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Does the Inclusion of Second Generation Genetically Modified Plants in Feeds have any effect on Animal Performance?

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ABSTRACT

The need for studies on the nutritional value of plants depends on their composition. The first generation genetically modified Plants (GMPs) have the same composition as their near-isogenic lines. Therefore, they have the same nutritional value, and most of the animal feeding studies have found no significant differences in the production and health parameters of animals that consumed first-generation GMPs in comparison to non-GMPs. Due to the recent production of transgenic plants with specific nutritional properties (second generation GMPs), their use as feed for animals is viewed with skepticism in very many countries. In this critical review, it is concluded that most of these nutritionally improved plants have not shown adverse effects on the performance of various animals compared to their near-isogenic lines and can therefore be considered in the animal feed industry. However, most of the experiments were conducted on laboratory animals. There is a need to conduct them with animals that are mainly consumed by humans, such as ruminants. There is also a need to feed the whole plant to these animals and not just certain parts of the plant to get a clear picture of its overall safety. In addition, there is a need to determine a suitable long-term nutritional and toxicological approach assessment.

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Introduction

The use of Genetically Modified Organisms (GMOs) in food and feed is not new. As far as 10,000 years ago, there has been a continuous effort of improving plants, microbes and animals. From food fermentation which is known as the earliest old/ancient biotechnology, to the selection of plants or animals, to improve performance and obtain adaptable genotypes with instinctive breeding (Vispo, 2018). After the discovery of the function and structure of DNA in the mid-20th century by altering DNA organisms, this led to a new biological revolution of the old biotechnology. These studies paved the way for a new wave in biotechnology (production of recombinant DNA) where genes can be manipulated and inserted from bacteria into plant and animal cells. This development of recombinant DNA production led to genetic engineering/cloning and thus the latest technology of creating GMOs and new transgenic cells (Daubenmire, 2019). Since the initial commercial planting of transgenic plants in 1996, agricultural biotechnology has spread rapidly around the world (Sissener et al., 2011).

"GMOs are organisms (plants, animals, or microorganisms) in which the genetic material (DNA) has been altered in a way that does not occur naturally through mating and/or natural recombination", according to the definition of the World Health Organisation (WHO). In most cases, this involves introducing a new genetic trait into the plant that does not occur naturally, such as pest and disease resistance, tolerance to harsh environmental conditions, reduction of spoilage, tolerance to chemical treatments, or increasing the nutrient composition of the plant. In the case of non-food crops such as microbes, applications of GMOs include the manufacturing of biofuels, pharmaceutical ingredients, and other industrially important products (James, 2013).

Countries have invested heavily in crop biotechnology to increase agricultural productivity and meet food and feed needs (Li et al., 2020). In 2018, with 23 years of Genetically Modified (GM) crop commercialization, twenty-six (26) countries had cultivated 191.7 million hectares of GM crops an increase of 1.9 million hectares (4.7 million acres), or 1% from 189.8 million hectares in

2017 (ISAAA, 2018). In 2018, according to ISAAA, the US grew 75 million hectares of biotech crops, then Brazil (51.3 million hectares), Argentina (23.9 million hectares), Canada (grew 12.7 million hectares), and lastly India (grew 11.6 million hectares) for a total of 174.5 million hectares, representing 91% of the global area. Three (3) developing countries (Brazil, India, Argentina) and two (2) industrial countries (USA and Canada) grew 91.3% of the biotech crops in 2018 (ISAAA, 2018).

Maize, soybean, canola, and cotton were the most embraced GM crops by 26 countries. Soybeans were grown on 95.9 million hectares and accounted for 50% of global GM crop adoption, which showed an increase of 2% from 2017. This was followed by corn at 58.9 million hectares, cotton (24.9 million hectares) and then canola at 10.1 million hectares. USA has the most number of approved events 544 approvals, with maize having the largest number of approved events 137 approved events in 35 countries. Herbicide-tolerant maize event NK603 has the most approvals, 61 approvals in 28 countries (ISAAA, 2018).

Many different studies have been published that assess GM food, compared to the GM feedstuff, although most GM plants and their biomass between 70 to 90% are used in animal feed (Giraldo et al., 2019). As for the few studies on GM feeds, most of the studies were conducted on first GMPs, many of which were shown to not affect animal performance and nutritional value. This paper is looking at feeding studies on second generation genetically modified plants when they are applied in animal nutrition.

