A Molecular Approach for Screening of Toxigenic Fusarium graminearum in Feedstuff

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SUMMARY

Fusarium contamination is a major agricultural problem as quality and yield can be reduced, but more importantly many species in the genus produce mycotoxins responsible for serious diseases in humans and farm animals. The most common mycotoxin in cereals is deoxynivalenol (DON) produced by certain isolates of Fusarium sp. being prevalent worldwide in crops used for food and feed production. Identification of Fusarium species is critical to predict the potential mycotoxicogenic risk of the cereals, therefore the development of an accurate and complementary method, which permits a rapid, sensitive and reliable specific diagnosis of Fusarium species, is necessary. The DON chemotypes are expected to produce amplicons in Tri13DON and Tri7DON genes (Lee et al., 2001). DNA based approaches applied in this study have been already reported as rapid, sensitive and specific alternatives to identify the main trichothecene-producing Fusarium species. The biological material consisted of eight samples of commercial feeds, containing soybean, maize and sunflower. Mill grinded sample of 100 mg were used in the DNA extraction. The DNA was extracted using CTAB method (Querci et al., 2004). For PCR amplification, three sets of specific primers described by Sampietro et al. (2010), were used. Amplification was performed with the cycling conditions proposed by Sampietro et al (2010). Seven of the samples were found to be positives for F. graminearum and the TRI 7 and TRI13 biosynthetetic genes were detected in the same samples. Since the results were confirmed by ELISA tests we appreciate that the proposed method is suitable to be used as a screening test preceding quantification of mycotoxins levels in feedstuff matrices.

REFERENCES