Rice is generally reported as a salt sensitive crop, particularly when the NaCl content in soil solution is more than 8-10 dS/m. Breeding rice for salt tolerance has been done for a decade. Number of new cultivars was developed however, the cooking quality is inferior to Khao Dawk Mali 105 (KDM105), farmers therefore adopted a few of them. In order to develop salt tolerance-high cooking quality rice varieties, molecular markers assisted selection has been used as a tool in backcross breeding program since 2000.

Two recombinant inbred lines, IR66946-3R-196-1-1(FL496) and IR66946-3R-230-1-1 (FL530) which carry a salt tolerant QTL were selected to used as donor parents, while KDM105 was used as recipient parent. This QTL located on chromosome 1 and associated with high K absorption, low Na absorption and low Na\(^+\)/K\(^+\) ratio. Three markers: RM140, B1.1-1 and B1.1-11 flanking a salt tolerant QTL spanning 33 cM and two markers: RM00 and 10L03_FW for cooking quality: amyllose content and aroma scent were used to select BC\(_1\)F\(_1\), BC\(_2\)F\(_1\), and BC\(_2\)F\(_2\) which carrying the salt tolerant QTL and maintaining low amyllose content aromatic scent of KDM105. Salt tolerant ability was evaluated using salt tolerant scoring, Na\(^+\)/K\(^+\) ratio, survival days of seedling, relative water content (RWC) of BC\(_2\)F\(_3\) population grown in EC 12 dS/m nutrient solution. This population was also used for field evaluation. Cooking qualities; amyllose content (AC), aroma, gel consistency (GC) and gelatinization temperature (GT) were also evaluated using BC\(_2\)F\(_2\) population. Both BC\(_2\)F\(_1\) and BC\(_2\)F\(_2\) were subjected to genome scan.

Progenies carried salt tolerant QTL were tolerant to salinity at average score 3.8 in 12 dS/m nutrient solution and maintained KDM105 characteristic. Significant genotypic variation existed among the BC\(_2\)F\(_2\) lines for all traits. However, 81 lines out of 90 lines evaluated produced higher seed/panicle, 1000 grain weight and 74 lines had higher grain yield than that of KDM105. Genome scan indicated that aside from major QTL on chromosome 1, there were modified gene located on chromosome 4, 5, 6 and 10 associated with salt tolerant ability of this population.