1st, 2nd and 3rd Generation Genetically Modified Plants

The first generation of genetically modified crops generally includes those plants that have simple input traits such as increased resistance to pests or tolerance to herbicides and increased economic benefits to farmers through higher yields and cost efficiency (Bawa & Anilakumar, 2013). They usually consist of traits that are exclusively relevant to agricultural use (Kamle et al., 2017).

Recently, advances in the understanding of plant metabolic pathways and biosynthesis, consumer needs, and industrial demands have led to the evolution of second generation GMPs (2nd GMPs). In these, the nutrient profile or availability has been intentionally altered (de Santis et al., 2018). As a result, effects on the nutritional value of the feed are expected to increase or alter or decrease undesirable (anti-nutritional) substances (González et al., 2020). The embedded quality traits are intended to provide nutritional benefits for food, feed, and industrial applications (Kamle et al., 2017). Their commercial presence and production is still minor though increasing pipeline of GMPs. These traits include, but are not limited to, modified oil composition for an increased amount of omega-3 fatty acids, increased levels of basic micronutrients such as vitamins and amino acids, increased levels of nutrient precursors such as β-carotene, increased levels of a nutrient enhancer such as enzymes (e.g. phytase), the concentration of an anti-nutritional factor, e.g., phytate, glycosides, glucan, lignin or (g) the content of toxic substances, e.g. mycotoxins have been decreased (Parisi, et al, 2016; de Santis et al., 2018).

The third-generation GMPs (3rd GMPs), undergone minimal recombination or modification as they carry a transgene construct that has never been used in other known GM plants. They have been successfully commercialized for the manufacturing of industrial products, such as vaccines, monoclonal antibodies, biofuel and plastics (Kamle et al., 2017).

Common Genetically Modified Crops Used In Animal Feeds And Their Traits

On a larger scale, herbicide tolerance (Ht) and insect resistance (Bt) are the most widely used genetically modified traits in GM crops. GM soybean, maize, canola, and cotton are the most common examples of these crops on the market for use in animal feed (Kamle et al., 2017), and their safety has been evaluated/revised over the past 9-10 years (Domingo, 2016). Others that have been also genetically modified and are of importance to animal feed industry are sunflower, sweet potatoes, sugar beet, and cassava (Table 1). Although some of them are not yet approved because their licenses to grow or market them in various markets have expired or have been withdrawn, but various trials have been conducted on animals.

Composition of The First and Second Generation Genetically Modified Plants

The nutrient profile of feedstuffs is a prerequisite for the evaluation of its feeding and nutritional value. The nutritional value based on protein, carbohydrate, fats, fiber, vitamins, ash, and mineral content is used in the digestibility estimation for the different farm animals. First generation GM crops are considered substantially equivalent to conventional non-GM lines since the DNA insertion that leads to the synthesis of a gene product in these plants does not interfere or affect the overall metabolism of the plant cell (de Santis et al., 2018).

Several researchers have pointed out that the nutritional composition of the transgenic plants studied so far does not differ significantly in their nutritional and physiological composition from the near-isogenic original lines (Brouk et al., 2011; Warf, 2014; Naegeli et al., 2020). However, some variations in the chemical composition can be observed due to factors of climatic conditions, the season of the year, the age of the plant, fertilization, or soil conditions in addition to processing methods (Aumaitre, 2004). In second generation plants GM we expect differences in chemical composition as the plants are modified to increase performance traits such as nutritional traits or reduce antinutritional traits and they vary depending on the desired trait.

Feeding Studies with The Second Generation Genetically Modified Plants

The studies reviewed such as (Snell et al., 2012; Tufarelli et al., 2015; Domingo, 2016; de Santis et al., 2018**;** Blair and Regenstein, 2020)**,** show no significant differences in production and health parameters of animals that consumed first-generation crops in comparison to their conventional/non-GM crops.

