

Correlation and Regression Analysis of The Impact of Yellow Rust (*Puccinia Striiformis* F. Sp. *Tritici*) On Grain Quality Traits in Wheat Genotypes

Abbos Elmurodov

PhD student, Institute of Genetics and Plant Experimental Biology of the Academy Sciences of Uzbekistan

Oybek Kholliyev

Senior Researcher, Institute of Genetics and Plant Experimental Biology of the Academy Sciences of Uzbekistan

Dilafruz Qulmamatova

Head of laboratory, Institute of Genetics and Plant Experimental Biology of the Academy Sciences of Uzbekistan

Zafarjon Ziyaev

Senior Researcher, Institute of Plant Genetic Resources, Uzbekistan

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Abstract

In the present study, correlation and regression analyses were conducted to evaluate the impact of yellow rust disease on total gluten and protein content in widely cultivated wheat varieties of Uzbekistan and synthetic hexaploid wheat genotypes. The results demonstrated that the influence of yellow rust on grain quality traits was more pronounced in synthetic hexaploid lines compared to released cultivars. In released cultivars, yellow rust severity explained 38.25% of the variation in total gluten content and 16.34% of the variation in protein content. In synthetic hexaploid lines, yellow rust accounted for 20.18% of the variation in gluten content and 25.42% of the variation in protein content. However, the moderate coefficients of determination indicate that grain quality formation is governed by complex and multifactorial interactions beyond the effect of disease severity alone.

Keywords: Bread wheat, synthetic hexaploid wheat, yellow rust disease, correlation, regression, protein, gluten.

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1. Introduction

Yellow rust (*Puccinia striiformis* f. sp. *tritici*) is one of the most destructive fungal diseases of wheat,

significantly affecting the plant's photosynthetic activity, assimilate translocation, and grain filling process. The development of the disease not only leads to yield reduction but may also alter the main grain quality

components, particularly gluten and protein content. Therefore, the relationship between the level of resistance to yellow rust and grain quality traits—namely gluten and protein content—was evaluated using correlation and regression analyses of phenotypic traits. This approach provides a scientific basis for determining the degree of association among traits and enables a comprehensive assessment of disease resistance and grain quality traits.

From a physiological perspective, yellow rust infection damages the leaf blade, reducing photosynthetic activity and assimilate flow, which consequently suppresses protein synthesis during the grain filling period. At the same time, gluten composition includes high-molecular-weight glutenin proteins, the formation of which largely depends on nitrogen metabolism and photosynthetic assimilates. Therefore, an increase in disease severity may lead to a reduction in the percentage of gluten in the grain, which is of considerable importance for high-quality bread production.

Due to differences in genetic background and adaptability between released cultivars and synthetic wheat lines, the regression and correlation relationships between the severity of yellow rust infection and the levels of gluten and protein content may vary among these genotypes. Therefore, in the present study, the associations between yellow rust severity and grain quality traits were comparatively analyzed in released cultivars and synthetic wheat lines.

One of the primary objectives of the wheat breeding program in Uzbekistan is to enhance the adaptability of wheat genotypes to diverse soil and environmental conditions while improving grain quality. Achieving these goals would enable the country to attain wheat self-sufficiency and, in the long term, potentially become a wheat-exporting nation [1].

Yellow rust (*Puccinia striiformis* f. sp. *tritici*) causes a significant reduction in grain quality and substantial yield losses in bread wheat (*Triticum aestivum* L.) [2].

Wheat rust diseases are considered among the most serious diseases worldwide and pose a significant threat to global food security [3; 4].

This disease affects numerous physiological processes that are directly associated with wheat productivity. In particular, impairment of chloroplast function leads to a reduction in chlorophyll content in the leaves, resulting in a decreased green leaf area index and reduced

photosynthetic intensity [5; 6; 7].

Yellow rust disease reduces protein content in wheat grains, as the disease inhibits the activity of enzymes involved in protein synthesis, particularly nitrate reductase, and increases the activity of lytic enzymes in infected tissues during the grain development stage [8].

Regression analysis demonstrates a strong negative correlation between yellow rust severity and wheat grain quality parameters: as disease severity increases, grain yield, thousand-kernel weight, and nutritional composition decline significantly. Studies indicate that up to 62% of the variation in yield can be explained by yellow rust severity, with notable reductions observed in protein and gluten content [9].

