6.1 Range and Scope of Transgenic Crops

Globally, the use of transgenic crops has increased rapidly during recent decades; they are now grown for food in 31 countries and for feed in 19 counties (Aldemita et al. 2015). The most commonly incorporated trait is herbicide tolerance (HT; e.g. crop tolerance to glyphosate and glufosinate), followed by insect resistance (IR; e.g. crops containing genes that produce insecticidal proteins derived from the soil bacterium *Bacillus thuringiensis* (Bt)) (Aldemita et al. 2015). Crops with stacked traits, those containing more than one trait, are becoming increasingly common. The crop with the largest number of varieties that contain single or stacked traits is maize, with stacked traits representing 30% of the total trait approvals (Aldemita et al. 2015). As of September 2013, for example, the USA Animal and Plant Health Inspection Service (APHIS) had approved 96 petitions for 145 transgenic crop releases to be sold as follows: maize, 30; cotton, 15; tomatoes, 11; soybeans, 12; rapeseed/canola, 8; potatoes, 5; sugar beets, 3; papaya, rice, and squash, 2 each; and alfalfa, plum, rose, tobacco, flax, and chicory, 1 each (Fernandez-Cornejo et al. 2014).

In 2015, 77% of maize and 79% of cotton in the USA had both herbicide-tolerant and insect-resistant traits. Other traits, such as resistance to bacterial, fungal and viral pathogens, continue to be developed and many new trait combinations have been released in recent years. For example, releases of transgenic cultivars with properties such as drought resistance increased from 1043 in 2005 to 5190 in 2013 (Fernandez-Cornejo et al. 2014). Increasing numbers of reports of herbicide resistance in weeds and insect pest resistance to Bt crops make it very clear that more comprehensive assessments of risks over longer temporal and larger spatial scales are required. The increase in the number and types of traits being engineered into crops indicates a need for assessments that account for different types of potential environmental effects beyond those associated with herbicide and pest resistance.
For example, it is important to evaluate changes in use of herbicides and pesticides due to adoption of genetically engineered crops. In the USA, for example, adoption of transgenic crops with herbicide resistance caused an increase of 239 million kg of herbicides to be used but adoption of transgenic crops with pest resistance traits caused a reduction of 56 million kg pesticides used for an overall increase of 183 million kg or approximately 7% from 1996 to 2011 (Benbrook 2012) (see also Chapter 12). These figures may underestimate the increase in pesticide use from 1996 to the present as they do not include the recent rapid rise in the use of neonicotinoid seed treatments (Douglas and Tooker 2015).

Viewing trends from an alternate perspective, Brookes and Barfoot (2015) estimate that global pesticide use with transgenic crops is 8.6% lower than it would have been if the most likely alternative controls were used, presumably with a concomitant reduction in adverse environmental impacts. In the USA, insecticide use on maize declined 10-fold from 1995 to 2010, consistent with the decline in European corn borer populations shown to be a direct result of Bt crop adoption (Fernandez-Cornejo et al. 2014). However, pest resistance to Bt proteins has increased substantially as well. For example, out of 27 sets of monitoring data, seven showed severe field-evolved resistance, eight showed less severe field-evolved resistance and 12 showed no evidence of decreased susceptibility to Bt proteins (Tabashnik and Carrière 2015).

Herbicide resistance in weed species has also increased substantially. For example, since glyphosate-tolerant crops were introduced in 1996, 32 glyphosate-resistant weed species have been identified worldwide (Heap 2016). Because of the use of transgenic crops, total herbicide use in the USA has been projected to increase from ~1.5 kg ha\(^{-1}\) in 2013 to more than 3.5 kg ha\(^{-1}\) in 2025 (Mortensen et al. 2012).

### 6.2 Conceptual Framework

Although, as we detail below, the effects of transgenic crops or any pest management tactic can be compounded (additively, antagonistically or synergistically) over wide spatial and temporal scales, most pest management decisions are made at the scale of a single field in a single season. The major factor determining if a given effect is positive or negative from the perspective of an individual grower is the function or guild of the non-target species affected. We examine primary effects on two non-target guilds, herbivorous insects and non-crop plants, and then contrast these effects with the secondary effects on four guilds: pollinators, decomposer fauna, predators (in a broad sense) and micro-organisms. Finally, we examine the effects on all groups across a broader spatial and temporal scale. As far as possible, we try to draw a distinction between quantified or at least identified effects as distinct from potential effects.