Table 1. Showing the most common GM crops used in animal feeds and their traits

Genetic material introduced	Characteristic	Plant
Insect resistance		
	Resistance to attack by	
cry1A(b) and cry1A	Lepidoptera	Maize, cotton
cry9C	Lepidoptera	Maize
cry3A	Coleoptera	Potato
Virus resistance		
Gene encoding a viral coat protein	Resistance to attack by potato virus Y	Potato
Herbicide tolerance		
epsps (bacterial or engineered plant gene)	Tolerance to glyphosate	Sugar beet, soybean, cotton, rape, maize
pat encoding PPT acetyltransferase	Tolerance to glufosinate-ammonium	Maize, soybean, sugar beet, rape
oxy encoding nitrilase	Tolerance to oxynil herbicides	Cotton, rape
Modified *als* genes encoding acetolactose synthase	Tolerance to imidazolines	Maize, rape
Modified composition		
Fragments of endogenous FAD2-1A and FATB1-A genes	Oleic acid increase and reduce linoleic acid.	Soya bean
Pj.D6D gene	Conversion of linoleic acid to α-linolenic acid	Soya bean
Nc.Fad3	Conversion of α-linolenic acid to stearidonic acid	Soya bean
mRNA stability by intron switching Dzr1 target	Methionine increase	Maize
Maize 15kDa-zein	Sulphur amino acids increase	Maize
Resveratrol glucoside	+Resveratrol	Alfafa
Downregulation CoA 3-O-methyltransferase	Lignin decrease	Alfafa, ryegrass
Downregulation of caffeic acid 3-O-methyltransferase	Lignin decrease	Alfafa, ryegrass
fad2-1 gene	Modification of the lipid profile	Soya bean
Dihydrodipicolinate synthase	Lysine	Maize

(Aumaitre et al., 2002); (EFSA, 2008); (Snell et al., 2012); (de Santis et al., 2018), *http://ec.europa.eu/food/dyna/gm_register/index_en.cfm*, International Service for the Acquisition of Agri-biotech Applications(ISAAA) *https://www.isaaa.org/default.asp*

Studies show that GM plants (first generation crops) are nutritionally equivalent to their non-GM isogenic lines and therefore could be safely used in food and feedstuff. They show no biologically significant effects on feed intake and digestibility, or animal well-being (health), and furthermore, there are no unintended effects on animal production and fertility. In addition, they concluded that animal products such as milk, meat, and eggs produced by animals that consumed feeds containing approved first-generation ingredients are as healthy, nutritious, and safe as foods produced by animals that consumed feeds containing conventional feed ingredients. However, the issue comes in feeding animals with the second generation GM plants that are nutritionally altered therefore the following paragraphs are looking at different feeding studies that have involved the use of these plants in animal feeding.

Genetically Modified Plants with Improved Proteins

Proteins are large complex molecules comprising one or more long chains of amino acids. The essential amino acids, tryptophan, lysine, threonine, and methionine have received the most attention because they are the most limiting in cereals (particularly lysine and tryptophan) and legumes crops (particularly methionine), which are the major sources of animal feed worldwide (Sivaji et al., 2020). Extensive efforts have been made through conventional breeding methods and mutagenesis to enrich crops with these essential amino acids. However, there has been limited success, apart from some results obtained with maize (Galili and Amir, 2013). Therefore, additional efforts using genetic engineering approaches have focused on reducing the regulation of the synthesis pathways of some essential amino acids through negative feedback and reducing the catabolism of these targeted essential amino acids (Galili and Amir, 2013; Wang et al., 2017).

Tryptophan (Trp) Enhanced GMPs, Feeding Trials with Fish and Poultry.

A feeding trial was conducted with the rainbow trout (*Oncorhynchus mykiss*) fish. The objective was to evaluate the transgenic Trp soybean as a source of tryptophan for the fish culture. The diet of the GM seeds consisted of about twice as much total Trp as compared to that of the control seeds. The bodyweight of fish fed with transgenic seed meal was greater than that of those fed with the control seed trp unsupplemented diet (Ishimoto et al., 2010). When twenty-one (21) Boris Brown male birds were used in an experiment for three weeks. Bodyweight and feed intake in a diet that was supplemented with the tryptophan GM-brown rice (50% higher Trp than conventional rice) were significantly higher than those in the control group (non-transgenic tryptophan unsupplemented rice) (Takada & Otsuka, 2007).

