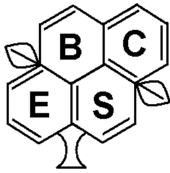

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OCCURRENCE OF GENETICALLY MODIFIED FOOD IN EGYPTIAN FOOD MARKET

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ABSTRACT

The use of genetically modified organisms (GMOs) as food or products is becoming widespread. The European Union has implemented a set of very strict procedures for the approval to grow, import and/or utilize GMOs as food or food ingredients. Recently, DNA-based techniques became very common for the detection of GMOs in food products. For rapid and easy detection of GMOs, polymerase chain reaction (PCR) screening methods, which amplify common transgenic elements, are applied in routine analysis. In this study, A total of 140 maize, maize products, soy and soybean products were collected from the Egyptian food market during 2005/2008. DNA based methods were used to detect the genetic modification in proportion above 1% in all samples. Maize samples were analyzed to detect the presence of maize line Bt 176, Bt 11, Mon 810, maize line T25 and starlink maize. On the other hand soy samples were analyzed to detect the genetic modified soybean line Roundup Ready, The results indicated that 18.57 % from maize samples were positive for maize line Bt176, 15.7 % positive for maize line Bt11, and 12.85 % positive for maize line StarLink™. On the other hand, 25.7 % from soybeen samples positive for the presence of Roundup Ready soy bean..

Keywords: genetically modified foods GMOs, PCR. DNA.

INTRODUCTION

Application of recombinant DNA technology (genetic engineering) in modern plant breeding has resulted in the development of plants with improved agronomic and nutritional properties. Food crops have been modified through the introduction of new agronomic traits or suppression of constituent genes which code for disease or pest resistance, herbicide tolerance, or inhibition of ripening or increase of nutritional value, reduce of toxins, remove undesirable characteristics, improve or add desirable characteristics. By using of recombinant DNA technology (genetic engineering) we can design what we want and need (Elsanhoty et al. 2006, Abdullah et al., 2006).

On the other hand, the application of recombinant DNA technology in agriculture, food and feed production has hazards. The hazards that may be introduced into foods through genetic engineering three, allergens, toxins, and reduced nutritional quality. Genetic engineering products could have unknown long-term effects. In addition, the potential risks exist from GM technology are: the transfer of the introduced genes to wild plants and non-GM crops and, the indirect effects of the GM crops in the environment, e.g., effects on non-target insect and weed population and the possible development of resistant insects and weeds. Also the indirect effect of GMO crop on the soil fertility, there is risk results from GMO food and crops to damage the useful soil microorganisms and brides, There is the possibility that the biodiversity of wildlife can be modified as a result of changes in the availability of food, increased pesticide resistance and genetic pollution, The risk from application of antibiotic resistance during the genetic engineering process, may be create super weeds, super pests, new virus and pathogens. It may also make genetic bioinvation, socioeconomic and ethical hazards. With the increasing development of genetically modified organisms (GMOs) (James, 2001). Several countries, including China, Japan and many members of the European Union, have set up food-labeling laws that incorporate threshold limits for the reason of safety concerning GM crops, which make the qualitative and quantitative detection methods for GMOs indispensable (Losey et al., 1999). Currently, the two most prevalent approaches for GMO detection are DNA-based PCR and antibody-based immunoassays (Malatesta, et al., 2008 ; Ahmed, 2002; Javier et al., 2008) but neither has been internationally accepted

regarding the validity of these two tests. At present, both PCR and multiplex-PCR protocols used for GMO screening are based on the detection of the 35S promoter in the cauliflower mosaic virus (CaMV) and the Agrobacterium tumefaciens nopaline synthase (nos) terminator sequences, and in some cases, the Neomycine-phosphotransferaseII (NptII) terminator (Lipp et al., 1999; Trapmann et al., 2002). These three genetic elements are presented in numerous but not in all GMOs, so the above methods have application limits. Furthermore, it is difficult to confirm PCR products by conventional methods when multiplex-PCR is used to amplify two or more DNA fragments simultaneously (Permingeat et al., 2002; Matsuoka et al., 2001; Demekea et al., 2002). Therefore, there is a demand for a more efficient approach capable of covering a broader range of GMO varieties and easily.