### 6.3 Primary Effects

#### 6.3.1 Effects on Non-target Herbivorous Insects

Non-target arthropods may be exposed to the insecticidal proteins termed ‘plant incorporated protectants’ or PIPs (www3.epa.gov/pesticides/chem_search/reg_actions/pip/index.htm) present in genetically modified crops. Exposure can occur by direct
feeding on plant tissues, ingestion of insecticidal proteins in the soil, feeding on prey that have ingested insecticidal proteins, and indirectly through reductions in prey/host populations (Figure 6.1) (Obrycki et al. 2001). We define primary exposure as effects from direct feeding on the focal transgenic crop and this narrows our scope to insects such as those in Lepidoptera (moths and butterflies) and Coleoptera (beetles) that feed on the two primary Bt crops (maize and cotton). Bt toxins are generally more specific than conventional insecticides and these two orders of insects are also the selective targets. However, toxicity to other orders has been demonstrated (Amichot et al. 2016).

In general, since any organism feeding on a crop plant can be considered a pest, growers will not alter their pest management strategies to minimize direct effects on species that feed on the crop plant even if these species are not the targeted pest. The monarch butterfly, Danaus plexippus, is one example of a species that is not a target pest but is affected by directly consuming a plant tissue (pollen) (Losey et al. 1999). Grower behaviour could change if aggregate impacts became severe enough that one or more directly impacted species was listed as endangered or threatened at broader levels. The probability that a directly affected species would be endangered is low since organisms that feed on common crop plants are generally not rare (Losey et al. 2003). It is important to note that some growers might choose to alter their use of transgenic crops to conserve iconic species even if such changes were not legally required or necessary to optimize profitability. The ‘willingness to pay’ or at least forego potential profits has been quantified for certain insects, including the monarch butterfly (Diffendorfer et al. 2013). Growers could decide to plant non-transgenic varieties to minimize environmental impacts and, in some cases, to take advantage of broader scale suppression of pests (e.g. Ostrinia nubilalis on maize in the USA) (Hutchison et al. 2010).

6.3.2 Effects on Non-crop Plants

Plants other than the focal crop (e.g. weeds) in a production field are potential competitors with the crop itself and are thus usually also considered pests. Since these plants can reduce yield and crop quality, any negative impact on them from the use of
transgenic crops would be seen as positive and would be facilitated rather than avoided by the grower. The use of herbicides, such as glyphosate, with herbicide-tolerant crops is very effective at removing essentially all weeds that have not developed resistance. In some situations, reduction in non-crop plant density and diversity creates an ‘ecological desert’ (Obrycki et al. 2001) that can lower the density or diversity of the animals that depend on those plant species. Plant diversity is known to enhance and facilitate ecosystem services (Egan and Mortensen 2012; Quijas et al. 2012) (see also Chapter 7), especially by supporting pollinators.

Although recent studies did not find significant impact of herbicide-tolerant crops on plant diversity in general (Schwartz et al. 2015; Young et al. 2013), this effect has been reported for specific herbivore groups including monarch butterflies (Pleasants and Oberhauser 2012) and birds (Taylor et al. 2006).

6.4 Secondary Effects

6.4.1 Effects on Beneficial Species

In contrast to the profile of effects of PIP crops on non-target plants or herbivorous insects, beneficial insects (i.e. those that enhance crop production) are presumably less likely to be affected because they are either unaffected by the insecticidal protein or do not ingest it – a prerequisite for the Bt protein to have insecticidal activity. However, any impact on beneficial species is also more likely to have a negative effect on the services they provide and this could lower yield and profitability (see Figure 6.1). Functional groups of beneficial insects (beneficials) that might be affected include pollinators, decomposers and predators (or parasitoids) of insect pests and weeds. Potential effects and consequences for each group of beneficials are described below.

6.4.1.1 Pollinators

The largest and most important group of pollinators is the Hymenoptera, specifically bees. No currently registered product is targeted to affect Hymenoptera so it is not surprising that there are very few effects reported. Malone and Burgess (2009) reviewed 22 studies (some within the same publication) that tested for effects of the Bt toxin on bees and only two found any effects and these were variable. They did find more potential for effects with other types of toxins (e.g. protease inhibitors) that may be more widely incorporated in the future (Malone and Burgess 2009). Loss of plant diversity following herbicide application could have a negative impact on pollinators. Soybeans and maize are not insect pollinated but there is potential for impact on cotton (Han et al. 2010) or other crops (e.g. fruits or vegetables) on the same farm.