Lysine (Lys) Enhanced GMPs, Feeding Trials With Mice, Poultry, And Pig

Insertion of the lysine-rich gene into grains like maize has shown an increase in the total protein and lysine content of transgenic varieties, leading to an improved amino acid score and hence an improvement in the nutritive value of such grains (Tang et al., 2013). In their experiment, Hua et al. (2012), compared the results in rats fed with the transgenic high lysine rice to those fed near-isogenic rice. There was no significant difference in body weight gain and it was clear that no adverse effects were observed in rats fed transgenic rice compared to those fed non-transgenic rice. Two transgenic rice lines HFL1 and HFL2 (High Free Lysine; HFL) containing a high concentration of free lysine were used in a 70-day rat feeding study to assess their nutritional value as compared to wild type (WT). The HFL groups had higher body weight, higher food intake, and higher food efficiency than the WT groups. In addition, the HFL diets had higher apparent protein digestibility, protein efficiency ratio, and lysine availability than the WT diet. Based on these results, it was concluded that rice high in free lysine resulted in improved growth performance, food efficiency, and lysine availability in growing rats (Yang, et al., 2017a).

In another 90-day experiment, body weight gain, food intake, and food efficiency were not affected in Sprague-Dawley rats fed rice diets of the HFL transgenic line compared to non-transgenic diets. Hematological parameters, serum chemistry, organ weights, and histopathology were assessed and there was no difference between rats fed the two diets (Yang, et al., 2017b). No adverse dietary differences in bodyweights, feed consumption/utilization, clinical chemistry, hematology, gross or microscopic pathology, absolute and relative organ weights were observed between rats consuming diets with Y642 transgenic lysine-rich maize grain compared with rats consuming diets containing Nongda 108 maize grain (control quality protein maize). These results clearly showed that Y642 lysine-rich maize is as safe and nutritious as conventional 108 maize grain (Yun et al., 2009).

The nutritional efficiency of LY038 maize with more lysine (0.360%), crude protein, and several other amino acids compared with the conventional maize (lysine 0.255%) was evaluated in a study on broiler chickens (Lucas et al., 2007). Body weight gain, feed conversion, and carcass yields of broilers fed GM high lys-based diets were similar to chickens fed conventional maize $_L$-lys HCl supplemented diets, but significantly better compared to chickens fed conventional corn diets without Lys supplementation. There were no unexpected effects of LY038 maize on health status or mortality (Lucas et al., 2007). In another study, three experiments were carried out to determine the nutritional value and to certify the performance of growing and finishing pigs (30 to 90 kg) fed on diets containing common corn (CC), high-lysine corn (HLC), and high-oil corn (HOC). There was no difference in performance and carcass variables between the corn types with different nutritional profiles (De Oliveira et al., 2011).

Genetically Modified Methionine Enhanced Crops, Feeding Trials with Poultry, Ruminant, And Fish

The leguminous bean of lupin (*Lupinus angustifolius* L.) was genetically modified to transfer a sunflower seed albumin gene resulting in increased methionine content (Molvig et al., 1997). In feeding trials with rats, the transgenic seeds diet gave statistically significant increases in live body weight gain, true protein digestibility, biological value, and net protein utilization, compared with wild-type seeds diet (Molvig et al., 1997). When the nutritional value of genetically modified lupin (*Lupinus angustifolius L.*) seeds was evaluated with broilers for 18 days, there was no significant difference in weight gain and feed intake between the conventional and transgenic lupin diets. However, gain of birds fed the conventional lupin diet was higher (1.82 vs 1.74) than that of birds fed the transgenic lupin diet (Ravindran et al., 2002). The average metabolizable energy for the transgenic lupin diet was high at 10.18MJkg^{-1}, which could be due to the lower content of soluble non-starch polysaccharides in the transgenic lupin (Ravindran et al., 2002).

In another experiment with 80 merino sheep fed cereal hay-based diet containing either the transgenic or parent lupin seed for 6 weeks. No significant differences were observed between the cereal diets in organic matter digestibility, rumen microbial protein synthesis, or *in Sacco* degradability of dry matter. Plasma urea nitrogen was lower in the sheep fed the transgenic grain than those fed the parent grain. They conclude that the magnitude and nature of the responses were consistent with the transgenic lupins providing more methionine to the tissues, a first-limiting amino acid for sheep (White et al., 2001). Feeding experiments also conducted on fish showed that in the first experiment, no obvious effect was observed on the growth of juvenile red sea bream fed transgenic lupins with increased methionine and non-transgenic control diets. In the subsequent second experiment, a positive significant effect on fish growth was observed with both the transgenic meal and the non-transgenic meal with added crystalline methionine compared to the nonfortified nontransgenic-meal (Glencross et al., 2003).

