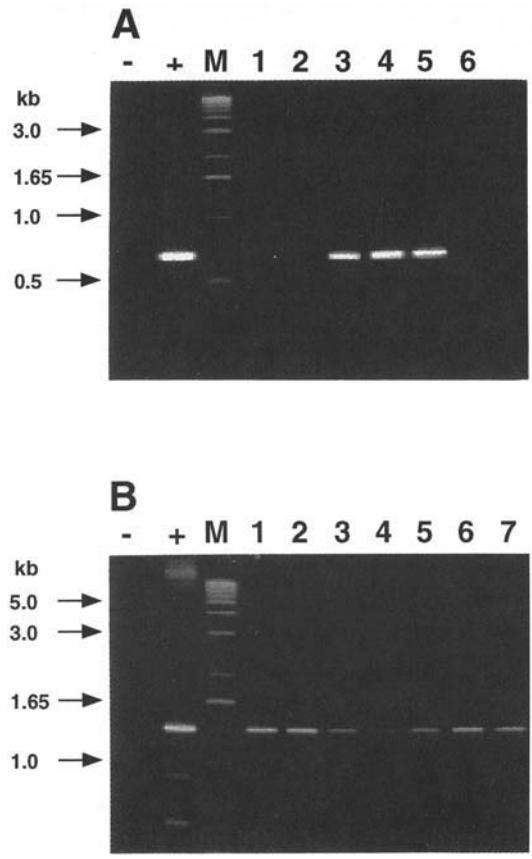

Fig. 1. PCR analysis of putatively transformed rice. DNA for PCR amplification was extracted from rice leaves and amplified as described in the text. The PCR products were size fractionated by electrophoresis through 1.2% agarose gels cast in Tris-borate buffer. **(A)** PCR amplification products obtained using green fluorescent protein gene (*gfp*)-specific sense (GFPS117; 5'-GAACTTTTCACTGGAGTTGTCC-3') and antisense (GFPA817: 5'-TATTTGTATAGTTCATCCATGC-3') primers. The PCR program (94°C, 30 s; 54°C, 30 s; 72°C, 60 s) was run for a total of 30 cycles. DNAs used as substrate in each lane were: –, reaction mix without added DNA; +, 10 pg *gfp* plasmid DNA mixed with 100 ng wild-type T309 DNA; 1–5, bialaphos-resistant transgenic rice cotransformed with chimeric *bar* ***(9)*** and *gfp* ***(10)*** genes; 6 and 7 T309 plants transgenic for a different gene of interest. Lane M contains BRL 1-kb ladder size standards. **(B)** PCR amplification products obtained using rice triose phosphate isomerase ***(11)*** gene-specific sense (TPIS4775: 5'-GAGACTCTCGAGCAGCGGG-3') and antisense (TPIA6122: 5'GCATTGCTCAAGCTGCAGG-3') primers. The PCR program (94°C, 30 s; 50°C, 30 s; 72°C, 60 s) was run for a total of 30 cycles. Lanes: As in A.