6.4.1.2 Decomposer Fauna

Most decomposer fauna live in or on the soil and are thus easily overlooked. However, between 60% and 90% of net primary production is processed by decomposer organisms (Brady and Weil 2008). While the bulk of this processing is accomplished by bacteria and fungi (addressed later in this chapter), larger organisms, including worms and arthropods, play an important role by modifying physical and chemical properties of the plant material and greatly enhancing decomposition efficiency (Meyer et al. 2011). There are
relatively few studies that address the potential effects of transgenic crops on meso- or macroinvertebrates, but one of the few studies found a negative impact on night crawlers (*Lumbricus terrestris*) (Zwahlen et al. 2003), while another found no effect on the earthworm *Eisenia fetida* or the springtail *Folsomia candida* (Clark and Coats 2006). These mixed results, coupled with the lengthy retention time of a few Bt proteins in soil (Cry1Ab, Stotzky 2000; Cry1Ac, Sun et al. 2007), suggest that further study in this area is warranted.

In a study combining assessment of both diversity and function, Londoño-R et al. (2013) examined in-field decomposition rates and diversity of microarthropod decomposers after 5 months in a field trial in which residues from two Cry1Ab Bt corn hybrids were compared to their non-transgenic counterparts in litterbags placed on the soil surface or buried at 10 cm depth. Microarthropod diversity varied by residue placement and by plant part, but there was no significant effect of genotype. Looking across a wide range of organisms, Saxena and Stotzky (2001) incorporated Cry1Ab Bt maize root exudates or plant biomass in soil in a laboratory experiment and found that these did not significantly affect populations of earthworms, nematodes, protozoa, bacteria or fungi 45 days after the soil was amended compared to non-transgenic maize.

### 6.4.1.3 Predators

Predators, used here in the broad sense of any organism (including parasitoids and parasites) that preys on either insect pests or weeds, suppress the majority of potential pest or weed populations before they reach economically damaging levels (Losey and Vaughan 2006). One unintended effect of the use of pesticides to control pests is that they can interfere with the pest suppression delivered by the natural enemies of pests. Since some of the most important predators of insect pests and weed seeds are beetles, there is the potential for negative impacts especially from crops expressing the Cry3 Bt toxin that is toxic to beetles.

Stephens et al. (2012) reviewed 24 laboratory and field studies involving the Cry1 Bt protein (primarily active against lepidopteran insects) and 11 studies involving the Cry3 protein. They reported five and two cases of negative impact for Cry1 and Cry3, respectively (Stephens et al. 2012). Based on multi-year large-scale field studies, this same study reports that densities of carabids and the coccinellid *Harmonia axyridis* were significantly lower in Bt maize plots compared to control plots. Using data from the same field study, DiTommaso et al. (2014) also report a reduction in the rate of weed seed feeding in Bt maize plots compared to control plots. It is important to note that, while these studies found differences between Bt and control plots, they did not find differences between the Bt and the insecticide plots, implying that the effects of Bt were no worse than the conventional (herbicide) alternative. This comparison is important because risk assessments should evaluate appropriate alternative management strategies in order to provide results that can support improved decision making by both growers and regulators.

### 6.4.2 Effects on Non-target Micro-organisms

Micro-organisms play a crucial role in decomposition so any negative effect on this group has implications for the system as a whole. Saxena and Stotsky (2001) reported reduced decomposition rates for Cry1Ab Bt maize in a laboratory experiment and attributed this
to a higher lignin content in the transgenic maize. Flores et al. (2005) also found reduced rates of decomposition for Bt residues of rice (Cry1Ab), tobacco (Cry1Ac), canola (Cry1Ac), cotton (Cry1Ac) and potato (Cry3A) compared to their non-Bt isolines in a laboratory study. These results could not be explained by differences in lignin content and no other potential mechanism for observed results was proposed. These results have not been replicated and a series of multi-year field trials in which different varieties of Cry1Ab rice, Cry3Bb maize and Cry1Ac cotton were grown did not yield similar results. Instead, in field-based litterbag studies where Bt and non-Bt residues were placed either at the soil surface or buried at 10 cm depth, no differences in decomposition between transgenic and non-transgenic varieties were found for two varieties of Cry1Ab maize (Londoño-R et al. 2013; Tarkalson et al. 2007), one variety of Cry3Bb maize (Xue et al. 2011), two varieties of Cry1Ab rice (Lu et al. 2010a, 2010b; Wu et al. 2009a) and one variety of Cry1Ac cotton (Kumari et al. 2014). Instead, in all cases, differences in decomposition were driven by residue placement (surface versus buried) and plant part, with leaves decomposing most quickly and cobs (for maize) and roots (for rice) decomposing more slowly. In no case was genotype a significant factor controlling residue decomposition.