Transgenic Crops with Enhanced Fatty Acids, Feeding Trials with Rats And Poultry

This article discusses feeding trials of genetically modified plants with enhanced fatty acid content as feeds but generally, oilseed plants are modified mainly for industrial benefits rather than for animal feeds or human food. As human food, the intention is to produce oil plants that are safe, such as oils with low or zero-saturated fat content and oils containing stearidonic acid (SDA) (de Santis et al., 2018).

In a feeding trial, different groups of rats were fed a diet containing 15% (w/w) of borage oil (BO), which contained 22% (w/w) of gamma-linolenic acid (GLA) and another was fed a diet containing 5, 10, and 15% a transgenic high-gamma-linolenic acid canola oil (HGCO) as a fat source. After 12 weeks, feeding with diets containing up to 15% HGCO resulted in no adverse effects on growth, organ weight, hematology, and serum biochemistry compared to the diet containing 15% BO, suggesting that HGCO may be a safe alternative source of GLA (Liu et al., 2004). In another study with two objectives; the first objective was to compare the effects of diets containing equal levels of GLA (23%) from either BO or HGCO on reproduction, pup development, and pup brain fractional anisotropy (FA) composition in mice. As a second objective, the effects of transgenic HGCO diluted to 23% GLA (GLA-23) were compared with those of undiluted HGCO containing 36% GLA (GLA-36). Compared to GLA-23, GLA-36 had larger effects on growth and brain FA composition but no differences in effects on reproduction and behavioral development. These findings suggested that the HGCO can be used as an alternative source of GLA (Wainwright et al., 2003).

Extensive research on modifying the oilseed plant composition to achieve increased concentrations of nutritionally valuable long-chain polyunsaturated fatty acids n-3 (LC PUFA n-3) has been a great task. Recently, the genes encoding desaturases and elongases enzymes from microbes were successfully expressed in oilseed plants. The principal objective of such genetic transgenesis was to increase the content of stearidonic (SDA, C18:4, n-3), eicosapentaenoic (EPA, C20:5 n-3) and docosahexaenoic acids (DHA, C22:5 n-3) (Venegas-Calerón et al., 2010). Transgenic soybean oils enriched with either SDA or EPA were incorporated into diets to test their effects on limiting the development of metabolic syndrome (MetS) in a mouse model of diet-induced obesity. Supplementation with SDA enriched oils improved features of MetS compared to feeding a control wild-type oil. The findings supported the utilization of SDA-enriched diets to modulate weight gain, glucose metabolism, and fatty acid profiles of the liver and adipose tissue (Munoz et al., 2020).

The effect on the fatty acid composition and sensory characteristics of chicken meat was investigated. Broilers fed with the diets supplemented with oil from soya beans genetically modified to produce relatively high concentrations of SDA produced meat with increased concentrations of SDA that is healthier for human consumption, also increased meat concentrations of eicosapentaenoic acid and DPA (docosapentaenoic acid, C22: 5n-3) were observed.

There was no significant difference in DM intake, weight gain, or feed conversion efficiency between the transgenic diet and that of the near-isogenic soya diet (Rymer et al., 2011). In addition to the latter study, two groups of broilers were fed diets containing either 50 g/kg CON (conventional soybean oil) or 50 g/kg of SDA-enriched oil (stearidonic acid (18:4n-3)-enriched soybean oil) derived from a genetic modification of soybean (SDASOY). There were no significant differences in weight gain, feed intake and efficiency between the diets. Compared to the CON treatment, dietary SDASOY increased ($P<0.01$) total VLC n-3 PUFA (VLC, Very Long Chain) contents of skinless and boneless breasts, tenders, and thighs by almost 3-fold (Elkin et al., 2016).

The transcription of the gm-fad2-1 gene fragment leads to a high level of oleic acid (18:1) in the soybean seed, and expression of the soybean acetolactate synthase protein (GM-HRA) encoded by the modified gm-hra gene is used as a selectable marker during transformation (Stepanek et al., 2014). In a study of 336 Hy-Line W-36 Single Comb White Leghorn hens, transgenic soybeans (DP-3Ø5423–1(305423)) containing the gm-fad2-1 gene fragment and the gm-hra gene were examined. Feeding of pullets hens with DP-3Ø5423-1 (305423) was shown to be nutritionally equivalent to the non-modified control as evidenced by body weight, hen-day egg production, egg mass, feed intake/efficiency as well as egg production and egg quality characteristics (Mejia et al., 2010). Similarly, in another study conducted on broilers, 305423 soybeans were found to be nutritionally equivalent to non-transgenic control soybeans (Mcnaughton et al., 2008).

