Do glyphosate resistant feral plants and hay fields spread the transgene to conventional alfalfa seed fields?

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Alfalfa is the fourth largest crop by land area and worth roughly $10 billion grown on more than 18 million U.S. acres according to the U.S. Department of Agriculture. The Western U.S. is the most important production area for both alfalfa forage and alfalfa seed. In addition to meeting domestic needs, large amounts of alfalfa seed and hay produced in the US are being exported overseas. Because alfalfa is an insect pollinated crop, gene flow is a concern. Adding to this alfalfa readily naturalizes along roadsides, irrigation ditches, and unmanaged habitats; and feral plants can contribute to gene flow. The situation has become more complicated since the introduction of genetically engineered (GE) alfalfa to resist glyphosate herbicide. Due to cross-contamination of GE traits, many alfalfa producers are impacted by market sensitivity. Our objective was to determine gene flow from glyphosate resistant (GR) feral plants and hay fields to conventional seed fields. Alfalfa feral plants, seed and hay fields were mapped in the Fresno County, CA and Canyon County, ID in spring 2013. GR feral plants and hay fields (source) and conventional seed fields (sink fields), located at various distances from GR sources, were identified. Conventional seed fields were combine and hand harvested along field edges every 30 m. Original samples (seed used to plant the fields in 2013) were collected for initial assessment of AP and for determining baseline contamination, if any. For fields where no original seed sample was produced, leaf samples were collected instead to determine baseline AP. Harvested seed samples were threshed, cleaned, scarified, and tested for the transgene using seedling germination assay. Leaf samples were tested for trangene using AgraStrip® RUR Leaf TraitChek™ test strips. Distance from GR hay fields, distance from GR feral plants, pollinator abundance, elevation, aspect, and slope were also obtained. The relationship between AP proportion and distance to GR source fields will be modeled using nonlinear models. No AP was observed in conventional seed fields located nearby GR feral plants suggesting there is less likely for gene flow to occur. Pending completion of the analysis, further results will be presented.