**CORRECTIONS**

1)Reviewer B: 1. It analyze the data with Griffing’s approach – now our molecular understanding leaded that for diallel analysis we can not fulfill its assumptions. So this analysis is of no use because there are several copies of a gene in the genomes – so several alleles. For diallel, there should be no multiple allelism. Now Transcription factors influenced by environment regulate the gene expression, so epistasis – as in the present paper two years data depicted huge differences for various trait. For diallel, there should be no epistasis. So I will suggest the authors to work on mean only and exclude this analysis of GCA and SCA.

We worked on mean only and exclude diallel analysis of GCA and SCA.

2) Reviewer B: 2. Second major concern is heterosis – better parent heterosis should be used or compare it with commercial heterosis. Mid-parent heterosis is of no use, and when BPH is being estimated then what MPH is giving benefit to be present. My recommendation is just to keep the BPH.

Further during 2007 performance is better and there is huge difference in the data of two years. It means there is significant year effect. Environmental features of two years may be given and should be discussed the reasons of these differences. ANOVA of genotype and year effect may be given.
In view of these two major concerns, I would recommend that this paper is not publishable in its current form.

We cancelled mid-parent heterosis and just to keep beter-parent heterosis. We gave ANOVA of genotype and year effect.