

## Co-existence challenges in small-scale farming when farmers share and save seeds

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### Abstract

Gene flow by means of pollen and seeds in maize influences local, regional and global maize biodiversity. Developing countries are centers of diversity for maize and preserve seeds also in informal seed systems. Particularly in poor communities, seed saving and sharing often co-occur with farming on small fields. We present preliminary investigations from a small-scale maize farming community, in Chongwe, Zambia, to illustrate the significance of seed saving and sharing for patterns of gene flow. The potential introduction of genetically modified (GM) plants brings in new dimensions of challenges for farmers e.g. related to: i) co-existence of GM and non-GM varieties; ii) potential infringement of intellectual property rights; and iii) trans-boundary movement of products to countries that do not accept certain GM products. Small-scale farming is vulnerable to cross-contamination due to limited separation between fields. If transgenes are introduced into small-scale agricultural contexts, uncontrolled diffusion and further spread seems unavoidable. Removal of transgenes as well as the regulatory implications of transgenes would require control of innumerable small informal seed stores kept by farmers.

### Introduction

Maize is an important cereal crop and staple food in many regions of the world, especially in Sub-Saharan Africa. In this study we provide concepts necessary for the elucidation of gene flow, with emphasis on potential transgene flow, in an African environment where small-scale and subsistence farms are dominant landscape components. We identify basic needs for measurement and analysis, and chart future needs for research in this field. It is worthy to note that from its center of origin, in Mesoamerica, farmers have for thousands of years experimented, spread, mixed and selected favorable maize plants for different environmental conditions on all continents.

This diversification process has until relatively recent times been based on informal seed systems, free sharing and no intellectual property rights on genes or germplasm. The ultimate consequence of this primarily *seed*-based maize gene-flow experiment, driven by farmers, is the highly appreciated richness of maize food and culture that we have today.

However, gene flow studies in maize have focused on the role of pollen movement and cross-hybridization (Dyer et al. 2009; Gray et al. 2011). Maize cross-pollination decreases rapidly within 30 m, but includes a long tail with low cross-pollination occurring over several hundred meters (Beckie and Hall 2008). Cross-pollination is still not zero at 800 m distance (Kawashima et al. 2011). Open pollinated varieties have higher outcrossing than hybrid cultivars (Sanvido et al. 2008).

Pollen flow has become particularly relevant with the introduction of transgenic or genetically modified (GM) plants which are protected by intellectual property rights (IPR) and bringing with them specific regulatory and risk assessment demands. Specific recommendations for isolation distances have been proposed to ensure that products comply with the EU labelling threshold of 0.9 %. For small-scale farming, proposed isolation distances are varying, e.g. 20 m (Gustafson et al. 2006), or 25-50 m (Beckie and Hall 2008). Further, a pollen barrier of 20 m has been recommended (Messeguer et al. 2006). Devos et al. (2005) argued that large fields (> 5 ha), did not need any isolation distance but small fields (< 1 ha) requires a 50 m isolation distance. In a South-African context, (Viljoen and Chetty 2011) recommended isolation distances of 135 m for cross-pollination levels between <1.0% and 0.1%, 503 m for <0.1 % to 0.01% and 1.8 km for <0.01% to 0.001% based on high cross-pollination values. In Zambia, isolation distances recommended in order to ensure seed purity in the production of certified maize seed and basic maize seed is 200 m and 400 m, respectively (MAFF 1995).

In the context of small-scale farming, quantitative recommendations as referred to above may clearly be of little or no use when i) fields are smaller than the isolation distance between fields, and ii) isolation barriers would consume a significant part of individual fields.

Adventitious presence of transgenes may also come from the spread of seeds. Seed sharing make people effective vectors of genetic material; over large distances, over natural and regulatory borders. This is difficult to manage and control, even in Europe where tighter controls may be expected than in developing countries. Bannert and Stamp (2007) reported from a GM maize field trial in Switzerland that unwanted mixing of seeds may contribute more to the GM content in receptor fields than the pollen for cross-pollination.

In this study we present preliminary data on field sizes and spatial arrangement of fields, as well as data from questionnaires about farmer activities like seed saving and sharing, in a small-scale maize farming community in Chongwe, Zambia. We discuss the link between gene flow and the feasibility for co-existence of GM maize (if introduced) and non-GM maize in this particular agricultural context.

## **Methods**

We mapped the spatial patterns of cultivated fields in a maize farming community of Chongwe, Zambia, using GPS devices (Garmin 62S) in March 2012. The coordinates (UTM, GCS Arc 1950) of the waypoints of each field were transformed to a polygon layer by means of ArcGIS 10.0, and field centroids and acreage were calculated. Analysis of the spatial distribution, and average distances to nearest field neighbours with respect to field centroids were performed using SIMULA-based written programs (Dahl 1968).

Additionally, we interviewed farmers (n=32) that used these same fields (but not all of them) about their practice related to seed saving and sharing.

