

14: RISK ASSESSMENT OF 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 MAIZE

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Country Taking Decision:	South Africa
Title:	Risk Assessment of the stacked-event maize product 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in South Africa. This risk assessment is in support of the Syngenta SA (Pty) Ltd. application for Commodity clearance release.
Contact details:	Name and Address and contact details of the Applicant Syngenta SA (Pty) Ltd. Thornhill Office Park 94 Bekker Street Midrand, 1685 Tel: +27 11 541 4000 Fax: +27 11 541 4072
LMO information	
Name and identity of the living modified organism:	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is a variety developed by Syngenta using conventional breeding techniques. 3272, Bt11, MIR604, TC1507, 5307, and GA21 maize were used to produce the breeding stack 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize. No further genetic modification to produce this stack has taken place.</p> <ul style="list-style-type: none"> • 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize stably inherit the <i>amy797E</i>, <i>pmi</i>, <i>cry1Ab</i>, <i>pat</i>, <i>mcry3A</i>, <i>MIR604 pmi</i>, <i>cry1F</i>, <i>ecry3.1Ab</i> and <i>mepsps</i> genes, retaining the hybridization patterns as predicted. • Maize plants derived from transformation Event 3272 contain the genes <i>amy797E</i> and <i>pmi</i>. • Maize plants derived from transformation Event Bt11 contain the genes <i>cry1Ab</i> and <i>pat</i>. • Maize plants derived from transformation Event MIR604 contain the genes <i>mcry3A</i> and <i>pmi</i>. • Maize plants derived from transformation Maize event TC1507 contain the genes <i>cry1F</i> and <i>pat</i>. • Maize plants derived from transformation Event 5307 contain the gene <i>ecry3.1Ab</i> and <i>pmi</i>. • Maize plants derived from the transformation Event GA21 contain the gene <i>mepsps</i>.
Unique identification of the living modified organism:	SYN-E3272-5 × SYN-BT011-1 × SYN-IR604-5 × DAS-01507-1 × SYN-05307-1 × MON-00021-9
Transformation event:	Stacked maize event 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21
Introduced or Modified Traits:	Altered growth, development and product quality: Insect control and herbicide tolerance
Techniques used for modification:	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is produced by conventional breeding techniques that combine six individual maize transformation events, 3272, Bt11, MIR604, TC1507, 5307 and GA21.</p> <ul style="list-style-type: none"> • 3272 maize was produced by transformation of immature maize embryos derived from a proprietary <i>Zea mays</i> line via <i>A. tumefaciens</i>-mediated transformation. • Bt11 maize was produced using a protoplast transformation/regeneration system (Negrutiu <i>et al.</i>, 1987). • MIR604 maize was produced by transformation of immature maize embryos derived from a proprietary <i>Zea mays</i> line via <i>A. tumefaciens</i>-mediated transformation (Negrotto <i>et al.</i>, 2000).