Genetically Modified Crops with Increased Phosphorus Availability, Feeding Trials with Poultry and Pigs

Plants contain significant amounts of phosphorus (P), although the main storage form of P in crops is phytic acid, as phytate salts, i.e. myo-inositol 1, 2, 3, 4, 5, 6 – hexakisphosphate (Yang, et al., 2017c). The P that is bound in phytates is not efficiently utilized in the gastrointestinal tract of monogastric animals due to its poor solubility (Swiatkiewicz & Arczewska-Włosek, 2011). In order to improve P availability in crops, genetic engineering methods leading to the expression of transgenic phytase (phy gene), the enzyme that hydrolyzes phytate bonds, in seeds are used (Gao et al., 2014).

Phytase transgenic corn (PTC) and non-transgenic conventional corn (CC) were fed to laying hens. The feeding of PTC to laying hens had no adverse effects on serum biochemical or organ weight parameters. The phosphorus digestibility of hens fed the PTC-based diet was (58.03%) greater than that of hens fed the CC -based diet (47.42%), implying that with PTC-based diet less undigested phosphates were excreted in the feces, thus reducing phosphorus contamination of soil and water (Gao et al., 2014).

When measuring performance through egg production and quality of eggs, hens fed diets containing transgenic corn (PTC) was similar to that of hens fed diets containing CC. No fragments of the phyA2 gene or protein translocation were detected in the blood, tissues, or eggs (Ma et al., 2013). Wang et al. (2013), in their study showed no effect on production in laying hens with the use of the Phytase transgenic corn. According to Lu et al. (2015), concluded that PTC had no adverse effect on the quantity and diversity of gut microorganisms and the transgenic phyA2 DNA or protein was not transferred to the tissues of broilers, implying that it was rapidly degraded in the intestinal tract.

In growing pigs, phytase transgenic corn had a higher digestibility of energy than common corn and reduced fecal P excretion (Li et al., 2013). With nursery pigs fed a corn-expressed phytase (GZ; GraINzyme, Agrivida Inc., Woburn, MA) for 41 days showed a linear increase in average daily gain, apparent total tract digestibility of P, bone-breaking strength, and bone ash characteristics as GZ inclusion increased (Broomhead et al., 2019). In the diets of weanling pigs, the inclusion of corn expressing an *E. coli*-derived gene to a P-deficient diet increased the growth performance and indices of P utilization in pigs (Nyannor et al., 2007). Feeding LPC (low-phytate hybrid corn) in pig diets reduced P excretion in swine waste by 50 and 18.4% in the semipurified and practical diets, respectively, compared with NC (near-isogenic corn). Using an *in vitro* procedure designed to simulate the digestive system of the pig, the availability of P for pigs was approximately 56% for LPC and 11% for NC (Veum et al., 2001). This study is similar to that of Hill et al. (2009), as they reported that feeding with low phytic acid (LPA) corn, LPA soybean meal significantly improved P digestibility.

Genetically Modified Plants with Reduced Anti-Nutritive Factors (Low-Oligosaccharide, Lignin, Beta-Glucan), Feeding Trials with Poultry and Ruminants

The metabolizable energy (ME) of soya bean meal (SBM) is quite low and is mainly due to the very poor digestibility of the carbohydrate fraction. The main reason for the low ME of SBM is the oligosaccharides i.e. raffinose and stachyose, which cannot be digested in the small intestine of humans, swine, and poultry. Due to plant breeding technologies, efforts have been made to reduce or nearly eliminate the oligosaccharides raffinose and stachyose through genetic engineering (Hagely et al., 2020), to produce LOSBM (low-oligosaccharide soyabean meals). Nutritional evaluation of SBM varying in oligosaccharide was done. The mean metabolizable energy values (kcal/kgDM) for the conventional soybean meals (CSBM) and LOSBM were 2,739 and 2,931 respectively, which represented a difference of 7% (Parsons et al., 2000). The feeding of broiler chicks with SBM produced from low-oligosaccharide (LOSBM) and conventional (CSBM) varieties of soybeans showed no differences between the diets for body weight gain or feed efficiency. In addition, LOSBM is required at lower concentrations in diets fed to broiler chicks because it has a higher nutritional value than CSBM (Baker et al., 2011).