In several of these field trials, bacterial and fungal decomposer community diversity in the litterbag samples was also investigated using molecular fingerprinting methods. For three varieties of Cry1Ab rice (Lu et al. 2010a, 2010b; Wu et al. 2009b), one variety of Cry3Bb maize (Xue et al. 2011) and one variety of Cry1Ab maize (Londoño-R et al. 2013), no differences in bacterial or fungal communities colonizing the residues could be attributed to genotype (Bt versus non-Bt), except as found by Lu et al. (2010b). Rather, residue placement and plant part were again the major drivers of changes in community composition observed. The singular difference in community composition observed for Cry1Ab rice in a paddy soil was in the fungal community decomposing Bt rice roots compared to the non-Bt rice (Lu et al. 2010b). However, no differences in the fungal communities decomposing rice straw were observed.

Overall, these results indicate that plant tissue composition is a very strong driver controlling decomposition rate, regardless of the presence of the Bt protein. Bacteria and fungi produce exoenzymes, such as proteases, to decompose soil proteins, such as the Bt protein. There is no mechanism that has been demonstrated or proposed that would suggest microbial decomposers would be directly affected in their ability to decompose these proteins. The persistence of the Cry1Ab protein from Bt maize reported by Stotzky (2000) is most probably due to adsorption of the protein on clays or soil organic matter such that proteases are unable to access them. For Cry3Bb maize, residue and protein decomposition is rapid, with the protein detectable in the rhizosphere only during active plant growth and undetectable after harvest (Xue et al. 2014). Icoz and Stotzky (2008) also found that the Cry3Bb protein does not persist in soil. The Cry3Bb maize is intended to control the corn root worm (Diabrotica spp.). Xue et al. (2014) found that, among 15 different genotypes of Cry3Bb maize, including several with stacked HT resistance traits, all displayed low expression in the roots and the protein decomposed very readily. These combined characteristics produced a relatively weak, short-lived presence of the toxin. While that profile of traits could represent relatively weak selection pressure, it apparently also posed only a minor barrier that the target pest overcame relatively rapidly. The variety expressing this protein (MON863) is no longer sold commercially as a result.

Debare et al. (2004, 2007) studied the effects of Cry3Bb Bt maize and tefluthrin pesticide (Force G, Dow Elanco, St Louis, MO, USA) on soil microbial biomass, nitrogen
mineralization potential, short-term nitrification rate and respiration rate in a 3-year field trial. While there was variation across time and significant differences in all variables between the bulk and rhizosphere soil, there was no effect of genotype on nitrogen mineralization potential or short-term nitrification rate. Using molecular fingerprinting, no differences were observed between bacterial or fungal communities colonizing the rhizosphere or bulk soil attributable to maize genotype. However, the authors did find that soils sampled from the Bt maize had increased levels of microbial biomass and microbial respiratory activity. While ‘more’ is not necessarily ‘better’, these results suggest that the Bt maize did not have any repressive effects on soil microbial abundance or activity and thus is unlikely to be harmful. For plants treated with the pesticide tefluthrin, they found depressed respiratory activity midseason for 2002 samples only.

In only one study (Wu et al. 2009b) was the community composition of rhizosphere bacteria found to differ substantially in Cry1Ab rice, compared to its non-transgenic counterpart in a paddy soil. Wu et al. (2009b) used phospholipid fatty acid analysis to characterize these bacterial communities. They suggested that potential differences in the content or extent of root exudation between the transgenic and non-transgenic rice could have led to the bacterial community level differences observed. Arbuscular mycorrhizal fungi spore abundance and root colonization were examined in field studies with Cry3Bb maize and non-transgenic isolines over a 5-year period (Zeng et al. 2015). Only minor effects on the arbuscular mycorrhizal fungi community were observed over the 5-year span of these trials.

Lastly, Liu et al. (2008) studied the effects of Cry1Ab Bt rice and the insecticide triazophos [3-(o,o-diethyl)-1-phenyl thiophosphoryl-1,2,4-triazol] in a paddy soil on microbial activity and community composition. Molecular fingerprinting was used to assess changes in bacterial and fungal communities in the rhizosphere of Bt rice compared to the non-transgenic isolate. Measurements were taken at four stages in the rice developmental cycle over a 2-year period. No significant differences in phosphatase activity, dehydrogenase activity, respiration, methanogenesis or fungal community composition were found in the transgenic compared to the non-transgenic variety.