Monitoring the presence of GM plants in a wide variety of food, feed and seeds matrices is important to countries with labeling laws for approved GM varieties. In addition, countries may want to test for unapproved GM varieties. In the United States, which does not require labeling of GM products, two recent events with implications for human health have emphasized the importance of being able to detect GM foods and feeds. The first incident occurred in 2000 with the detection in human food of a GM maize that was only approved for use in animal feed (Dorey, 2000). The second was the accidental shipment of an unapproved GM maize variety for cultivation between 2001 and 2004 (Herrera, 2005).

Although Egypt mainly depends on imported soybeans and maize, the control and evaluation of these crops only depends on its nutrient content and the acceptable level of mycotoxins without paying any attention to genetic manipulation. Consequently, there is no idea about the presence or absence of GM crops for both human and/or animal consumption in Egypt. Furthermore concepts for safety evaluation are urgently needed. Therefore, this work was planned to monitor the incidence of genetically modified foods in Egyptian market. To achieve this purpose, 140 samples of soybean or soybean products, maize and maize products have been randomly collected from the Egyptian market. The samples were subjected to detection techniques based on Polymerase Chain Reaction (PCR) using the official detection methods according to Article 35 of the German Federal Foodstuffs Act (Anonymus, 2002).

MATERIALS AND METHODS

Materials

Seventy samples from each of commercially available soybean, soybean products, maize and maize products were collected randomly from markets in Cairo and Giza, or provided by the Food Technology Research Institute or the Central Laboratory for Food and Feed (Egypt) throughout the years 2005 / 2008. Samples included diverse processing steps from relatively mild treated ground soybeans to highly processed bakery products and snacks.

Reference Materials

Certified reference materials (CRMs) standards consisting of dried soybean powder with 2%, 0.5% and 0% Roundup Ready soy and dried maize flour with 5%, 0.5% and 0% Bt-176 maize and 2%, 1% and 0% Bt-11 maize produced by the institute for reference material and measurements (Geel, Belgium) were used as negative and positive controls for soy and maize lines CRMs were purchased from Fluka.

Because there is no CRM available for maize lines MON 810 and T 25, samples containing 1% GMO were prepared in the laboratory from these lines and used as positive controls, whereas, the negative control that was used was the normal non GMO maize. For the Star Link maize, the positive control as well as the negative control, were provided with the commercial detection kit used for detection of this maize line (Commercial GMO/dent Star Link™ kit produced by Europe Gene Scan, Bremen Germany. Cat. No.: 5221102810).

Extraction, purification and quantification of genomic DNA

Soybean seeds, and maize samples were ground in an electric grinder. Frozen products were placed at room temperature till thawed, 200 mg samples as well as from the CRMs were used for the extraction of the genomic DNA according to the official German methods for soybean (Anonymus, 1998) and maize (Anonymus, 2002) by the cetyltrimethyl ammonium bromide (CTAB) method. DNA from CRMs as well as from all investigated samples was extracted twice in independent procedures. Furthermore, a blank sample consisting of 200 µl autoclaved bi-distilled water was used to control reagents used in the work.The concentration and purity of the

extracted DNA were measured by absorbance at 260 and 280 nm using a spectrophotometer.

Reagents

Suitable molecular biology grade reagents were used and all procedures were carried out under substantially sterile conditions. The water used was bi-distilled and autoclaved or of equivalent quality. This specified solution (aqueous solution), was filtrated through 0.2 mm filter paper and autoclaved before use.

Oligonucleotide primers used in this section of study together with their target specific part of the investigated DNA are listed in Table (1). All primers were synthesized by Bio Syntesis, Inc USA and obtained in a lyophilized state. All primers were solved before use to obtain a final concentration of 20 pmol/µl each. For Star Link maize the primer pair as well as the complete master mix without the polymerase enzyme were provided with the commercial detection kit used the GMOIdent StarLink™ test kit (GeneScan Europe AG)

DNA amplification and PCR condition

PCR was carried out on a PTC-150 Minicycler (MJ Research,Inc,USA) ,. Each PCR reaction mix had 25 µl total volume and contained 2.5 µl ReddyMix buffer (10 x concentrate, Thermo Scientific), 2 µl $MgCl_2$ solution (25 mM), 1 µl dNTPs solution (0.2 mM each of dATP, dCTP, dGTP and dTTP), 0.5 µM of each primer, 0.625 Unit Thermoprime *Taq* polymerase (Thermo Scientific), 2 µl of template extracted DNA and was completed to 25 µl with water. For Star Link detection 1 Unit AmpliTaq Gold polymerase (Perkin Elmer) was added to the master mix obtained with the commercial kit prior to PCR.

