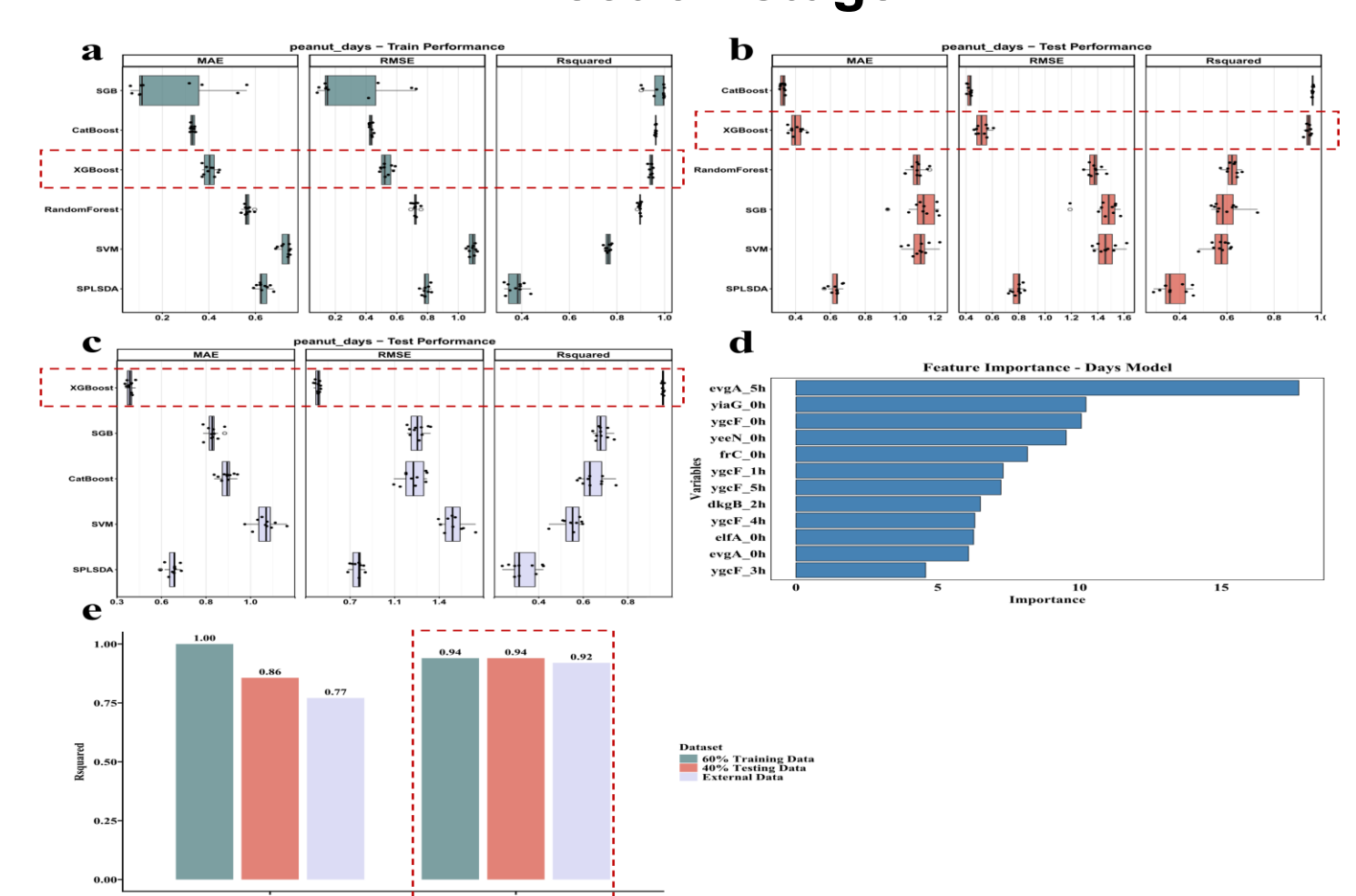
Fig.1. Schematic representation of our methodology.

For maize: XGBoost consistently achieved superior performance in internal validation, with R² values of 0.94 and 0.98 for maize infection staging and AFB₁ quantification, respectively.

