Evaluation of kernel health in selected winter wheat cultivars grown in different regions of Poland with the use of conventional and molecular methods

Winter wheat is one of the most important and most widely grown crops in the world. Fungal diseases of cereals and, in particular, the occurrence of mycotoxin-producing fungi, affect crop yields and quality under changing climatic conditions. The aim of this study was to evaluate grain health in four winter wheat cultivars from different regions of Poland under various levels of agricultural inputs, and to determine deoxynivalenol (DON) concentrations in grain. The experiment was carried out using a conventional culture method and the qPCR technique with specific primers for *F. culmorum, F. graminearum, F. avenaceum*/*F. tricinctum, F. poae,* trichothecene-producing *Fusarium* spp. (*TRI5*), and *P. verrucosum.* Deoxynivalenol concentrations were determined by high-performance liquid chromatography (HPLC) with the use of a UV-Vis detector. The following saprotrophic fungi: *Alternaria alternata*, *Epicoccum purpurascens* and *Cladosporium cladosporioides,* and toxin-producing fungi of the genera *Fusarium* and *Penicillium* were identified by the culture method in the grain of the analyzed winter wheat cultivars. *Fusarium avenaceum* and *F. poae* predominated in the group of fungi potentially capable of producing toxins, whereas *F. culmorum*, *F. graminearum* and *P. verrucosum* were encountered sporadically. The analyzed winter wheat cultivars different in the levels of grain colonization by pathogens, which were most prevalent in the grain of cv. KWS Ozon (165 isolates) and least prevalent in the grain of cv. RGT Kilimanjaro (84 isolates). The highest number of pathogen isolates were obtained from grain samples collected in Ruska Wieś (135 isolates), and the lowest number of isolates were obtained from grain samples collected in Pawłowice (29 isolates) and Tomaszów Bolesławiecki (26 isolates). A mycological analysis of grain demonstrated that chemical control (A2) led to an 18% reduction in the incidence of pathogenic fungal species in the grain of the analyzed winter wheat cultivars. The qPCR technique revealed that the evaluated grain was most severely contaminated with *F. avenaceum,* followed by *F. poae, P. verrucosum* and *F. graminearum,* and least severely – by *F. culmorum.* A statistical analysis revealed correlations between the amount of DNA of *F. avenaceum* and *F. poae,* determined by qPCR, and the number of fungal cultures isolated from wheat grain (R=0.58 and R=0.77, respectively), as well as between the abundance of DNA of *F. culmorum* and *F. graminearum,* and the DNA of trichothecene-producing fungi (R=0.49 and R=0.91, respectively). The qPCR technique confirmed that the grain of cv. Artist was most contaminated by toxin-producing fungi, whereas the lowest amount of DNA was determined in the grain of cv. RGT Kilimanjaro. The qPCR analysis demonstrated

that the high-input technology (A2) reduced the amount of DNA of toxin-producing fungi by 11.44% relative to technology A1. The highest and lowest levels of fungal DNA were detected in wheat grain from Ruska Wieś and Bezek, respectively. The concentrations of DON in wheat grain were also determined in this study. The analyzed winter wheat cultivars differed significantly in the DON content of grain. The average DON content of grain reached 98 µg/kg in cv. Artist, and 57.6 µg/kg in cv. RGT Kilimanjaro. It was also found that DON concentrations varied depending on the origin of grain samples. The highest average DON content of grain was noted in Sulejów [162 µg/kg], and the lowest – in Kościelna Wieś [25.4 µg/kg]. Positive correlations were observed between the abundance of DNA of *F. culmorum, F. graminearum* and trichothecene-producing fungi and the concentrations of DON in grain samples (R=0.56, R=0.92 and R=0.94, respectively), whereas a negative correlation was noted between the levels of DNA of trichothecene-producing fungi and the presence of DNA of the *F. avenaceum/F. tricinctum* genotype in grain (R=-0.33). A statistical analysis confirmed that weather conditions affected the amount of DNA of fungi causing Fusarium head blight (FHB) in wheat grain. A positive correlation was found between the abundance of DNA of the *F. avenaceum/F. tricinctum* genotype and mean daily temperatures in the first ten days of May (R=0.54). Spike colonization by *F. avenaceum/F. tricinctum* and *F. poae* was influenced by precipitation levels in the first ten days of July (R=0.58 and R=0.64, respectively).