2. Methods

The conduct of the study commenced in 2017–2019 at the Tashkent Region of Uzbekistan (41.2322° N and 69.2754° E). The experiments ran at the Dormon Experimental Site, Institute of Genetics and Plant Experimental Biology, Academy of Sciences of Uzbekistan, Tashkent Region, Uzbekistan.

The obtained from International Winter Wheat Improvement Program 24 synthetic wheat lines, as well as released varieties were used.

The total protein and gluten contents of wheat grain samples were determined according to the manufacturer's instructions using a Zeutec Spectra Analyzer (Zeutec Opto-Elektronik GmbH, Germany) based on near-infrared spectroscopy (NIRS).

In wheat genotypes, the disease severity scoring ran two to three times in each experiment using the modified Cobb's scale Peterson et al. [10], with the host response to infection determined according to Roelfs et al. [11].

Regression analysis was performed using Statgraphics 18, and correlation coefficients were calculated in Excel 2016.

3. Results and Discussion

Regression analysis conducted on the released cultivars revealed a statistically significant negative relationship between the severity of yellow rust infection (*Puccinia striiformis* f. sp. *tritici*) and gluten content in wheat grain ($P = 0.01$). The regression coefficient was -0.04 , indicating that a 1% increase in disease severity resulted in an average decrease of 0.04% in gluten content.

As a result, Yellow rust infection significantly affected gluten content; however, the relatively moderate coefficient of determination ($R^2 = 0.3825$) indicates that disease severity alone does not fully explain variations in grain quality. Since gluten accumulation depends on nitrogen remobilization and protein synthesis during grain filling, the partial reductions observed under infection may be attributed to altered assimilate partitioning rather than a complete disruption of protein formation.

Furthermore, the ANOVA results ($P = 0.0107$) confirmed the overall significance of the regression model, while the Durbin–Watson statistic ($DW = 2.31$; $P > 0.05$) indicated the absence of autocorrelation in the residuals, suggesting that the model predictions are reliable (Figure 1).

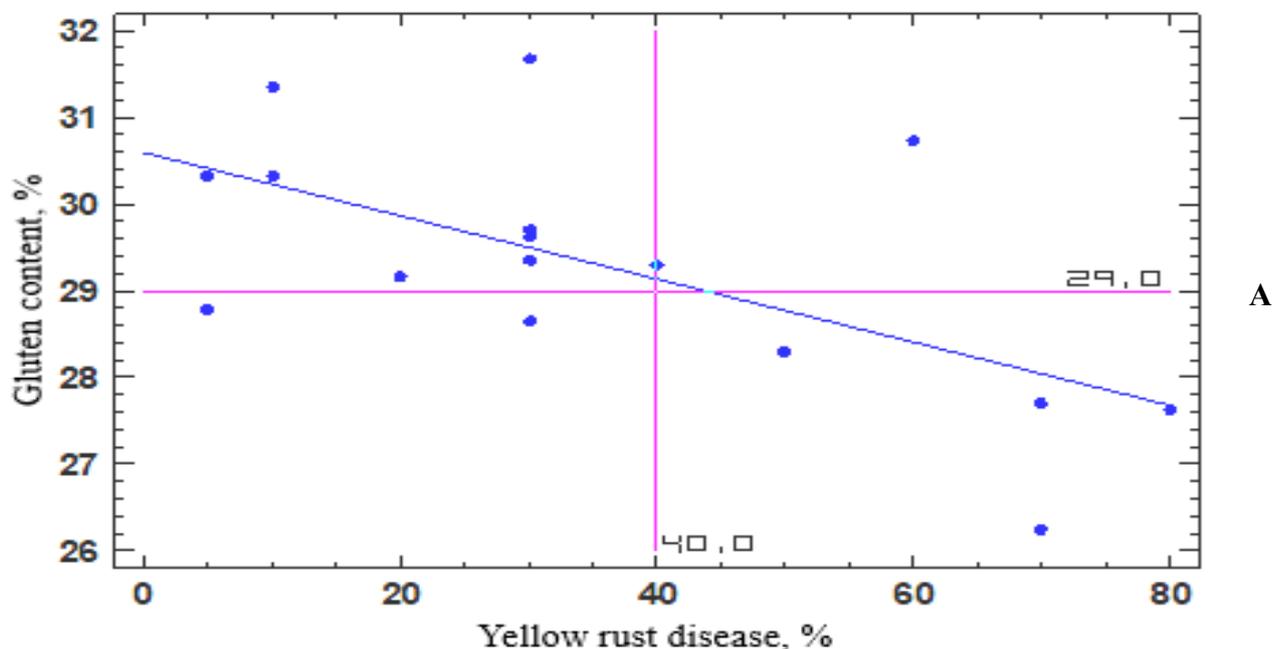
However, the relatively low R^2 value implies that multiple factors contribute to grain quality formation, highlighting the multifactorial nature of this trait.