Fewer studies have been conducted to examine the effects of herbicide-tolerant crops on the soil microbial community. Glyphosate inhibits the enzyme 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase that is required for the biosynthesis of the aromatic amino acids phenylalanine, tyrosine and tryptophan via the shikimate pathway in bacteria, fungi and plants. Roundup Ready crops (herbicide-tolerant crops) contain a gene derived from Agrobacterium sp. strain CP4 that encodes a glyphosate-tolerant enzyme (CP4 EPSP synthase) (Funke et al. 2006) and are thus relatively unaffected by glyphosate application. Nakatani et al. (2014) examined the effects of herbicide-tolerant soybean on soil microbial biomass-carbon and nitrogen and the activities of the enzymes beta-glucosidase and acid phosphatase. They worked at six sites in Brazil across 2 years. Their results show no significant effect of genotype on any of the variables measured.

6.5 Tertiary Effects: Broader Spatial and Temporal Scales

While pest management decisions are made at the field level, effects often accrue across broader spatial and temporal scales and these scales need to be considered as regulations for transgenic crops continue to be developed and refined. Traditionally, data for risk assessments of transgenic crops have usually been collected at the plot or field
scale. However, many environmental impacts occur at landscape and larger spatial scales and may not be apparent at small plot or field scales. Assessments of the effects of transgenic crops are performed on a case-by-case basis in order to address the specific characteristics of the trait, crop and environment where the transgenic crop is to be deployed (Andow and Zwahlen 2006; Andow et al. 2006; Peterson et al. 2000; Wolfenbarger and Phifer 2000). Recent research has highlighted the importance of considering landscape context and extended spatial and temporal scales when evaluating the impacts of land use changes associated with introducing new genetically engineered crops. Since broad-scale effects take longer to accrue and have not been as rigorously assessed, we will address them primarily in terms of risks of future effects.

Given the current widespread use of transgenic crops in several parts of the world and the projected rapid adoption of next-generation transgenic crops with stacked traits (Mortensen et al. 2012) (see also Chapter 12), there is an urgent need for improved tools and methods for assessing risks at regional to national spatial scales and multidecadal time scales so that these methods are ready to use on the next generations of transgenic crops.

There has been a large amount of work devoted to developing and standardizing risk assessment methods. The United States Environmental Protection Agency (USEPA) has produced numerous guidance documents for conducting ecological risk assessments. However, a recent compilation indicates that only three of the 38 documents address landscape-scale analyses, and none of these are focused on pesticides (USEPA 2012). In other countries, guidance for risk assessment for other topics such as maintaining biodiversity in Australia (Smith et al. 2013) and managing invasive (alien) species in Norway (Sandvik 2013) may be applicable to genetically engineered crops.

For genetically engineered crops, landscape and regional geospatial analysis is critically important because these traits are deployed on a large portion of the landscape and interspersed with non-genetically engineered crops, organic fields and other sensitive, non-target vegetation and ecosystems. Because the benefits and risks of genetically engineered crops are often landscape dependent, it is critically important to represent these landscapes accurately in risk assessments. For example, in some regions, genetically engineered crop fields may dominate the landscape, so effects that are small in a single plot or field may become large as they accumulate in a watershed or region. Conversely, in other regions, genetically engineered crop fields may be interspersed in a patchwork of non-agricultural lands, non-genetically engineered row crop fields including organic systems, and high-value horticultural crops.

The risks of a particular genetically engineered trait may be mitigated or magnified by these spatial arrangements at the landscape to regional scale. Furthermore, if a genetically engineered crop has increased yields compared with the non-genetically engineered alternative, it could contribute to ‘land-sparing’ such that less area is required for the crop, providing the opportunity for land use change toward other uses. But if a genetically engineered crop allows commercial production to occur on lands that are marginal for alternative crops, including conservation lands, there could be land use change toward more intensive use with the potential to contribute to cumulative risks. For these reasons, a geospatial approach to risk analysis can improve upon current approaches by better representing spatial patterns of genetically engineered crops and other land uses, how these spatial patterns affect risks, and how patterns may change with the introduction of a new genetically engineered crop.
For transgenic crops, increasing attention has been paid to the need to develop geospatial methods to conduct ecological risk assessment and management in Europe. For example, a web-based geographical information system has been designed that incorporates data on the location of all genetically engineered crop production in Germany, facilitating analysis with geospatial data on climate, soil and agricultural patterns (Kleppin et al. 2011). Models have also been developed to scale up from plot and field scale data to perform landscape and regional ecological risk assessments for transgenic crops, particularly in Europe (Breckling et al. 2011; Reuter et al. 2011; Wurbs et al. 2012). Unplanned release of genetically engineered crops may occur along transportation corridors such as railways, as has been documented for herbicide-tolerant rapeseed in Switzerland (Schoenenberger and D’Andrea 2012). These types of approaches are required to address both local and regional environmental impacts of transgenic crops.