Alfalfa (*Medicago sativa L.*) is grown worldwide and used fundamentally to meet the nutritional requirements primarily for the ruminant livestock. However, the nutritional value of alfalfa is severely limited by indigestible cell wall components such as lignin. Lignin reduction has been achieved by the down-regulation of two specific enzymes in the lignin biosynthesis pathway – COMT (caffeic acid 3-O-methyltransferase) and CCOMT (caffeoyl CoA 3-Omethyltransferase) (Barros et al., 2019).

In a study designed to compare the difference in forage nutrient quality between reduced-lignin alfalfa hay and conventional alfalfa hay, it was found out that there were no differences in forage nutrient quality between alfalfa treatments. They concluded that animal performance did not differ for growing Angus heifers consuming the two diets (Peterson et al., 2018). In the study with lambs, dry hay alfalfa genotypes with down-regulated COMT or down-regulated CCOMT were compared to their respective nulls (same genotype without genetic modification). During the study, free choice intake was measured at refusal levels of 9-15% of feed offered. There was no difference in these intakes (as a percentage of body weight/day) between the treated hay diets. Digestibility of NDF organic matter (aNDFom) was greater for COMT than its null for all cuttings for free choice and restricted intakes. For the CCOMT down-regulated alfalfa, the digestibility of aNDFom was greater than its null for all cuttings at restricted intakes (Mertens, 2009).

GM barley with reduced (1,3-1,4)-β-D-glucan has nutritional benefits for the chicken feeding industry. β-D-glucan is identified in barley grain as an anti-nutritive factor because it is not easily digested. β-D-glucan binds water in the intestine which results in the formation of gels and increased viscosity of the intestinal contents which reduces nutrient availability in the diet (Stepanek et al., 2014). Barley with reduced β-glucan improves the feeding efficiency and the nutritive value of the feeds. Also when transgenic barley grains were fed to broilers showed no effect on weight gain and can be the best alternative to a maize-based diet for broilers, especially in regions that cannot produce enough maize (Von Wettstein et al., 2003).

Transgenic Plants with Improved Biological Active Compounds, Feeding Trials with Pigs, Rats, And Poultry

Determination of whether genetically modified rice that expresses human lactoferrin (hLF rice) or lysozyme (LZ) which protects the intestinal tract similarly to subtherapeutic antibiotics was done. The results demonstrated the potential of genetically produced lactoferrin (LF) and LZ rice to be used as a substitute for antibiotics in broiler diets (Humphrey et al., 2002). The hLF rice was evaluated on the basis of components, nutrient digestibility in pigs, protein availability in rats and protein digestibility corrected amino acid score (PDCAAS) in comparison with its parental rice variety (PR rice). The hLF rice did not affect the digestibility of protein, carbohydrates, fat, and crude fiber. The revised protein efficiency ratio of hLF rice was improved to 2.50, which was significantly higher than that of PR rice. The PDCAAS of PR rice was 52.66, while the PDCAAS of hLF rice was improved to 54.06. In general, the nutritional quality of hLF rice is better than that of PR rice (Hu et al., 2010).

Silage from transgenic inulin synthesizing potatoes was compared to that of the parental cultivar. The starch content and the digestibility of fiber fraction decreased (73 vs 81%) and the feed energy value was 14.3 MJ ME/kg DM for the silage of transgenic and 14.6 MJ ME/kg DM for the silage isogenic potatoes. The average daily weight gain of pigs fed the transgenic silage was 43g lower than that of the controls. From the energetic point of view, the modification was a disadvantage for the pigs (Böhme et al., 2005).

Conclusions and Recommendations.

In general, feeding with second generation genetically modified plants has shown a positive effect on the performance of the different animals.

However, most experiments have been carried out in sample animals, I think that it is necessary to conduct most of these feeding trials with nutritionally modified plants with other animals that are consumed by humans, such as ruminants. In addition to this, most tests are being done on laboratory animals especially the mice. These animals are fed only small and specific parts of the GM plant, not the entire plant, whereas most farm animals consume almost the entire plant from leaves to roots. This means that using these lab animals may not give a clear picture of the overall safety of the GM plants for both the animals and the plants.

In addition, for these plants and their products to be accepted for commercial production and distribution to the general population in most countries, an appropriate long-term evaluation of the nutritional and toxicological approach is required.

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