## **Results**

A total of ninety-seven fields were found within an area of 1 km<sup>2</sup> in the Zambian community of Chongwe. The mapped fields were small with an average size of about half a hectare (0.49 ha). The fractional area of cultivated maize as a percentage of the total study area was 48 %. Two thirds of the fields were smaller than 0.5 ha and only 5% of the fields were larger than 2.0 ha. All fields had neighbouring fields that were closer than 10 m away. Based on data from questionnaires, about two thirds of the farmers both saved and shared seeds from the previous season, involving both local varieties and commercial hybrids. Sharing happened mostly within the local community (i.e. to very nearby farmers and up to 800 m away), but also across communities, i.e. up to a distance of 100 km.

## **Discussion**

Much progress has been made in understanding transgene flow in large, industrial agricultural settings, but by contrast our knowledge of gene flow is very restricted for cases where small-scale and subsistence agriculture dominates the ecosystem. In particular, there is a knowledge gap on this issue in the case of Africa.

The community of Chongwe, Zambia, represents a small-scale farming system in Africa. Given the density, sizes and distances between fields we observed, pollen will interchange genetic material between farmers at a high rate. Thus, this kind of farming seems incompatible with a segregated and parallel growing of GM and non-GM maize. Fields would rapidly be cross-contaminated by pollen flow. However, this describes a hypothetical scenario since Zambia has not allowed growing of GM maize. Open pollinated varieties, which are in use in Chongwe (but in a minority proportion compared to commercial hybrids), have higher outcrossing rates than hybrid cultivars (Sanvido et al. 2008). Farming practices that use an increasing proportion of open pollinated varieties/landraces (termed 'local maize' or 'Gangata' in Chongwe) will thus be more vulnerable to cross-contamination by pollen.

The role of pollen in gene flow is important. However, the vital role of seeds as a vehicle for gene flow must not be forgotten (Dyer *et al.*, 2009). In particular, the human-driven gene flow through intentional and unintentional seed movement is relevant. Farmer's behavior, including management, preservation and selection of seeds have contributed to the diversification of maize landraces (Bellon and Berthaud 2004). Such behaviors, including seed saving and sharing are practices that often go hand in hand with small-scale farming.

The practice of re-using seeds was found to be a common feature among the farmers of Chongwe and was seen as an important part of the local food security and independence. The farmers re-used not only the local maize varieties, but sometimes also commercial hybrid maize varieties. This practice constitutes a link between the informal and the formal seed system. Transgenes would likely be introduced as commercial hybrid seeds in the formal seed system, but might find their way into the informal seed system sooner or later. The combination of pollen flow and the tradition to re-use of seeds would potentially spread and keep transgenes, if introduced, in circulation from year to year. A secondary consequence of such process would be that seeds protected by intellectual property rights (IPR) might be found in local on-farm seed stores, with a risk of patent infringements. The open pollinated local maize varieties would be particularly vulnerable to cross-pollination by transgenes.

The practice of sharing seeds to family members and friends was also common in Chongwe, primarily within the local community. Again, in a GM maize scenario, seed sharing would spread transgenes quickly within the community, and also across communities as exemplified by a farmer sharing seeds up to a distance of 100 km. This would mean that the diffusion of transgenes would not be limited to the community of introduction, but also lead to spread across a larger region. The example illustrates the central role of human agents for gene flow.

Apart from the airborne pollen in anemophilous plants such as maize, it is therefore crucial that decision-makers factor in human driven processes that impact gene flow. Intentionally or unintentionally, humans are the main drivers of gene flow in maize in Mexico (Dyer *et al.* 2009). The same can be expected in Southern Africa although the scientific data is limited from that region. Small- and subsistence farmers dominate in poor regions and base their agriculture on subsistence practices including seed saving and sharing. These activities must be taken into account in models and understanding of gene flow. Small- and subsistence farmers (commonly referred to among policy makers as the "informal" sector) tend however to be invisible when governmental or commercial analyses and decisions of gene flow are considered. Yet they have to be considered as a substantial component of the biosafety development process.

## **Conclusion**

The agricultural practice under study in the small-scale community of Chongwe is working well in sustaining selection, exchange and re-use of local seed varieties. Thus the farmers uphold the traditional agriculture with its central processes to the local

livelihood and food production. It is clear that the studied agricultural practice would not be able to uphold segregation of GM and non-GM maize if transgenes were introduced to that system. Both pollen flow between closely positioned maize fields, and sharing of seeds between farmers represent high rates of gene flow. We need more data to evaluate how representative Chongwe is for other small-scale farming areas and practices, with a focus on field sizes, isolation distances, and proportion of farmers that save/share seeds. For the future, mapping larger areas of local maize field cultivation should enable quantification of transgene maize flow by means of dispersal models for different cultivation patterns and scenarios (see e.g. Reuter et al. 2008).

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