The linear regression analysis conducted in the released cultivars evaluated the relationship between grain protein

content and yellow rust severity. The regression coefficient was negative (-0.03), indicating that a 1% increase in yellow rust infection severity resulted in an average decrease of 0.03% in grain protein content.

However, the model was not statistically significant ($P = 0.1204 > 0.05$). According to the ANOVA results, the overall model was also not significant ($F = 2.74$; $P = 0.1204$). Although a moderate negative correlation was observed between yellow rust severity and grain protein content ($r = -0.40$), this relationship was not confirmed at the 95% confidence level.

The coefficient of determination (R^2) was 16.34%, indicating that yellow rust severity explained 16.34% of the variation in grain protein content. The adjusted R^2 value (10.37%) further suggests a low explanatory power of the model. These results indicate that protein accumulation is a multifactorial trait. Grain protein content is strongly influenced by the genotype’s genetic background, nitrogen availability, agroclimatic conditions, and other agronomic factors.



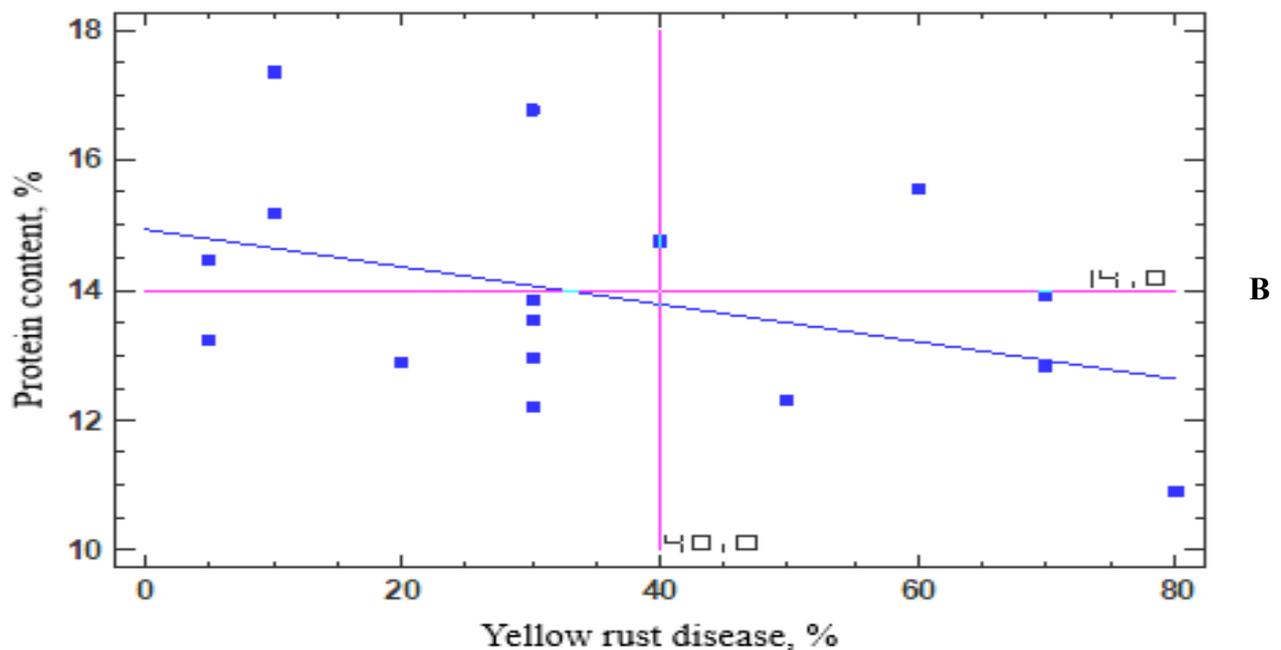


Figure 1. Regression relationships between yellow rust severity and grain quality traits in released cultivars: (A) gluten content and (B) protein content.

