doi 10.18699/PlantGen-2025-257

The selection of target genes for detection of plant impurities in feeds

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During the analysis of domestic and foreign literature, fragments of constitutive genes and Lime elements were selected for the detection of plant impurities in feed. Constitutive genes are expressing almost all tissues and cells at a relatively constant level. Diversity in expression of any reference genes is not constant and in different experimental environments can vary greatly, so the choice of genes is a necessary stage of the experiment, the use of reference genes widely used in modern research requires a prior assessment of gene stability. In the laboratory of Eurofins Genomic Europe, the actin gene is using for plant identification. A significant disadvantage of its use is the short conservative region of this gene, which leads to the selection of degenerate primers or the use of another gene for internal control. The plant ingredients of greatest interest are soy, corn, and rice due to the frequent occurrence of genetically modified events. In European techniques, the target genes for soybean are *lec* (lectin), *ADH* (alcohol dehydrogenase), *Sus4* (sucrose synthase 4), and *APX2* (ascorbate peroxidase 2) genes, for maize – *ADH1* (alcohol dehydrogenase), *hmga* (high-mobility protein group), *ivr1* (invertase1), *zein* (zein) genes, for canola – *BnACCg8* (acetyl-CoA carboxylase), *PEP* (phosphoenolpyruvate carboxykinase), *FatA* (gene encoding an enzyme involved in fatty acid biosynthesis), *HMG-I/Y* (high-mobility group of proteins I/Y), *CruA* (cruciferin A) genes. In GMO testing the techniques of «The Russian State Center for Animal Feed and Drug Standardization and Quality» use *lec* (lectin), *ADH1* (alcohol dehydrogenase) and *hmga* (highly mobile protein group), *CruA* (cruciferin A) genes for the detection of soybean, corn and rapeseed, respectively. Another gene that can be used as an internal control is the PCNA (proliferating cell nuclear antigen) gene. This protein is found in all plant cells and is highly conserved. The third possible version is the use of Lime elements (long identical multispecies elements). There are elements that in the process of evolution moved from the plastid genome (chloroplasts, mitochondria) to the nuclear genome. In plastids they acquired polymorphisms, while in the nucleus they are ultraconservative. Accordingly, when they are used as internal controls, there should be no cross amplification with mitochondrial DNA sequences. Thus, in the future, these elements can be used in our work.