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
	<ul style="list-style-type: none"> • TC1507 maize was produced with particle acceleration technology on embryogenic maize cells. • 5307 maize was produced by transformation of immature maize embryos derived from a proprietary <i>Z. mays</i> line via <i>A. tumefaciens</i>-mediated transformation (Negrotto <i>et al.</i>, 2000). • GA21 maize was produced via micro-projectile bombardment of maize suspension culture cells.
Description of gene modification:	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is a variety developed using conventional breeding techniques that combined the six individual transformation events 3272, Bt11, MIR604, TC1507, 5307 and GA21. No further genetic modification to produce this stack has taken place.</p> <ul style="list-style-type: none"> • 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize produces the transgenic proteins, AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS
Vector characteristics:	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize was developed by using conventional breeding techniques that combines transformation events 3272, Bt11, MIR604, TC1507, 5307 and GA21.</p> <ul style="list-style-type: none"> • No vector was involved in development of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize • The plasmid pNOV7013 was used for transformation of 3272 maize. • The plasmid pZO1502, cut with a <i>NotI</i> restriction enzyme, was used to produce Bt11 maize. The plasmid is a derivative of the commercially available plasmid pUC18. • The plasmid pZM26, a binary vector used for <i>Agrobacterium</i>-mediated plant transformation, was used to generate MIR604 maize. • The PHI8999A fragment of vector PHP8999 was used for the transformation of TC1507 maize. • Plasmid pSYN12274 was used to generate 5307 maize. • A <i>NotI</i> restriction fragment from the plasmid pDPG434 was used to transform GA21 maize. The plasmid is derived from a pSK-vector which is commonly used in molecular biology and is derived from pUC19.
Insert or inserts (Annex III.9(d)):	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize was developed using conventional breeding techniques that combines 3272, Bt11, MIR604, TC1507, 5307 and GA21 maize.</p> <p>Southern blot analyses confirmed that the DNA hybridization patterns for 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize corresponds to the hybridization bands observed for the single events. Thus, 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize produces the transgenic proteins, AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS present in the six individual transformation events. This indicates that the integrity of the transgenic inserts from the single events were preserved during conventional breeding to produce 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize.</p>
Recipient organism or parental organisms (Annex III.9(a)):	
Taxonomic name/ status of recipient or parental organisms:	<p>Family name: Poaceae Genus: <i>Zea</i> Species: <i>Z. mays</i> L. Subspecies: <i>Z. mays</i> ssp. <i>mays</i></p>
Common name of recipient or parental organisms:	<p>Maize.</p>
Point of collection of recipient organisms:	<p>Maize originates from the Mesoamerican region, i.e. Mexico and Central America (CFIA, 2003).</p>

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Characteristics of recipient or parental organisms related to biosafety:	<p><i>Z. mays</i> reproduces sexually via the production of seed. Although maize is an allogamous species (capable of cross-fertilization), both self-fertilization and cross-fertilization are usually possible.</p> <p>Most maize varieties are protoandrous so pollen shedding precedes silk emergence by up to five days. Pollen dispersal is limited by several factors, including large size (0.1 mm diameter), rapid settling rate and short survivability. Greater than 98% of the pollen settles to the ground within a maximum distance of 25-50 meters of its source (EEA, 2002; Jarosz <i>et al.</i>, 2005). Shed pollen typically remains viable for 10 to 30 minutes, but may remain viable longer under refrigerated and humid conditions (Coe <i>et al.</i>, 1988; Herrero and Johnson, 1980; Hoekstra <i>et al.</i>, 1989; Jones and Newel, 1948). Fertilization is affected by a number of complicating factors, such as genetic sterility factors and differential growth rates of pollen tubes.</p> <p>1. Sexual compatibility with other cultivated or wild plant species, including the distribution in South Africa of the compatible species. As there are no wild relatives of maize in South Africa, the potential for genetic transfer and exchange with other organisms is limited to other maize plants. Maize is wind pollinated and pollen distribution and viability depends on prevailing wind patterns, humidity, and temperature. The frequency of cross-pollination and fertilization depends on co-availability of fertile pollen and receptive plants. Wild <i>Zea</i> species have no pronounced weedy tendencies (CFIA, 2003).</p> <p>2. Survivability</p> <p>(a) Ability to form structures for survival or dormancy Maize is an annual crop. Seeds are the only survival structures; they cannot be dispersed without mechanical disruption of the cobs and show little or no dormancy. Natural regeneration from vegetative tissue is not known to occur.</p> <p>(b) Specific factors affecting survivability Survival of maize is dependent upon temperature, seed moisture, genotype, husk protection and stage of development. Maize seed can only survive under a narrow range of climatic conditions. The biology of maize means that other than deliberate cultivation, the only means by which it can persist in the environment is accidental dispersal of kernels into disturbed ground during harvest or transport; maize cannot reproduce vegetatively (OECD, 2003). Maize kernels spilled in fields during harvest may germinate immediately and seedlings may be killed by frost (Miedema, 1982; OECD, 2003); however, maize can occur as a volunteer weed in areas with mild winters, or when seeds germinate in the spring (OECD, 2003). Volunteers are easily controlled with herbicides or other agronomic practices (Owen, 2005).</p> <p>Maize kernels spilled into disturbed soil outside agricultural field can germinate to produce occasional feral plants; however, even in areas with mild winters, persistent or invasive populations of feral maize are not observed in South Africa, presumably because of low seed dispersal and low seedling survival due to retention of kernels on the ear (Doebley, 2004; Warwick and Stewart, 2005; OECD, 2003).</p> <p>3. Dissemination:</p> <p>(a) ways and extent of dissemination Maize dissemination may be accomplished through seed dispersal. Seed dispersal does not occur naturally due to the structure of the ear (OECD, 2003). Maize has a large ear with 500 or more kernels attached to its central axis.</p>