According to the Durbin–Watson test results ($DW = 1.89$; $P = 0.4205$), no statistically significant autocorrelation was detected among the regression residuals. The DW value being close to 2 indicates that the residuals are independent. This confirms that the regression model is statistically well specified. However, the P-value of the independent variable—yellow rust severity—was 0.1204. Since this value exceeds the conventional significance threshold, yellow rust severity was not statistically confirmed as a significant predictor of the dependent variable.

The multiple regression analysis conducted in synthetic wheat lines revealed a statistically significant negative relationship between yellow rust severity and grain gluten content (regression coefficient = -0.03 ; $P = 0.0165$). These results indicate that a 1% increase in yellow rust severity leads to an average decrease of 0.03% in gluten content.

The results demonstrated a moderate negative correlation between yellow rust severity and gluten content in synthetic lines ($r = -0.45$). In this context, plants

exhibiting higher levels of disease infection tended to show reduced gluten content. However, the coefficient of determination ($R^2 = 20.18\%$) indicates that approximately 20% of the variation in gluten content can be explained by yellow rust severity, while the remaining 80% is associated with genetic factors, agroecological conditions, and other agrobiological influences.

According to the Durbin–Watson test results ($DW = 2.447$; $P > 0.05$), no statistically significant serial correlation was detected among the regression residuals (Figure 2).

This indicates that one of the key classical assumptions of regression analysis—the independence of residuals—was satisfied, thereby confirming that the regression coefficients and their levels of significance were reliably estimated.

In synthetic hexaploid wheat lines, a statistically significant negative correlation was identified between yellow rust severity and total grain protein content ($r = -0.50$). The P-value ($0.0062 < 0.05$) confirms a significant negative effect at the 95% confidence level.