Table (2) explains the time/temperature profiles used in PCR for each primer pair including the conditions for the detection of Star Link. All amplicons were stored at 4 ºC until gel electrophoresis.

Table (1) Oligonucleotide primer pairs sequence and their target element

Primer	Sequence	Fragment Length	Target element	References
GM03 / GM04	5'- gCC CTC TAC TCC ACC CCC ATC C - 3' 5- gCC CAT CTg CAA gCC TTT TTg Tg – 3'	118 bp	Soy lectin gene.	Meyer et al., (1996)
P35s-f2/ Petu-r1	5' - TgA TgT gAT ATC TCC ACT gAC g -3' 5' -TgT ATC CCT TgA gCC ATg TTg T-3'	172 bp	Transition site from the CaMV35S promoter sequence to the petunia hybrida chloroplast-transit-signal sequence in **RRS**.	Wurz (1997)
IVR1-F/ IVR1-R	5 - CCg CTg TAT CAC AAg ggC Tgg TAC C- 3' 5 – AAT TTg CgC gCC TgC TgC CTT CC- 3'	226 bp	Maize invertase gene.	Ehlers et al., (1997)
Cry03 / Cry04	5' - CTC TCg CCg TTC ATg TCC gT - 3' 5' - ggT CAg gCT CAg gCT gAT gT - 3'	211 bp	Transition site from the CCDPK-promoter into the amino terminal sequence of synthetic Cry1A(b) gene in **Bt 176** maize.	Hupfer et al., (1998)
IVS2-2 / PAT-B	5' - CTg ggA ggC CAA ggT ATC TAA T - 3' 5' - gCT gCT gTA gCT ggC CTA ATC T – 3'	189 bp	Transition site from the intron IVS2 into the PAT-gene in **Bt11** maize.	Anonymus (2002)
T25-F7 / T25-R3	5' - ATg gTg gAT ggC ATg ATg TTg - 3' 5' - TgA gCg AAA CCC TAT AAg AAC CC- 3'	209 bp	Transition site from the CaMV-terminator into the PAT gene in **T25** maize.	Anonymus (2002)
VW01 / VW03	5'- TCg AAg gAC gAA ggA CTC TAA Cg - 3' 5' - TCC ATC TTT ggg ACC ACT gTC g – 3'	170 bp	Transition site from the genomic maize DNA into the CaMV-promoter in **MON810** maize.	Anonymus (2002)

Table (2) Time / temperature profiles for qualitative PCR with DNA extracted from maize and soybean samples using the primer pairs described in Table (1)

Primer pair	Initial denaturation	Denaturation	Annealing	Extension	Cycles	Final elongation
GM03 /GM04	10 min. at 95 °C	30 sec. at 95 °C	30 sec. at 60 °C	1 min. at 72 °C	35	3 min. at 72 °C
P35s-f2 /petu-r1	10 min. at 95 °C	30 sec. at 95 °C	30 sec. at 62°C	25 sec. at 72 °C	35 – 40	10 min.at 72 °C
IVR1-F /IVR1 - R	12 min. at 95 °C	30 sec. at 95 °C	30 sec. at 64 °C	30 sec. at 72 °C	42	10 min. at72 °C
Cry03 /Cry04	12 min. at 95 °C	30 sec. at 95 °C	30 sec. at 63 °C	30 sec. at 72 °C	38	10min. at 72 °C
IVS2-2 /PAT-B	12 min. at 95 °C	30 sec. at 95 °C	30 sec. at 64 °C	30 sec. at 72 °C	38	10min. at 72 °C
T25-F7 /T25-R3	12 min. at 95 °C	30 sec. at 95 °C	30 sec. at 64 °C	30 sec. at 72 °C	40	10min. at 72 °C
VW01 /VW03	12 min. at 95 °C	30 sec. at 95 °C	30 sec. at 64 °C	30 sec. at 72 °C	40	10 min. at 72 °C
Star Link Kit	10 min. at 94 °C	25 sec. at 94 °C	30 sec. at 62 °C	45 sec. at 72 °C	50	3 min. at 72 °C