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Characteristics of recipient or parental organisms related to biosafety:	<p>The kernels are naked and easily digested (cannot survive through the digestive tracts of birds and mammals) and so cannot be dispersed by animals. As ears of maize do not shatter, any ears left on the plant fall to the ground with all the kernels attached; when the hundreds of seeds on the ear germinate, the emerging plants are unable to obtain adequate light and soil to grow and reproduce (Doebley, 2004).</p> <p>Dissemination may also occur via pollen and pollen flow. Pollen dispersal is influenced by wind and weather conditions and is limited by several factors, including large size (0.1 mm diameter), rapid settling rate, short survivability, and physical barriers. Greater than 98% of the pollen settles to the ground within a maximum distance of 25-50 meters from its source (EEA, 2002; Jarosz <i>et al.</i>, 2005).</p> <p>(b) specific factors affecting dissemination</p> <p>Maize has a polystichous (arranged in many rows) female inflorescence (group of flowers), called the ear, on a stiff central spike (cob) enclosed in husks (modified leaves). Because of the structure of the ears, seed dispersal of individual kernels does not occur naturally. Maize is non-invasive of natural habitats (OECD, 2003). The rate of dissemination via pollen will be influenced by the size of pollen, wind direction and speed, other weather conditions such as rainfall, the presence of barriers and the degree of synchrony of flowering. Maize pollen is large and heavy and tends to be deposited close to the source plant. In addition, most maize varieties are protoandrous so pollen shedding precedes silk emergence by up to five days.</p> <p>Pollen dispersal is influenced by wind and weather conditions and is limited by several factors, including large size (0.1 mm diameter), rapid settling rate, short survivability, and physical barriers. The pollen grain has a relatively thin outer membrane that gives little environmental protection, consequently shed pollen typically remains viable only for 10 to 30 minutes, but may remain viable longer under refrigerated and humid conditions (Coe <i>et al.</i>, 1988; Herrero and Johnson, 1980; Hoekstra <i>et al.</i>, 1989; Jones and Newel, 1948). Pollen release can be prevented by detasselling and genetic sterility.</p> <p>4. Geographical distribution of the plant.</p> <p>Maize is the world's most widely planted cereal with very diverse morphological and physiological traits; it is grown on approximately 185 million hectares worldwide (FAOSTAT, 2015¹⁵). Maize is distributed over a wide range of conditions: from latitudes 50° North to 50° South, below sea level of the Caspian plains up to 3000m in the Andes Mountains and from semi-arid regions to arid regions (Russell and Hallauer, 1980). The greatest maize production occurs where the warmest month isotherms range between 21° and 27° C and the freeze-free season lasts 120-180 days.</p> <p>5. Other potential interactions, relevant to the GMO, of the plant with organisms in the ecosystem where it is usually grown, or elsewhere, including information on toxic effects on humans, animals and other organisms.</p> <p>Maize is known to interact with other organisms in the environment including insects, birds, and mammals. It is susceptible to a range of fungal diseases and insect pests, as well as to competition from surrounding weeds (OECD, 2003). Maize is extensively cultivated and has a history of safe use for human food and</p>