In addition to accounting for landscape-dependent effects, risk assessments at larger scales may detect effects that are not apparent at plot scales. While genetically engineered traits are generally intended to improve yields, for soybean, small yield decreases have been found at the regional scale in the USA of 0.07 t ha⁻¹ in the Central Corn Belt and 0.11 t ha⁻¹ elsewhere (Xu et al. 2013). Furthermore, these results demonstrate that effects that are important at regional and national scales may be difficult to detect at the field scale. During recent years, USA maize yields have averaged 8–10 t ha⁻¹, so detecting small losses of 0.07–0.11 t ha⁻¹ could be quite difficult at the plot or field scale, but not difficult at regional scales due to the very large sample size and concomitant statistical power to detect small differences.

Recent advancements have contributed to the development of the field of probabilistic regional geospatial environmental risk assessment, for example by analysing climate change effects on forest growth (Woodbury et al. 1998), improving methods for spatially explicit risk assessments (Woodbury 2003) or identifying promising methods for probabilistic assessment of multiple types of risks to agricultural and forest ecosystems at the regional scale (Woodbury and Weinstein 2010). Careful attention to appropriate temporal and spatial scales and to cumulative impacts has been recommended for all types of ecological risk assessments (Dale et al. 2008), as have regional risk assessments that cover multiple types of environmental stressors (Landis and Wiegers 2007). There is a need and an opportunity to apply these approaches of cumulative, probabilistic, regional geospatial risk assessment to transgenic crops at landscape, regional and national scales. For example, there is evidence that widespread deployment of Bt crops has reduced insect pest populations in China at the landscape scale. Specifically, adoption of Bt cotton caused an increase in the abundance of generalist predators in non-Bt crops that increased the biological control of aphid pests beyond the genetically engineered crop fields (Lu et al. 2012). In Europe, geospatial modelling suggests that Bt maize pollen could cause mortality to the protected butterfly *Inachis io* in southern Europe where it is multivoltine, but not in northern Europe where it is univoltine (Holst et al. 2013).

Increasing the temporal scale will also provide a more comprehensive risk assessment compared to assessments exclusively at shorter time scales. Incorporating multidecadal time scales is important because environmental benefits and impacts may change over time. For example, glyphosate-resistant genetically engineered crops have provided a benefit to farmers and others due to improving the ease of weed management, and replacing older, more toxic herbicides with glyphosate (Green 2012). However, the relatively
rapid development of multiple populations of glyphosate-resistant weeds after introduction of glyphosate-resistant crops was an unpleasant surprise to many growers and policy makers (Powles 2008, Shaner et al. 2012). Development of glyphosate-resistant weeds has prompted development of genetically engineered crops resistant to synthetic auxin herbicides. A multidecadal time scale is required to more fully evaluate both benefits and risks of herbicide-resistant crops and the effects of management practices.

6.6 Quantifying Risks and Benefits of Transgenic Traits

Although much of the research and regulation for transgenic crops is based on assessment and management of risk, there are also benefits from genetically engineered crops that should be balanced against the risks in order to assess the overall impacts. For example, expressing the Bt protein in crop tissues reduces insect damage and increases yield due to improved efficacy of pest control in treated fields. It also reduces insecticide application and concomitant risks, as discussed earlier. Such co-benefits may also provide economic savings to farmers despite the increased cost of genetically engineered seeds. There is evidence for both yield increases and economic benefits due to deployment of genetically engineered traits in the USA. For example, for maize in the USA, yield increases with full adoption of genetically engineered traits are estimated to be 1.3 t ha\(^{-1}\) in the Central Corn Belt and 0.6 t ha\(^{-1}\) elsewhere (Xu et al. 2013). For European corn borer in five Mid-Western states in the USA (IL, MN, WI, IA, NE), recent analyses suggest economic benefits of Bt maize over 14 years as high as US$6.8 billion, with US$4.3 billion of this total due to indirect effects, specifically reduction of pests in fields without the Bt trait (Hutchison et al. 2010). These results also highlight the value of retaining non-Bt maize refugia to slow development of resistance to Bt in maize pests. In China, increases in arthropod predators and decreases in aphid pests were found in Bt cotton, along with potential improvement in biocontrol in neighbouring crops including maize and soybean (Lu et al. 2012).