Gel electrophoresis

Agarose gel preparation as well as electrophoresis were carried out using Tris-base/borate (TBE) buffer solution (pH 8.0), containing 45 mmol/L Tris-base / boric acid and one mmol/L EDTA adjusted with hydrochloric acid. To determine the size of the DNA fragments, DNA of known size (50, 100 bp DNA marker, Gibco BRL, USA and Vivantes, Singapore) together with the different amplicons were separated on 2% w/v agarose gel (LE, Roche)/TBE buffer stained with 0.01% ethidium bromide solution (0.5 mg/L). 10 µl of all amplicons and DNA marker were stained before gel electrophoresis by 2 µl xylenecyanol dye solution (1 mg xylenecyanol, 400 mg sucrose and completed to 1 ml with water), and then subjected to electrophoresis for 45 min. The amplicons were made visible by ethidium bromide staining and documented using UV transillumination (254 nm.)

RESULTS AND DISCUSSION

The presence of GM-soy in Egyptian food samples

The presence of soybean in collected samples was checked by using the soybean lectin specific primer pair GMO3/GMO4 (118bp) (Table 1 and 2). All examend samples containing soya were positive to the lectin gene. The results are shown in figure (1) as an example for the PCR analysis in detected the presence of the lactin gene (118bp). No amplification were observed in PCR control without DNA. For the detection of Roundup ReadyTM (RRS) soybean PCR with RRS soybean-positive samples results in an amplicon of 172 bp in length using the primer pair P35s-f2/petu-r1 (Table 1 and 2).

Which is specific for the genetic modification in Roundup Ready soybean™ The amplicon was only detected in 18 transgenic samples out of 70 samples tested or 25.7% as shown in table (3) and example for the PCR analysis is given in figure (2) lane 2, 3, 8, 9, and 11).

The presence of GM-maize in Egyptian food samples

The presence of was checked by using the maize invertase specific primers pair IVR1-F/IVR1-R (226bp) (Table 1 and 2). All tested samples gave positive results as shown in the example in Figure (3). No amplification was observed with the PCR control without DNA For the detection of GM maize in maize and maize food products the collected samples (Table 4) were analysed using specific primer pairs to detect Bt176 (211bp), Bt11 (189bp), MON810 (170

bp), T25 (209 bp) and StarLink™ (134bp) in PCR (Table 1 and 2). Bt176 was identified using the primer pair CRY03/CRY04. The expected 211 bp amplicon only appeared with the transgenic samples and GMO containing CRM as shown in the example in Figure (4) (lanes 2, 3, 4,5, and 6). By using primers specific for Bt11 maize (IVS2-2/PAT-B) an amplified sequence of 189 bp length was obtained with maize grain samples imported from the US and the positive control (Figure 5 lanes 4,5, 7 and10). Primer pair T25-F7/ T25-R3 is used for the detection of T25 maize yields a PCR product of 209 bp. The amplicon only appear in GMO containing CRM as shown in the example in Figure (6). For the identification of maize MON 810 the primer pair VW01 / VW03 expected 170 bp shown in the example in Figure (7). The identification of StarLink™ maize was detected The expected 134 bp fragment which only appeared with the maize grain samples from USA as shown in the example in Figure (8) (lane 2,3,4 and 6).

The results for all 70 maize samples under investigation are compiled in Table (4). In particular maize grains imported from the USA, maize grains imported from the Argentina, maize grains imported from the Ukraine and one sample of ground maize of unknown origin were tested positive for Bt176, Bt11 and/or StarLink™. Thirteen samples contained Bt176 maize (18.57 %) and 11 samples Bt11 maize (15.7 %). Nine samples contained StarLink™ maize Table (2). The latter was found in combination with Bt176 and Bt11 in imported US maize. Especially for this GMO event, health risks can not be fully excluded based on the investigations described in the authorisation by The U.S. *Environmental Protection Agency* (EPA) for the purpose of feed production. No MON810 or T25 maize was detected. No GM maize was identified in maize flour and kernels or food samples of Egyptian origin.

