Estimation of transgene introgression from GM soybean into Japanese wild soybean population

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Wild soybean (Glycine soja), the closest wild relative of GM soybean (Glycine max), is distributed widely in eastern Asia. Because of the low degree of hazard and exposure, Japanese government has permitted cultivation and the commodity of herbicide-tolerant GM soybean to be distributed in Japan. Currently, the question is being asked whether the scientific principles underlying the ERA already completed GM soybean can also be applied to the insect-protected or abiotic stress-tolerant GM soybean. The current paradigm that risk is a function of a hazard intensity and exposure degree is well accepted. So we are trying to establish a quantitative evaluation method for hazard intensity using the artificial hybrids and its progenies between the wild and non GM soybean. In order to predict future consequences of transgenes in wild populations, we have developed a computer simulation model for gene introgression. The simulations based on the parameters collected in experimental fields indicated that a transgene can be purged rapidly, within the first few generations, after hybridization under conditions of no selection pressure. The evaluation has been extended to natural habitats of wild soybean but this has posed some difficulties. The reaction of hybrids is far more complex in the competitive native weed population. The simulations of various parameter combinations from the natural habitats revealed that transgenes can persist in wild populations at very low frequency for a long time even with no selection pressure. This means that a quantitative evaluation of the hazard is necessary even if exposure is low. The focus of our studies has gradually shifted to the ERA of insect-protected GM soybean. Recent attempts to understand the degree of selection pressure on the Bt gene by insects in natural wild soybean population will also briefly introduce.

Keywords: Simulation, Hybrids, Natural habitats