6.6.1 Quantifying Effects on Ecosystem Services at Landscape and Regional Scales

Humans derive an array of services from ecosystems, which can be classified as provisioning, regulating, supporting or cultural (MEA 2005) (see also Chapter 7). Agriculture provides services such as crop production, a provisioning service. But to do so, it relies on supporting and regulating services such as nutrient and water cycling, pollination, pest regulation, and maintenance of soil quality and biodiversity (Power 2010). Such services are extremely valuable; for example, a limited set of ecosystem services provided by wild insects in the USA were found to be worth US$57 billion per year (Losey and Vaughan 2006).

To incorporate the many services provided by and required by agriculture, risk assessments should address a broad suite of ecosystem services. As an example of a screening-level risk assessment of the impacts of future bioenergy crop production on a comprehensive suite of ecosystem services across a 12-state region of the upper Mid-Western USA, Bruins et al. (2009) identified a large number of services and endpoints that are relevant because of the focus on both annual and perennial crops (including
maize, soybean and switchgrass) at the regional scale. As another example, both quantitative models and semi-quantitative estimates were used to analyse the impact of cover crops on the temporal dynamics of 11 ecosystem services and two economic metrics in a 3-year soybean–wheat–maize rotation in a typical Mid-Atlantic climate (Schipanski et al. 2014) (Figure 6.2). These studies illustrate that it is feasible to account for both risks and benefits to ecosystem services in a quantitative regional risk assessment framework for genetically engineered crops. However, it will be an ongoing challenge for risk assessment methodologies and for collecting data needed to conduct risk assessments as the pace of transgenic technology increases.

One example of these types of advances is the recent development of CRISPR (clustered regularly interspaced short palindromic repeats) technology that has the potential to greatly increase the ease and speed of transgenic crop trait development by allowing straightforward ‘editing’ of genomes. Crops have already been developed using advanced genome editing technologies including oilseed rape (canola), maize and wheat (Ainsworth 2015). If these crops produced with gene editing technology do not include genetic material from other species, they may not be defined as ‘transgenic’, and in fact the first such crop has already been planted in California (Ainsworth 2015). However, this same crop may be considered transgenic in Europe, thus further complicating risk analysis and management for crops that may be traded internationally.

Figure 6.2 Example of the effects of an agricultural management practice (cover cropping, CC) on a suite of indicators of ecosystem services, with higher numbers indicating increased ecosystem service benefit. Source: Adapted from Schipanski et al. (2014). Reproduced with permission from Elsevier.

### 6.6.2 Risk Management Impacts for Transgenic, Non-transgenic and Best Management Practices

Most crops in the USA are highly managed, and management practices substantially affect risks. For example, for synthetic auxin herbicides such as 2,4-D and dicamba that have the potential for vapour and spray drift, best management practices such as...
low-vapour formulation, correct timing of application, accounting for wind speed and direction, correct rate, correct type of spray nozzles and thorough cleaning of equipment can greatly reduce or eliminate problems of drift damage (Mueller et al. 2013; Parker 2011). Conversely, widespread use of these herbicides without best management practices has the potential to substantially damage sensitive crops (Egan et al. 2014; Mueller et al. 2013; Parker 2011). Thus, management strongly influences the risk of damage to non-target crops and other vegetation. However, risk assessment guidance and risk assessments rarely focus adequate attention on risk management. For the USA, for example, a recent compilation indicates that only four of 38 USEPA guidance documents directly address risk management, while another 11 ‘touched upon’ this subject (USEPA 2012).

This issue is discussed in the current draft genetically engineered synthetic auxin herbicide Environmental Impact Statement prepared by APHIS (USDA-APHIS 2013). This document notes that the ‘Save our Crops Coalition,’ a group of growers who raise crops sensitive to 2,4-D, was opposed to 2,4-D-tolerant (Enlist™; Dow AgroSciences; www.enlist.com/en) crops due to concerns about off-target drift of 2,4-D. However, once they became familiar with the Stewardship Agreement that adopters of the Enlist™ plants must enter into with the developer, data on the volatility of proposed 2,4-D formulations and requirements for drift reduction planned for the label, they were no longer opposed (www.regulations.gov/document?D=APHIS-2012-0032-0143). Concerning this, it is important to evaluate the impacts of different degrees of compliance with these best management practices, as they will have strong impacts on risks.

In a broader sense, more case studies are needed to support quantification of impacts of different management practices at landscape to regional scales.

6.6.3 Quantitative Uncertainty Analysis

In any risk assessment, there is uncertainty about the magnitude and effects of a particular stressor (any physical, chemical or biological entity that can induce adverse responses). This is particularly true for assessing potential risks of genetically engineered crops, since agricultural systems are complex, with different environments, management practices and landscape contexts in different fields, farms and regions of the world. Furthermore, both uncertainty and variability are important in risk assessments, and it is useful to distinguish between them. Uncertainty may be caused by lack of knowledge or lack of data. Variability is a property of natural systems, including agricultural systems, with variation within and among plants, pests and non-target species, as well as biophysical properties of the environment such as soil characteristics.