Table (3): Soybean and soybean products analysed for the presence of Roundup Ready™ specific DNA

Tested materials	Number of samples	Number of RRS positive samples	Percentage of GMO
Local soybean seeds	4	0	0 %
Soybean granules from USA	22	12	54.5 %
Soybean granules from Brazil	2	1	50 %
Soybean ground	4	1	25 %
Tofu	3	0	0 %
Soybean flour	3	2	66.5 %
Natural soybean milk	1	0	0 %
Biscuit with soybean flour	10	1	10 %
Soybean mix for hamburger	3	0	0 %
Natural cheese supported with soybean milk	1	0	0 %
Cerelac with soybean protein	2	1	50 %
Soybean milk with chocolate flavour	2	0	0 %
Soybean milk with strawberry flavour	2	0	0 %
Soybean ice cream	2	0	0 %
Bread with soybean flour	3	0	0 %
Snack with soybean	2	0	0 %
Soy sauce	4	0	0 %
Total number of samples	70	18	25.7 %

Legend to table (1) DNA was extracted and analysed by PCR as discribed in Materials and Methods. For PCR the primers p35s-f2 and petu-r1 were used to detect the transgene from RRS; the limit of detection for this PCR system is about 0.5 % of RRS; "-" indicates a negative RRS result (concentration below 0.5% RRS).

Table (4). Presence of Bt176, Bt11, T25, Mon 810 and StarLink™ specific DNA in maize and maize products

Tested materials	Number of samples	Number of Positive Samples					Percentage of GMOs
		Bt176	Bt11	T25	MON 810	StarLink ™	
Maize flour	1	0	0	0	0	0	0 %
Maize starch	2	0	0	0	0	0	0 %
Biscuits with maize flour	6	0	0	0	0	0	0 %
Petit four with maize flour (5%)	1	0	0	0	0	0	0 %
Bread 100% maize flour	1	0	0	0	0	0	0 %
Baladi bread 20% maize	2	0	0	0	0	0	0 %
Maize cake	2	0	0	0	0	0	0 %
Maize flour for maize cake	1	0	0	0	0	0	0 %
Corn flakes	3	0	0	0	0	0	0 %
Maize ground (feed)	3	1	1	0	0	0	66.5 %
Snacks with cheese flavour and pepper flavour	7	0	0	0	0	0	0 %
Sweet kernel corn	3	0	0	0	0	0	0 %
Local maize granules	15	0	0	0	0	0	0 %
Maize grains from Argentina	2	1	1	0	0	0	100 %
Maize grains from Ukraine	3	1	0	0	0	1	33.3 %
Maize grains from USA	18	10	9	0	0	8	55.5 %
Total number of samples	70	13	11	0	0	9	
Percentage of GMOs		18.57 %	15.7 %	0 %	0 %	12.85 %	47,1%

Impact of processing

The quality of the DNA extracted from food samples is generally influenced by these factors: the grade of damage (e.g., depurination) of the DNA, the presence of PCR inhibitors in food matrices and the average fragment length of the DNA extracted. These factors are dependent on the samples itself, the processes carried out during the production of the food, physical and chemical parameters of extraction method utilized (Peano et al., 2004). The exposure to heat is known to cause fragmentation of high molecular weight DNA (Hupfer et al., 1998, Greiner et al., 2004, Toyota et al., 2006), and physical and chemical treatments will cause random breaks in DNA strands, thus reducing the average DNA fragment size. Many foods, such as vegetables and fruits are characterized by their acidity, thus accelerating the acid-catalyzed reactions in course in thermal treatments. On the other hand, processing at alkaline pH is part of the production of other foods; a typical example is use of strong alkaline and or acidity solution in the initial stages of the prepration of bread, starch and other similar foods from maize. The DNA is very sensitive to acid and alkaline agents because of mechanism of hydrolytic degradation of DNA. At acid pH, purines are removed from the nucleic backbone due to thecleavage of N-glycosidic bonds between deoxribose residues and bases. Subsequently, adjacent 3$^-$, 5$^-$ - phosphodiester linkage are hydrolyzed, leading to the shortening of DNA strands (Anklam et al., 2002; Yamaguchi et al., 2003).

Conclusion

Soybean and maize play a relevant role in human nutrition and animal feeding in Egypt. Moreover, the consumption of soybean as a basic food component is promoted by the government. The results clearly demonstrate the incidence of genetically modified maize and soybean in the Egyptian food market. Furthermore, the existence of StarLink™ maize in the food chain supplies evidence for uncontrolled arrival of even unauthorised GMOs for food use in Egypt.

