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Poster Abstract - H.03

DEFINITION OF AN ANALYTICAL METHOD TO QUANTIFY GM SOYBEAN CONTAMINATION IN FEED

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Italian livestock system can not provide a convenient soybean supply to satisfy internal animal feed need. Thus, over the 95% of the soybean employed in the formulation of complementary and concentrated feed in Italy is imported from countries where GMO cultivation is allowed. As a consequence, soybean is often present as accidental contamination in feed, and often, such component results genetically modified. At the present, however, no analytical solution for quantifying soybean contamination entity is published. In the aim of giving our contribution to solve this problem, we developed an analytical method based on Real Time PCR. Firstly, in the view of settling up the method, we exploited a single component feed. Corn meal was chosen, being the major energy source in feed. As calibrator for the standard curves, we constructed four pGEM-t plasmids (Promega), each one containing a single copy of soybean (*lectin*) and corn (alcohol dehydrogenase *Adh1*, high mobility group protein *hmga*, invertase 1 *inv*1 and *zein*, respectively) endogenous genes. The Real-time quantification experiments were carried out on samples prepared by mixing together defined amounts of corn meal with soybean RR powder certified material (Fluka). In this strategy, the percentage of soybean contamination can be calculated from the ratio between the copy numbers of the soybean and corn endogenous genes, on the basis of the relative haploid genome sizes. Besides, the quantification of the transgenic component percentage on the total sample can be estimated. For each plasmid, method accuracy and precision were evaluated. Further assays are in progress where feed samples at more complex composition are analysed.

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