Executive Summary: Herbicide-Tolerant MZHG0GJ Corn

Syngenta Crop Protection LLC, on behalf of Syngenta AG and its affiliates, has developed MZHG0JG corn (maize; *Zea mays* L.), a new cultivar that has been genetically modified to tolerate glyphosate and glufosinate-ammonium herbicides. Most corn currently grown in the United States and Canada consists of herbicide-tolerant transgenic varieties. MZHG0JG corn will offer growers much-needed flexibility to use herbicides with two alternative modes of action in their weed management programs and will help mitigate and manage the evolution of herbicide resistance in weed populations.

MZHG0JG corn plants contain the transgene *mepsps-02*, which encodes the enzyme mEPSPS, and the transgene *pat-09*, which encodes the enzyme phosphinothricin acetyltransferase (PAT). The native 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from *Z. mays* is involved in the synthesis of aromatic amino acids and is inhibited by glyphosate. The mEPSPS produced by MZHG0JG corn has low affinity for glyphosate, thus conferring tolerance to glyphosate in herbicide products. The transgene *pat-09* was derived from the soil bacterium *Streptomyces viridochromogenes.* PAT acetylates glufosinate-ammonium, thus inactivating it and conferring tolerance to glufosinate-ammonium in herbicide products. PAT was used as a selectable marker in the development of MZHG0JG corn.

MZHG0JG corn was produced by transformation of immature embryos of proprietary variety NP2222 via *Agrobacterium tumefaciens*–mediated transformation. The region of the plasmid vector, pSYN18857, intended for insertion into the corn genome included gene-expression cassettes for *mepsps-02* and *pat-09*. The *mepsps-02* expression cassette consisted of the *mepsps-02* coding region regulated by a corn ubiquitin promoter (Ubi58-02) and terminator (Ubil58-02), as well as the figwort mosaic virus (FMV-05), cauliflower mosaic virus 35S (35S-05), and tobacco mosaic virus (TMV-03) enhancer sequences and an optimized transit peptide (OTP-02). The *pat-09* expression cassette consisted of the *pat-09* coding region regulated by a 35S promoter from cauliflower mosaic virus (35S-19) and the nopaline synthase (NOS) terminator sequence from *A. tumefaciens* (NOS-05-01).

Genetic characterization studies demonstrate that MZHG0JG corn contains, at a single locus within the corn genome, a single copy of each of the following functional elements: *mepsps-02*, *pat-09*, FMV-05 enhancer, 35S-05 enhancer, OTP-02 transit peptide, Ubi158-02 promoter, TMV-03 enhancer, Ubi158-02 terminator, 35S-19 promoter, and NOS-05-01 terminator. No extraneous DNA fragments of these functional elements occur elsewhere in the MZHG0JG corn genome. Similarly, plasmid backbone sequence from transformation plasmid pSYN18857 is not present in the MZHG0JG corn genome. Analyses comparing the corn genomic sequence flanking the MZHG0JG insert with sequences in public databases indicate that the inserted DNA does not disrupt any known endogenous corn gene.

Southern blot analyses demonstrated that the MZHG0JG T-DNA insert is stably inherited from one generation to the next and that the MZHG0JG corn genome contains a single T-DNA insert. The observed segregation ratios for *mepsps-02* and *pat-09* in three generations of MZHG0JG corn plants indicated that they are inherited in a predictable manner, according to Mendelian principles. Analyses of grain and forage demonstrate that MZHG0JG corn is nutritionally and compositionally similar to, and as safe and nutritious as, conventional corn.

Well-characterized modes of action, physicochemical properties, and a history of safe use demonstrate that the mEPSPS and PAT proteins present in MZHG0JG corn present no risk of harm to humans or livestock that consume corn products or to wildlife potentially exposed to MZHG0JG corn.