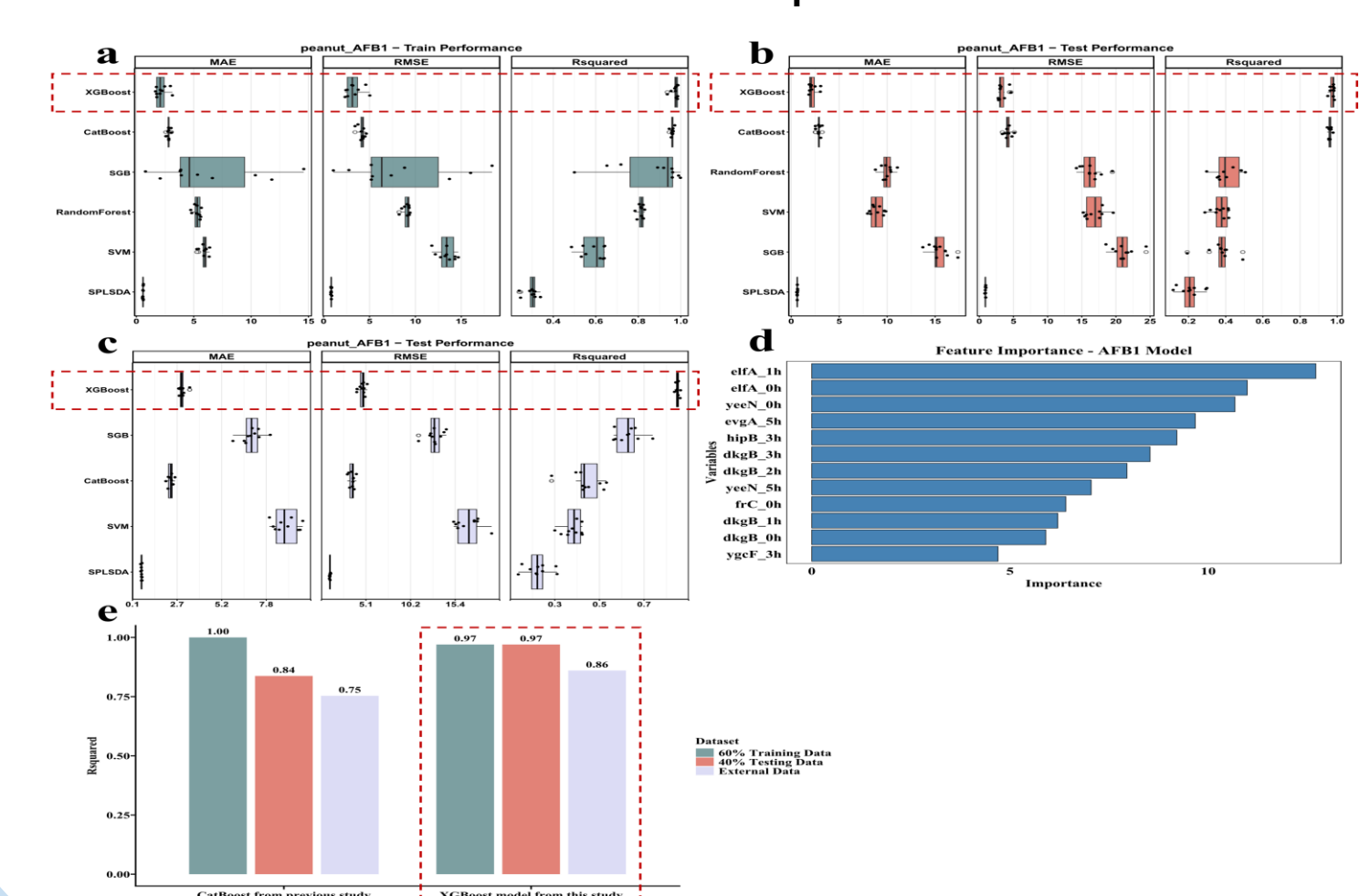


The model also maintained strong generalization in external validation using independent *A. flavus* isolates, achieving R² values of 0.92 and 0.91.

