

Precaution and GMOs: an Algorithmic Complexity Approach

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SUMMARY: *This is a supplement to our Precautionary Principle paper presenting the problem from the perspective of Computational/Algorithmic Complexity, which can clarify the risks of GMOs. The point is that—in addition to the change in risk classes—the difference between conventional breeding and transgenics may change the complexity class associated with the problem of harm evaluation.*

Our PP approach

Our analysis of the risk of GMOs in the preliminary version of the PP paper [1] was probabilistic, based upon the conjunction of three problems

- the opacity of tail risks: the difficulty of obtaining information *now* about potential deferred *future* harm to health or the environment
- the systemic consequences of fat tailed events in GMO risks that are not present in conventional breeding and agricultural technology innovation—the difference lies in the absence of passive barriers or reactive *circuit-breakers* (a term also used in market regulation) that limit the propagations of errors for GMOs to prevent wider damage.
- that measures of harm scale nonlinearly with measures of impact, e.g., a reduction of 10% in crop production or genetic diversity can multiply the harm to social systems or ecologies by orders of magnitude.

The problem of identifying the harm analytically arises because of the many ways that, e.g., insertion of a gene from another species, can affect molecular, cellular, physiological, and other organismal aspects of the organism, and those modifications may impact long term health or agricultural and ecological systems—impacts that may be unobserved due to the complexity of societal changes in the absence of monitoring. Unintended effects arise from the many interactions that are possible, and increasing global connectivity that converts local to systemic risks. The ecosystem and civilization are at risk due

to the absence of boundaries of GMO use in human consumption or ecological systems globally.

Boundedness of conventional breeding

Counter to the idea that GMOs are similar to natural evolution or breeding, the viability and other qualities of offspring from the mating of two members of the same species implies the range of outcomes of breeding is bounded. Offspring that arise within a species must have high probability of long term compatibility with other members of the species and contextual ecology. Otherwise the species and the ecosystem of which it is part would not have persisted over many generations. The same statement need not be true of GMOs.

Indeed the reason that GMOs are being introduced is that (1) GMOs depart significantly from the set of organisms that can arise through breeding, (2) Many of the advantages of breeding have been explored and exploited.

Unfortunately, the FDA does not require testing of GMOs as it has accepted industry claims that GMOs are no different from conventional breeding. This means there are few, and surely insufficient, tests of the harm that might be caused—or monitoring of the effects.

Some believe—and have convinced others—that they can "figure out" what the effect of GMO modifications is and consider that unintended consequences will not occur. This is a stretch: "Figuring out" the impact of GMO modifications may very well not be possible. We do not mean unlikely due to current computational restrictions and the state of science, but literally impossible.

NP computational limits and impossibility

There are many problems that are intractable because the level of effort to solve them grows rapidly with the dimension of the problem. Thus, for example, it is widely believed by mathematicians that NP-complete problems (e.g. traveling salesman problem, boolean satisfiability problem) cannot be solved for large enough problems because the level of effort grows more than polynomially

in the size of the system. We may check a solution *if we know it* in polynomial time but cannot guarantee that we can derive it. Whether NP-complete or not, there is a wide range of problems whose computation time grows exponentially.

These problems—those exponential rather than polynomial growth—are deemed impossible to solve for large systems.

Is the determination of harm from GMOs such a “hard” problem? Identifying all of the possible consequences of GMO modifications may very well involve combinatorially many effects to consider in the interaction of one (or more) new genes with the other genes, other organisms, agricultural and ecological processes. (The need for combinatorial numbers of observations for behavioral characterizations of such complex systems has been previously discussed [2].) On the other hand, the limitations that exist on the traits of members of the same species suggest that the probability of harm in breeding is constrained, and the generally incremen-

tal impact of breeding suggests a much lower if not well characterized computational effort to determine it. Therefore outcomes of breeding are more amenable to testing or analysis in comparison to GMOs, including the projection of future harm.

Advanced complex systems science methodologies exist that can identify large scale impacts without characterizing all details of a system [3]. However their application to the system of harm and risk in the context of genetic modification that is pervasively present in the system has to be established, and is not yet available to address the current risks being taken.

REFERENCES

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