Quantitative uncertainty analysis has long been recommended to help understand and quantify the sources and magnitudes of uncertainties, and how they may affect risk management decisions (Hammonds et al. 1994; Thompson and Graham 1996; USEPA 2001; Warren-Hicks and Moore 1998). Such techniques have been used to improve previous analysis of environmental risks (Nagle et al. 2007, 2012; Woodbury et al. 1998) and should also be utilized to improve risk analyses for genetically engineered crops.
6.7 Variation Among Countries in Risk Assessment and Management

Approaches to regulation and concomitant adoption of genetically engineered crops vary substantially among countries, reflecting broad cultural, social and political differences (Heinemann et al. 2013; NAS 2016). During the late 1990s, adoption of genetically engineered crops increased 20-fold worldwide, prompting an explosion of concern, particularly in Europe, over the health and environmental impacts of these crops (Peterson et al. 2000). Since that time, genetically engineered crop area has grown globally each year such that in 2014, 18 million farmers in 28 countries planted more than 181 million hectares (James 2014). However, very large differences in adoption of genetically engineered crops among countries and global regions have continued, with very rapid adoption in North America, most of South America, especially Brazil, as well as South and East Asia, contrasted with adoption in only a few countries in Europe and in Africa (James 2014). These differences appear to be driven not so much by different data on environmental impacts of genetically engineered crops in different parts of the globe or by use of entirely different risk assessment methods, but rather by differences in the approach to regulating risks and benefits (NAS 2016). For example, in both the USA and Europe, risk assessment and regulation are in theory based on a requirement for review of each crop variety produced by a specific set of genetically engineered techniques, while similar varieties developed through other breeding technologies are not regulated (Bartsch 2014; NAS 2016). However, as discussed earlier, genetically engineered crop adoption is very widespread in the USA, while in Europe a precautionary approach has dominated, and there was adoption in only five European Union countries as of 2014 (James 2014).

In part, this difference may be because the policy goals specified in many countries may be so broad that it is difficult to translate them into specific assessment endpoints for risk assessment (Garcia-Alonso and Raybould 2014). Additionally, regulations in some countries go well beyond food safety and environmental protection to address social goals such as protecting organic production systems and product labelling for consumers (NAS 2016). More generally, there are political, social and psychological factors that affect approval of genetically engineered crops that go beyond scientific assessments of environmental risk (Bartsh 2014; Devos et al. 2014; NAS 2016). Therefore, even with increasing amounts of data on various types of environmental impacts of genetically engineered crops, it is likely that there will continue to be large differences in policy, management and adoption among countries and regions.

6.8 Conclusions

Improved assessment tools that comprehensively consider the impacts of genetically engineered crops on non-target organism and ecosystem services are clearly needed. These assessments need to be conducted not just at the field scale, but at longer temporal and larger spatial scales as well.

Effects on soil ecology provide a salient example to consider, especially if lands where transgenic crops are grown are to be transitioned to organic agriculture in the future. Any
carryover effects could adversely affect the ability of land owners to obtain and maintain organic certification (Thies 2015). However, when do we consider sufficient data to have been collected to determine whether a particular transgenic crop has no harmful effects on the soil microbial community? In many cases, for the Bt crops, Bt protein constructs are beginning to change as resistance in target pests escalates. Once one protein has been ‘retired’ and another comes on line, what data will we still need to gather to assure environmental safety of this new trait? And, if a given Bt protein is no longer detectable in soil after a single season, is there a need to continually monitor? Some rationale is needed to target those ‘risks’ that may persist and continue to measure those while we ‘cease and desist’ where the weight of the evidence suggests this is prudent to do.

Besides prospective risk assessment, there is a need for ongoing risk management, including analyses of new data collected after release of a transgenic cultivar. Ongoing technological developments such as CRISPR technology will pose a challenge for risk assessments, especially to the extent that genetically engineered crops may not be defined as transgenic and thus could fall out of the infrastructure in place to assess effects and risk for genetically engineered crops. Furthermore, uncertainty should not be ignored, but rather addressed using quantitative uncertainty analysis.

All of these recommendations would improve our knowledge of the environmental impact of genetically engineered crops and provide better decision support for risk management and sustainable crop production.

References

Effects of Transgenic Crops on the Environment


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