The StarLink™-positive maize imported from the US was freely accessible on the local markets and the use of grains for food or feed purposes is not strictly defined nor monitored to the population. Although the amount of StarLink™ in the samples was less than 1 % the allergenic potential is still a matter of discussion. Apart from StarLink™, Bt176 and Bt11 maize was detected in US imported raw

or ground maize. The presence of further GMOs cannot be ruled out since the material was investigated only for the most abundant maize lines, which are approved for food use.

Because it was no longer possible to determine the origin of the maize and soybean material under investigation, it cannot be ruled out that, for instance, the grain samples could be homogenous batches which were imported and distributed all over the country. However, all the samples of the 18 US maize grains were taken randomly from different places and at different time in Cairo and Giza. In particular, the percentage of StarLink™ contained in these samples is not equally distributed which strongly indicates different batches. In the case of soybean samples, RRS positive material was also identified in processed products like biscuit, which is used as infant formula in Egypt. Taken together, GM material could mainly be detected in grains or meals representing the starting point for further processing but also in processed products. Thus, the question is whether the concentration in products is likely to be below the detection limits of the used methods. The German official methods according to the § 35 of the German Foodstuffs Act, which were applied here, are reported to detect 0.1 % GM material. However, the positive controls within the framework of this study were carried out with materials between 0.5 – 5 % GMO. Therefore, it is possible that GM material contents below this range have not been detected.

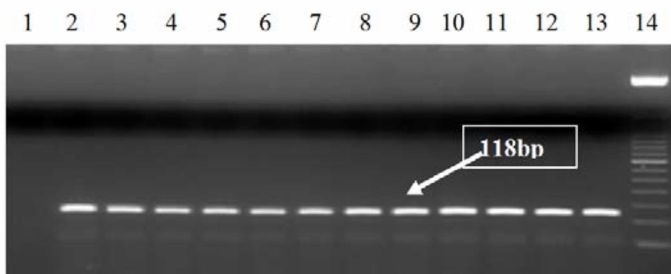

Figure (1) Example for the detection of the soybean lectin gene .

lane 1: PCR control without template-DNA; lanes 2,3: DNA from soybean granules; lanes 4+5: DNA from soybean tofuo; lanes 6+7: DNA from soybean bread; 8+9: DNA from soybean milk; 10 +11: DNA from soybean granules;; lane 12: DNA from non GMO soybean; lane 13: DNA from 2 % RRS; Lane 14 : 50 bp molec

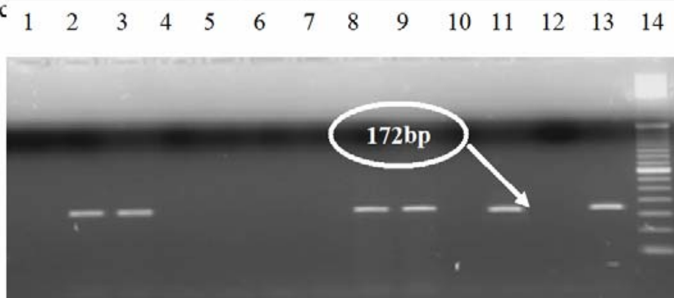

Figure (2) Example for the presence of RRS specific DNA.

lane 1: PCR control with out template DNA; lanes 2+3: DNA from soybean granules from USA; lanes 4+5: DNA from soybean tofuo;6+7+ 8: DNA from soybean ground; 10+11: DNA from soybean granules from Brazil;; 12: DNA from non GMO soy bean; 13: DNA from 2% of RRS; Lane 14: molecular weight marker 50 bp ladder.

