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**NOVEL APPROACH TO MODELING FOOD CONSUMPTION OF PLODIA
INTERPUNCTELLA LARVAE: SHAP INSIGHTS**

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Abstract

The Plodia interpunctella (Indian meal moth, IMM) is one of economically most important pests of stored maize worldwide. Biotest was conducted using kernels of 37 Serbian maize genotypes as nutritional and rearing media (whole and crushed/ damaged) for IMM while amount of consumed kernel was recorded across two generations. The obtained empirical data were used for modeling with the aim of identifying the influence of two factors: genotype and kernel state (whole/crushed) on kernel consumption by IMM larvae. A regression-based approach was applied, as it is suitable for analyzing continuous output variables and allows interpretation of the contribution (influence) of individual properties. This approach is particularly important for evaluating the effects of genotypes, which was further enhanced by the application of SHAP (SHapley Additive exPlanations) analysis. The analysis of SHAP values indicated that both, maize genotype and kernel state had great influence on the quantity of consumed kernels by IMM larvae. In addition to ranking variable importance, SHAP analysis enabled the identification of specific genotypes that contribute most to increasing or decreasing the output variable-in this case, the amount of consumed kernels. Practically, the model allows the identification of genotypes that are more palatable to IMM larvae and therefore were more susceptible to IMM attack and at higher risk of facing greater storage losses when infestation occurs. Additionally, the model evaluated the impact of IMM bionomy parameters such as larval body length and fecundity on the output variable (food consumption), and results show that those parameters had a lower impact, as they represent consequences of developmental processes rather than causal factors driving increased feeding. This confirms that the selected model successfully captures the causal drivers of the observed outcome.

Keywords: *Plodia interpunctella, consumed food, SHAP modeling, maize genotype, kernel*

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