¹⁵ FAOSTAT. 2015. Statistic Division, Food and Agriculture Organization of United Nations, Rome Italy. <http://faostat3.fao.org/download/Q/QC/E> (accessed June 2015)

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Characteristics of recipient or parental organisms related to biosafety:	<p>animal feed. No significant native toxins are reported to be associated with the genus <i>Zea</i> (CFIA, 2003). As there are no wild relatives of maize in South Africa, the potential for genetic transfer and exchange with other organisms is limited to other maize plants.</p> <p>Maize is wind pollinated and pollen distribution and viability depends on prevailing wind patterns, humidity, and temperature. The frequency of cross-pollination and fertilization depends on the co-availability of fertile pollen and receptive plants.</p> <p>6. Wild plant species</p> <p>Wild <i>Zea</i> species have no pronounced weedy tendencies (CFIA, 2003). The only wild taxa known to hybridise spontaneously with maize are species of teosinte (OECD, 2003; Owen, 2005). Annual teosinte is a wind-pollinated grass. Out-crossing and gene exchange between <i>Z. mays</i> ssp. <i>mexicana</i> and <i>Z. mays</i> ssp. <i>mays</i> do occur, but hybrids have reduced seed dispersal and often reduced viability (OECD, 2003). The natural distribution of <i>Z. mays</i> ssp. <i>mexicana</i> is limited to Mexico and Central America (CFIA, 2003). Although some <i>Tripsacum</i> species (<i>T. dactyloides</i>, <i>T. floridanum</i>, <i>T. lanceolatum</i>, and <i>T. pilosum</i>) can be crossed with <i>Z. mays</i> ssp. <i>mays</i>, hybrids have a high degree of sterility and are genetically unstable. Out-crossing of maize and <i>Tripsacum</i> species is not known to occur in the wild (OECD 2003). No <i>Tripsacum</i> species are present in South Africa.</p> <p><i>Tripsacum</i> species are geographically restricted to the Americas (CFIA, 2003). Only two species are known to be found north of Mexico: <i>T. floridanum</i> which is native to the southern tip of Florida, USA; and <i>T. dactyloides</i> (Eastern gammagrass), which can be found in the northern US. The center of diversity for <i>Tripsacum</i> is the western slopes of Mexico, the same area where teosinte is frequently found (CFIA, 2003). <i>Tripsacum</i>-annual teosinte hybrids have not been produced.</p>
Centre(s) of origin of recipient or parental organisms:	Maize originates from the Mesoamerican region, i.e. Mexico and Central America (CFIA, 2003).
Centres of genetic diversity, if known, of recipient or parental organisms:	Maize originates from the Mesoamerican region, i.e. Mexico and Central America (CFIA, 2003).
Habitats where the recipient or parental organisms may persist or proliferate:	Maize originates from the Mesoamerican region, i.e. Mexico and Central America (CFIA, 2003). Please refer to information provided above regarding geographical distribution of the maize plant. Maize is incapable of sustained reproduction outside domestic cultivation and is non-invasive of natural habitats (OECD, 2003).
Donor organism or organisms (Annex III.9(b)):	
Taxonomic name/status of donor organism(s)	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize was developed using conventional breeding techniques that combines 3272, Bt11, MIR604, TC1507, 5307 and GA21 maize.</p> <p>The donor organisms of the single events are:</p> <ul style="list-style-type: none"> • <i>Thermococcales</i> The AMY797E α-amylase enzyme is a chimeric enzyme derived from wild-type α amylases from the archaeal order <i>Thermococcales</i>. <i>Thermococcales</i> are anaerobic Archaea belonging to the kingdom Euryarchaea. Archaeal organisms are widespread in nature (Landry <i>et al.</i>, 2003). <p>An alpha-amylase derived from the same wild-type α-amylases of the archaeal order <i>Thermococcales</i> as AMY797E was developed for use as</p>