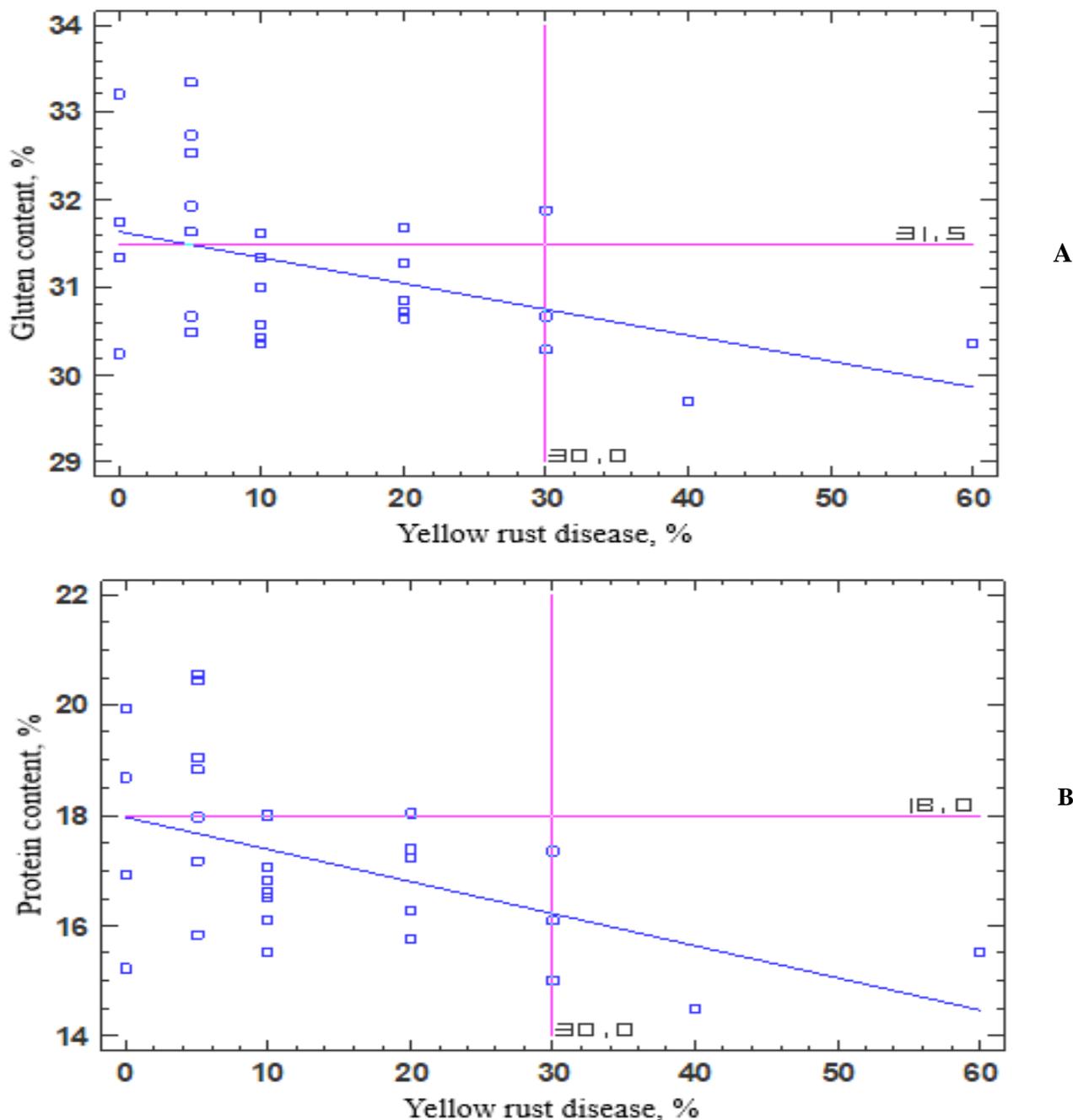


Figure 2. Regression analysis of the effect of yellow rust disease on grain quality in synthetic wheat lines: (A) gluten content; (B) protein content.

The regression coefficient was -0.06 , indicating that an increase in yellow rust severity was associated with an average decrease of 0.06% in total grain protein content. The model's coefficient of determination ($R^2 = 25.42\%$) suggests that approximately 25% of the variation in protein content can be explained by yellow rust severity, while the remaining proportion is attributable to genetic factors, agroecological conditions, nutrient availability,

and other agrobiological influences.

The Durbin-Watson statistic ($DW = 2.397$; $P > 0.05$) indicated the absence of serial correlation in the residuals.

These findings indicate that although synthetic lines represent valuable sources of genetic diversity and disease resistance genes, their grain quality stability

under biotic stress may require further selection and stabilization. The stronger disease–quality interaction observed in synthetic germplasm highlights the importance of integrating both resistance and nitrogen use efficiency traits in breeding programs. Similar genotype-dependent responses to foliar fungal diseases have been reported by [12], emphasizing that grain quality responses are not solely determined by disease severity but also by the genetic background and physiological resilience of the genotype.

Although considerable research has addressed the effects of abiotic factors, particularly nitrogen nutrition, on wheat processing and end-use quality [13; 14], comparatively less attention has been given to the influence of biotic stresses such as stripe rust and their interaction with nitrogen dynamics. The present findings contribute to this area by demonstrating that disease severity explains only a moderate proportion of gluten variation, highlighting the complex interaction between pathogen pressure, nitrogen remobilization, and genotypic background.

4. Conclusion

Regression and correlation analyses demonstrated that yellow rust infection negatively affects grain quality traits in wheat genotypes. The impact on gluten and protein content was more pronounced in synthetic hexaploid wheat lines than in released cultivars, indicating greater physiological sensitivity of synthetic germplasm to pathogen pressure.

However, the moderate coefficients of determination confirm that grain quality formation is a complex and multifactorial process influenced not only by disease severity but also by genetic background, nitrogen dynamics, and agroecological conditions. Therefore, wheat breeding programs should integrate the evaluation of grain quality traits with resistance to yellow rust to ensure both productivity and end-use quality under biotic stress conditions.

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