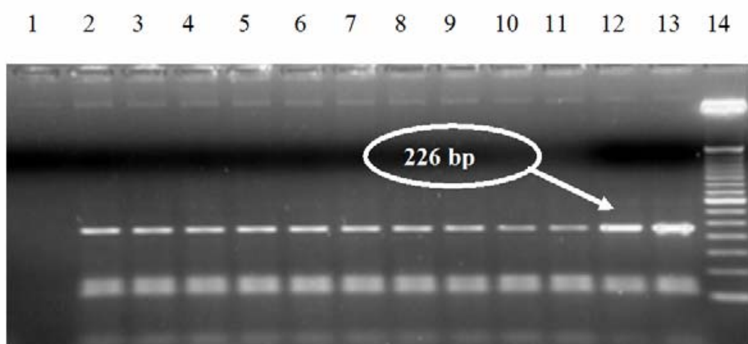

Figure (3) Example for the detection of the maize invertase gene .

lane 1: PCR control without DNA template; lanes 2 -11; DNA from different maize samples; lane 12: DNA from non GMO maize; lane 13: DNA from 0.5% genetically modified Bt 176 maize; Lane 14: 50 bp marker DNA ladder.

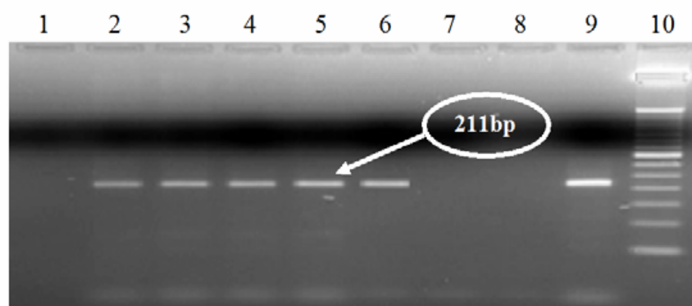

Figure (4) Example for the detection of the transgene from Bt 176 maize.

Lane1: PCR control without DNA; lanes 2 + 6: DNA from maize granules, USA; lane 7: DNA from egyption maize granules, ; lane 8: DNA from non GMO maize; lane 9: DNA from 5 % Bt 176 maize; Lane: 10: molecular weight marker 50 bp DNA ladder.

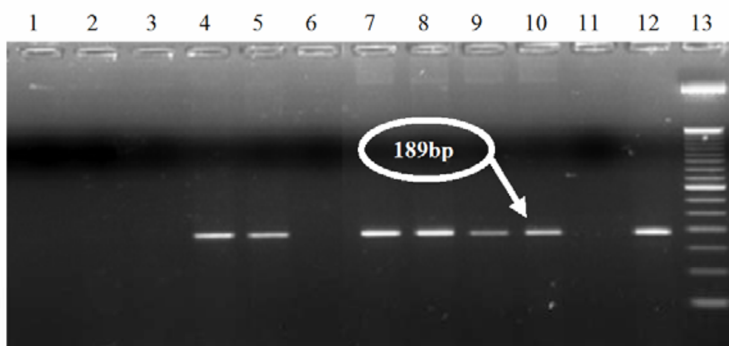

Figure (5) Example for the detection of the transgene from Bt11 maize

Lane 1: PCR control without DNA template; lanes 2 + 3: DNA from egyptian maize samples; lanes 4 + 5: DNA from maize granules derived from the USA; lane 6: DNA from maize flour from the USA; lanes 7+10: DNA from maize granules from the USA; lane 11: DNA from non GMO maize; lane 12: DNA from 2 % Bt11 maize; Lane: 13: 50 bp marker DNA ladder.

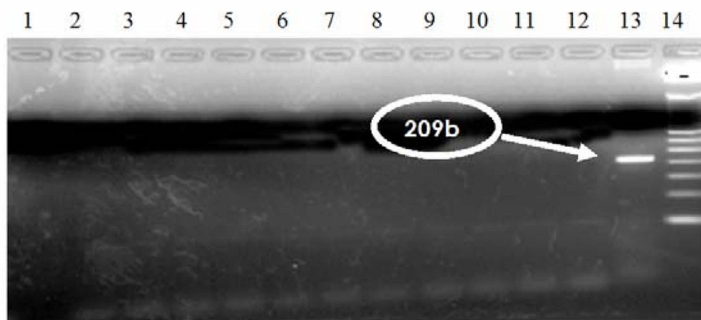

Figure (6) Example for the detection of the transgene from maize T25

Lane 1: PCR control without DNA; lanes 2-11: DNA from raw and processed maize samples; lane 12: DNA from non GMO maize; lane 13: DNA from 1% GMO maize T25; Lane 14: 50 bp marker DNA ladder.