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Taxonomic name/ status of donor organism(s)	<p>an enzyme in the hydrolysis of edible starch to produce various food products and for ethanol production for use in alcoholic beverages.</p> <ul style="list-style-type: none"> • <i>Bacillus thuringiensis</i> The source of the native <i>cry1Ab</i>, <i>cry3A</i>, <i>eCry3.1Ab</i> and <i>cry1F</i> genes is <i>B. thuringiensis</i>. The species is a member of the genus <i>Bacillus</i>, a diverse group of rod-shaped, gram-positive, facultative anaerobic, spore forming bacteria. <i>B. thuringiensis</i> occurs naturally and ubiquitously in the environment. It is a common component of the soil microflora and has been isolated from most terrestrial habitats (Glare and O'Callaghan, 2000). • <i>Escherichia coli</i> The source of the <i>pmi</i> gene is the common bacterium <i>E. coli</i>, K-12 strain. <i>E. coli</i> belongs to the Enterobacteriaceae, a relatively homogeneous group of rod-shaped, gram-negative, facultative bacteria. Members of the genus <i>Escherichia</i> are ubiquitous in the environment and found in the digestive tract of vertebrates, including humans. The K-12 strains from <i>E. coli</i> have a long history of safe use and are commonly used as protein production systems in many commercial applications. • <i>Streptomyces viridochromogenes</i> The source of the <i>pat-09</i> gene is the aerobic bacterium <i>S. viridochromogenes</i> strain Tu494, a gram-positive, sporulating, soil inhabiting bacterium widespread in the environment and with a long history of safe use (OECD, 1999). • <i>Zea mays</i> The source of the <i>epsps</i> gene is maize (<i>Z. mays</i>). Maize is the world's most widely planted cereal. It is grown between latitudes 50° north and 50° south and from below sea level to altitudes of more than 3000m. Maize is believed to have been domesticated about 6000 to 10000 years ago from teosinte (Doebley, 2004). Maize is now a main commodity crop used for food and feed with a long history of safe use (OECD, 2003).
Common name of donor organism(s):	<i>B. thuringiensis</i> , <i>E. coli</i> and <i>S. viridochromogenes</i> are bacteria. <i>Thermococcales</i> is a hyperthermophilic micro-organism Maize is a commodity crop.
Point of collection or acquisition of donor organism(s):	<i>B. thuringiensis</i> , <i>E. coli</i> , <i>S. viridochromogenes</i> , <i>Thermococcales</i> and maize are widespread in the environment.
Characteristics of donor organism(s) related to biosafety:	<i>B. thuringiensis</i> , <i>E. coli</i> , <i>S. viridochromogenes</i> , <i>Thermococcales</i> and maize are widely prevalent in the environment.
Intended use and receiving environment	
Intended use of the LMO:	Commodity clearance of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in South Africa.
Receiving environment:	No environmental release
Risk assessment summary	
Detection/ Identification method of the LMO:	<p>3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize contains all the transgenes in the component events and produces the following proteins: AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS.</p> <p>For the verification of the performance of the 3272, Bt11, MIR604, TC1507, 5307, and GA21 event-specific detection methods on 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize, DNA samples consisting of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 DNA and nontransgenic, near-isogenic DNAs were provided for internal verification by the European Union Reference Laboratory for Genetically Modified Food and Feed (EURL GMFF, Ispra).</p>