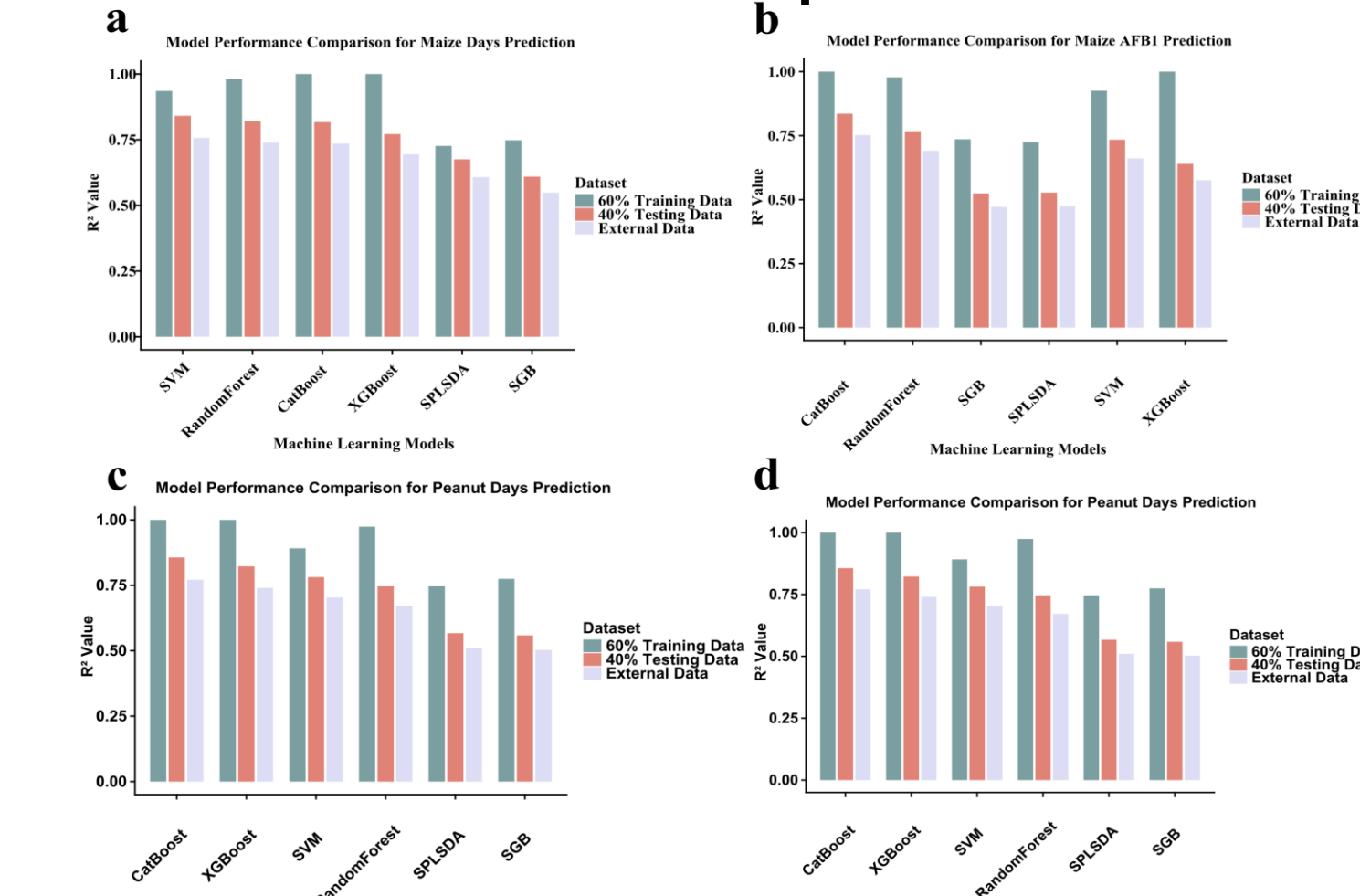
Infection stage



AFB₁



Model comparison



For peanuts: XGBoost achieved high accuracy in internal validation (R² = 0.94 and 0.97) and maintained robust performance in external validation (R² = 0.92 and 0.86).

Reference

Sun, L., Ma, J., Jiang, Y., Purcaro, G., Tian, Y., Wang, G., Li, W., Tai, B., & Xing, F. (2025). A novel approach for predicting aflatoxin B₁ production using regression models and whole-cell biosensors in moldy maize and peanut kernels. *Journal of hazardous materials*, 498, 139883. Advance online publication. <https://doi.org/10.1016/j.jhazmat.2025.139883>