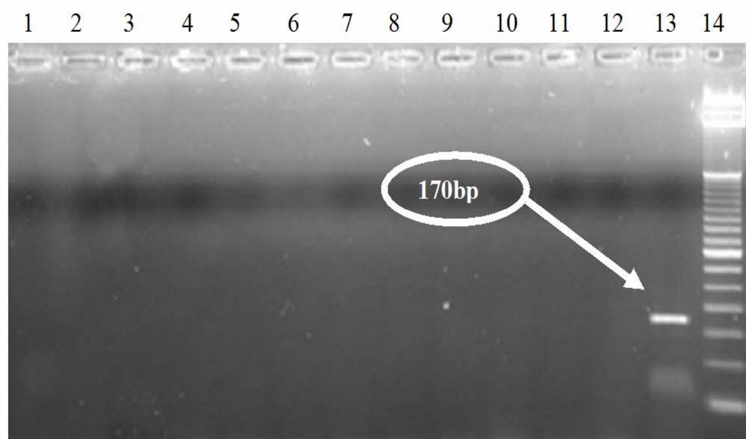

Figure (7) Example for the detection of the transgene from maize MON 810

Lane 1: PCR control without DNA; lanes 2-11: DNA from different raw and proceed maize samples, lane 12: DNA from non GMO maize, lane 13: DNA from 1% GMO maize MON 810; Lane14: 50 bp DNA ladder.

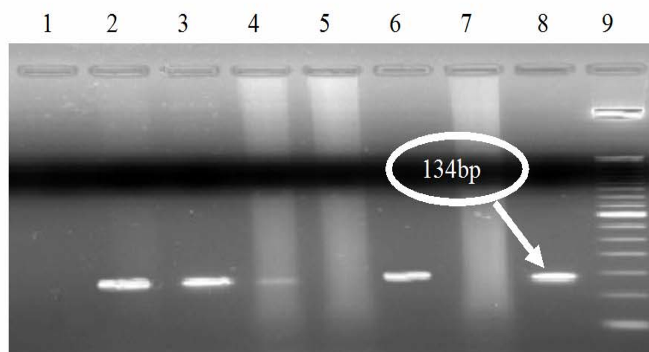

Figure (8) Example for the detection of the transgene from StarLink™ maize

Lane 1: PCR control without DNA; lanes 2+3+4+6: DNA from USA maize granules; lane 5: DNA from egyptian maize; lane 7: DNA from non GMO maize; lane 8: positive DNA from GMO*Ident* StarLink test kit; Lane: 9 : 50 bp DNA ladder.

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مدي تواجد الاغذية المعدلة وراثيا في سوق الغذاء المصري

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لقد انتشر استخدام الكائنات المعدلة وراثيا في الغذاء ، وقد وضع الاتحاد الاوربي مجموعة من الطرق الصارمة للموافقة علي انماء و استيراد او استخدام الاغذية المعدلة وراثيا سواء كغذاء او كمكون غذائي، وحديثا انتشر استخدام التقنيات التي تعتمد علي ال DNA في الكشف عن الاغذية المعدلة وراثيا، يتم استخدام تفاعل البلمرة المتسلسل PCR في التحاليل الروتينية والتي تعتمد علي تضخيم تتابع العوامل الوراثية الشائعةالاستخدام في الهندسة الوراثية، وتعتبر هذة الطريقة طريقة سريعة وبسيطة.

في هذة الدراسة تم تجميع 140 عينة من (الذرة، ومنتجات الذرة،و الصويا ، ومنتجات الصويا) وذلك من السوق المصري خلال الفترة من 2008/2005 ولقد استخدمت الطرق التي تعتمد علي ال DNA للكشف عن وجود التعديلات الوراثية والتي تكشف حتي نسبة 1% في جميع العينات.

تم تحليل عينات الذرة للكشف عن وجود سلالات الذرة ,Bt 176, Bt 11, Mon 810 T 25, Starlink™ ومن جهة اخري تم تحليل عينات الصويا للكشف عن السلالة المعدلة وراثيا Roundup Ready.

وتشير النتائج الي وجود عينات موجبة للسلالة BT 176 بنسبة 18.57% وللسلالة BT 11 بنسبة 15.7 % و للسلالة Starlink™ بنسبة 12.85% .، اما في عينات الصويا فكانت العينات الموجبة لسلالة Roundup Ready Soy بنسبة 25.7%.