MEASURING THE EFFECTS OF CROP GENETIC LOAD ON PRODUCTIVITY AND FITNESS IN WEEDY *BRASSICA RAPA* (WILD TURNIP) × *BRASSICA NAPUS* (OILSEED RAPE) HYBRID POPULATIONS.

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With the implementation of transgenic crops in agriculture, transgene flow to wild relatives is sure to occur. In the event transgenic hybrids are produced, the inherited transgene could supply a fitness advantage. This is a real agronomic and ecological concern, but only if transgene introgression occurs. In many cases, hybrids such as these exhibit lower fitness when compared to their wild parents. This may be due to the inheritance of disadvantageous crop/domestication genes present in the new host genome. These genes would certainly negatively impact transgene introgression and possible reduce the risk associated with many transgenes. In order to gain a better understanding of transgene introgression, we plan to assess how productivity and fitness of backcrossed hybrids are affected by the presence of a transgene in the company of crop/domestication alleles. Here, we use transgenic *Brassica napus* cv. westar as a model crop plant. *B. napus* has been transformed with the *Bacillus thuringiensis* endotoxin (*BtCry1Ac*) and the green fluorescent protein. Subsequently, we made hybrids between the transgenic *B. napus* and its wild weedy relative *Brassica rapa* ac. 2974. We produced mixed BC_1/F_2 populations in the field as well as advanced backcross generations (F_1, BC_1F_1, BC_2F_1 BC_2F_2, BC_3F_1 and BC_4F_2) by hand-crossing in controlled environment chambers. First, we plan to grow the BC_1/F_2 populations in competition with *Triticum aestivum* as well as with each other. Productivity and fitness data will be gathered for both the hybrids and wheat. Secondly, we will grow the advanced backcross populations under agronomic conditions. Productivity data such as seed yield and dry above ground biomass will be recorded. In addition, to gain an understanding of hybrid fitness, we will also grow these plants in competition with *B. rapa* and the number of transgenic progeny will be recorded. All of the above data will then be correlated to the amount of crop specific AFLP markers present in each population. These data together will determine if there is any relationship between inherited crop/domestication alleles and productivity or fitness of transgenic hybrids of *B. rapa* × *B. napus*.