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Detection/ Identification method of the LMO:	<p>The detection methods developed for the single events will also detect the individual events in 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize.</p> <p>For specific detection of Bt11 maize genomic DNA, a real-time quantitative TaqMan® PCR method has been developed using the taxon specific target sequence (<i>Adh1</i>) and the Bt11 target sequence. One of the oligonucleotide primers is located within the maize specific flanking sequence and the other is located in the insert. This method has been validated for use by the EU-RL GMFF and can be found on the EU-RL GMFF website: http://gmo-crl.jrc.ec.europa.eu/summaries/Bt11_CRLVL1007_Validated_Method%20doc.pdf and http://gmo-crl.jrc.ec.europa.eu/summaries/Bt11_CRLVL1007_Val_Report.pdf.</p> <p>For specific detection of MIR604 maize genomic DNA, a real-time quantitative TaqMan® PCR method has been developed by Syngenta using the taxon specific target sequence (<i>Adh1</i>) and the MIR604 target sequence. One of the oligonucleotide primers is located within the maize specific flanking sequence and the other is located in the insert. This method has been validated for use by the EU-RL GMFF and can be found on the EU-RL GMFF website: http://gmo-crl.jrc.ec.europa.eu/gmomethods/entry.do?db=gmometh&query=ac%3ASYN-IR604-5&id=qt_zm_013.</p> <p>For specific detection of TC1507 maize genomic DNA, a real-time quantitative TaqMan® PCR method has been developed using the taxon specific target sequence (<i>Adh1</i>) and the TC1507 target sequence. This method has been validated for use by the EU-RL GMFF and can be found on the EU-RL GMFF website: http://gmo-crl.jrc.ec.europa.eu/summaries/TC1507-WEB-Protocol-Validation.pdf and http://gmo-crl.jrc.ec.europa.eu/summaries/TC1507-report_mm.pdf.</p> <p>For specific detection of 5307 maize genomic DNA, a real-time quantitative TaqMan® PCR method has been developed by Syngenta using the taxon specific target sequence (<i>Adh1</i>) and the 5307 target sequence. One of the oligonucleotide primers is located within the maize specific flanking sequence and the other is located in the insert. This method has been validated for use by the EU-RL GMFF and can be found on the EU-RL GMFF website: http://gmo-crl.jrc.ec.europa.eu/gmomethods/docs/QT-EVE-ZM-002.pdf.</p> <p>For specific detection of GA21 maize genomic DNA, a real-time quantitative TaqMan® PCR method has been developed using the taxon specific target sequence (<i>Adh1</i>) and the GA21 target sequence. This method has been validated by the EU-RL GMFF and can be found on the EU-RL GMFF website: http://gmo-crl.jrc.ec.europa.eu/summaries/GA21Syngenta_validated_Method_correctedVersion1.pdf and http://gmo-crl.jrc.ec.europa.eu/summaries/GA21Syng_val_report_correctedVersion1.pdf.</p>
Evaluation of the likelihood of adverse effects:	<p>Maize is planted and harvested as an annual crop. Wild populations with which it could cross-pollinate are uncommon, and not prevalent in South Africa. Maize dissemination can only be accomplished through seed dispersal which does not occur naturally due to the structure of the ear (OECD, 2003). Natural regeneration from vegetative tissue in the field is not known to occur. Maize is predominantly wind pollinated. Plants produce pollen for 10-13 days according to the genotype. Shed pollen typically remains viable only a short time but may remain viable longer under humid conditions. Pollen dispersal is influenced by wind and weather conditions and is limited by several factors, including large size (0.1 mm diameter), rapid settling rate, short survivability, and physical barriers.</p>

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Evaluation of the likelihood of adverse effects:	<p>More than 98% of the pollen settles to the ground within a maximum distance of 25-50 meters from its source (EEA, 2002). The pollen grain has a relatively thin outer membrane that gives little environmental protection, consequently shed pollen typically remains viable only for 10 to 30 minutes, but may remain viable longer under refrigerated and humid conditions (Coe <i>et al.</i>, 1988; Herrero and Johnson, 1980; Hoekstra <i>et al.</i>, 1989; Jones and Newel, 1948). Thus, even in the rare event that small amounts of maize kernels of the stacked product could accidentally find their way into the environment during importation of this product by grain traders, their survival would be very unlikely as maize is highly domesticated and cannot survive without human intervention (Niebur, 1993; Owen, 2005). In addition, in the rare event that these maize plants were to survive they could be easily controlled using any of the current agronomic measures taken to control other commercially available maize.</p> <p>The comparative assessment of composition, whole food safety, phenotypic and agronomic traits conducted for 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize and near-isogenic nontransgenic maize has shown that the 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize does not contain altered agronomic and phenotypic characteristics apart from the intended modification, which is insect control and herbicide tolerance. It leads to the conclusion that this maize is substantially equivalent to conventional maize.</p> <p>The persistence or invasiveness of the 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize when compared to nontransgenic maize has not increased. There are no data indicating that AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS protein expression results in altered seed dormancy, over wintering capacity, or other characteristics that would alter the prevalence of volunteer maize in subsequent growing seasons.</p> <p>Maize has a long history of safe use and the crop itself causes few health problems. Expression of the proteins AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS in food and feed products derived from 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is unlikely to cause adverse effects through toxicity or allergenicity based on the following information:</p> <ul style="list-style-type: none"> • Well-characterized specificity of the biological activity of AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins. • No known adverse effects of prior exposure to AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins in food or feed. • AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins have no significant sequence identity to known toxins with known adverse effects in humans or animals. • AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins have no detectable acute toxicity in mice at high doses. • AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins have no significant amino acid homology to known or putative allergenic protein sequences that are biologically relevant or have implications for allergenic potential. • AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins are degraded in simulated gastric fluid.

