IDENTIFICATION OF PLANT RAW MATERIALS IN FEEDSTUFF BY QUALITATIVE PCR

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A simple and not expensive PCR-based method was developed to identify the species included in plant raw material used as feed mixture. Four species-specific genes have been selected to develop as many STS (Sequence tagged sites) markers to identify four target species: Lectin A gene (faba bean), Convicilin A gene (field pea), UDP-glucosyltransferase gene (grain sorghum) and Hordeindoline-a gene (barley). Identification of durum and common wheat (lipid transfer protein gene), soybean (Gly m Bd 30K allergen gene) and maize (invertase gene) was carried out using markers available from the literature. A large number of faba bean (19), field pea (27), barley (24), durum wheat (30), common wheat (25), grain sorghum (26), soybean (24) and maize (2) varieties were analyzed to improve accuracy. Cross-reactivity of the primer pairs was also tested against species that are not usually included in feed mixture, as oat, rye, kidney bean and lentil.

This method was applied for the analysis of flour mixtures. Eight flour samples, one for each species, were used to prepare eight serial dilution of flour mixtures. Within each series, each target species flour was included at different concentrations (0, 0.9, 5, 10 and 100%) while non target species were included at equal amount. The presence of the species included was confirmed by the STS markers as a clear amplification product. The seven STS markers amplified in all mixtures but 0%, where target species was absent.

The efficiency of the method was also verified with an extruded sample mix of soybean, faba bean and field pea where technological treatments could damage DNA integrity. DNA analysis confirmed the presence of the three species included and evidenced a slight maize contamination.

This research, funded by the Marche Region (LR37/99), could be a strategy applicable to traceability and certification of animal feeding systems based on locally produced forages and feeds, within high quality animal production chains, closely linked to production area.