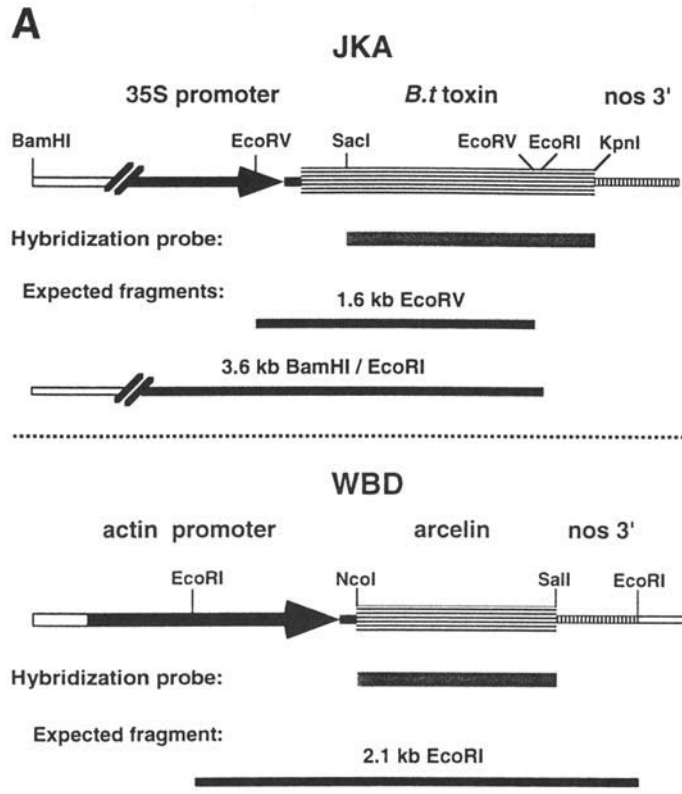

Fig. 2. Genomic blot analysis of rice. **(A)** Partial restriction maps of chimeric genes JKA and WBD that were introduced into rice. The DNA fragments used as hybridization probes and the fragments expected are shown.

be likely the promoter was disrupted and the likelihood of a functional gene being present would be low. Although additional genomic blots using different restriction digests could be used to determine the extent and location of the rearrangements, it is easier to amplify overlapping fragments using PCR (e.g., *see* Fig. 7 in **ref.** ***4***) to confirm the integrity of the gene.

In just the above few examples, it is easy to see that the copy number of introduced sequences can vary from low (1–2) to very high (>100). Because of the increasing number of reports of gene silencing ***(5-7)***, which are often attributed to the plant responding to multiple copies of genes, a challenge for future research is to determine how to regulate and limit the number of copies introduced. One mechanism that might explain, at least partially, how the copy number varies was presented at a recent meeting ***(8)***. Scanning E*M* photos of DNA-coated microcarriers showed some that had small precipitates of DNA