“Crop-to-wild gene flow” - a case study of NEWEST transgenes’ escape into wild rice (*Oryza longistaminata*) in Ghana

By

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Abstract

Background: To boost local rice production in Ghana, to meet demand, there are plans to introduce transgenic rice. Confined Field Trials (CFTs) of rice lines transformed for Nitrogen-Use Efficiency, Water-Use efficiency and Salt Tolerance ("NEWEST" rice), are on-going. NEWEST rice is multi-stacked with genes that make the plant better utilize available nitrogen, water and bind to excess salt in the soil which restore saline soils over time. Perceived ecological risk such as gene flow to wild species is associated with the release of transgenic crops. In Ghana the presence of the wild rice (*Oryza longistaminata*) has been reported. It is important to know whether NEWEST transgenes will escape to wild rice through gene flow, and the consequences on the weediness of wild rice in the case of NEWEST transgenes escape to the wild rice.

Methodology/key findings: In a survey of wild rice distribution in Ghana, we observed infestation of *O. longistaminata* in cultivated rice. The availability of nitrogen, water and salt was experimentally manipulated to determine their effect on the weediness of wild rice (*O. longistaminata*). The wild plants had a better growth with more access to water and nitrogen and were severely inhibited by salinity (p<0.05). Hand hybridization between cultivated rice and *O. longistaminata* was confirmed in this study with a success rate of 20 %. Gene flow frequency under field conditions was performed using 6 highly polymorphic SSR markers. We observed moderate gene flow under field conditions with an average of 10.17 migrants per generation.

Significance/conclusion: NEWEST genes may have the potential to increase the weediness of *O. longistaminata* if incorporated. Gene flow between NEWEST and wild rice can occur, which may lead to improved tolerance in wild rice. Mitigation strategies should be put in place before NEWEST rice is introduced to prevent the risk of transgene escape.