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
	<ul style="list-style-type: none"> • Low dietary exposure to AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins. <p>In addition, margins of dietary exposure have been calculated by comparing the NOEL from the acute oral toxicity studies of AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS protein to the expected intake level. The results indicate that expected levels of intake of AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS through consumption of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in South Africa will be very low. Margins of dietary exposure for the AMY797E, PMI, Cry1Ab, PAT, mCry3A, MIR604 PMI, Cry1F, eCry3.1Ab, and mEPSPS proteins, supporting the conclusion that no unacceptable risk is posed to consumers.</p> <p>Maize is known to interact with other organisms in the environment including insects, birds, and mammals. It is susceptible to a range of fungal diseases and insect pests, as well as to competition from surrounding weeds (OECD, 2003). However, the importation and use as food, feed or for processing of grain from stacked 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is highly unlikely to have environmental effects through interactions with non-target organisms.</p>
Evaluation of the consequences:	<p>Cultivation of maize derived from 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in South Africa is not within the scope of this application. As discussed above, the conclusion reached from the detailed evaluation of the characteristics of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize and the likelihood of any adverse effects, is that this maize is substantially equivalent to conventional maize and that it is highly unlikely to have any adverse effects on human or animal health or the environment.</p> <p>Therefore, no adverse consequences will result from the importation and use as food, feed or for processing of grain from stacked 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in South Africa.</p>
Overall risk:	<p>The overall risk of potential adverse effects from importation of and use as food, feed or for processing of grain from stacked 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is negligible. None of the components introduced into 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize are considered to be dangerous to human health or the environment.</p> <p>There is no indication that the combination of 3272, Bt11, MIR604, TC1507, 5307 and GA21 maize by conventional breeding would result in any adverse effects or changes in maize toxicity to humans or animals. None of the proteins expressed by 3272, Bt11, MIR604, TC1507, 5307 and GA21 maize are known to be toxic to humans or animals and there are no known precedents where interactions between non-toxic proteins lead to toxic effects (FIFRA SAP, 2004). In addition, compositional analysis and broiler feeding studies, have confirmed that the 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize is equivalent in composition to conventional maize and is as safe and nutritious as conventional maize. The overall risk for potential adverse effects on human and animal health or the environment as discussed in this document is thus negligible in the context of the intended uses of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize.</p>
Recommendation:	Full compliance with permit conditions and other risk management conditions imposed by the National Competent Authority.
Actions to address uncertainty regarding the level of risk:	Not applicable.

Syngenta 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize
September 2015
CONFIDENTIAL BUSINESS INFORMATION DELETED

Risk assessment: 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize in accordance with Annex III of Cartagena Protocol on Biosafety	
Additional information	
Availability of detailed risk assessment information:	More information on the stacked product and the assessment of risk can be obtained from the Commodity clearance application of 3272 × Bt11 × MIR604 × TC1507 × 5307 × GA21 maize.
Any other relevant information:	None
Attach document:	Not applicable
Notes:	Not applicable