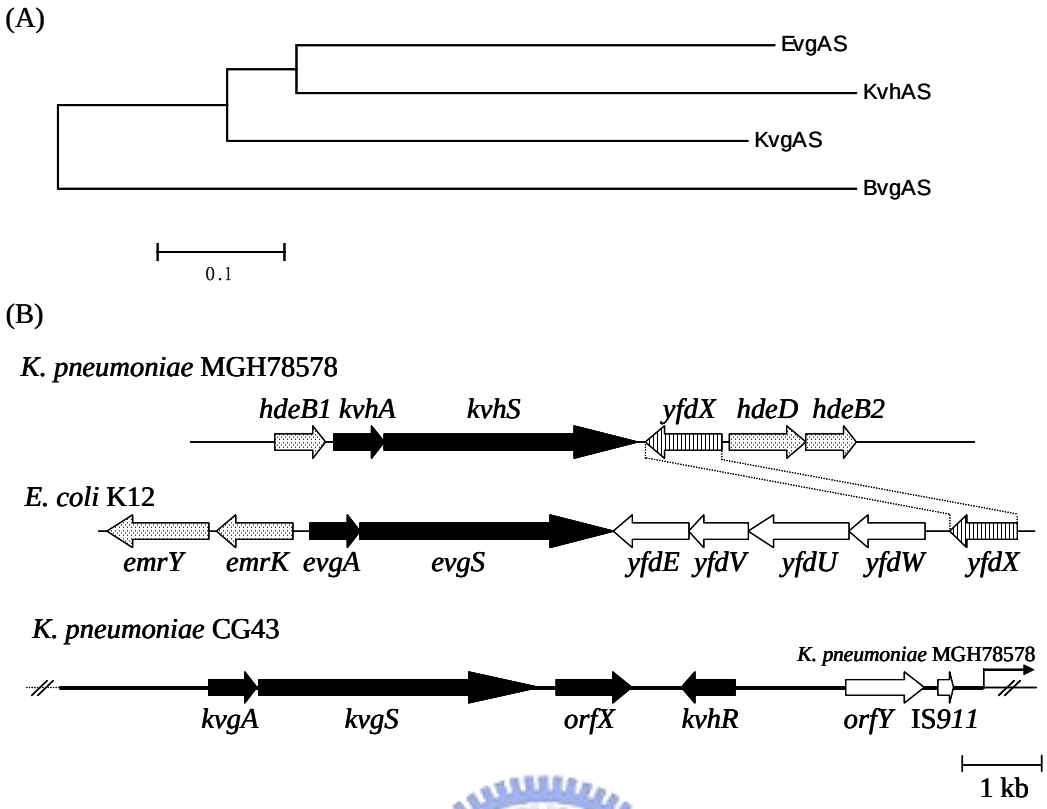

Fig. 1 Evolutionary relation*hAS* gene clusters. (**A**) The phylogenetic tree of KvgAS, K*A*S. The Neighbor-Joining tree was built by CLUSTAL W 1.81 (89) with the deduced amino acid sequences. The resultant tree was visualized by MEGA2 (47). The bar represents 10% sequence divergence. (**B**) Comparison of the respective gene clusters flanking *kvhAS*, *kvgAS*, and *evgAS*. The respective ORFs flanking *kvgAS* in *K. pneumoniae* CG43, *kvhAS* in *K. pneumoniae* MGH78578 and *evgAS* in *E. coli* K12 are shown. The amino acid identities are indicated.

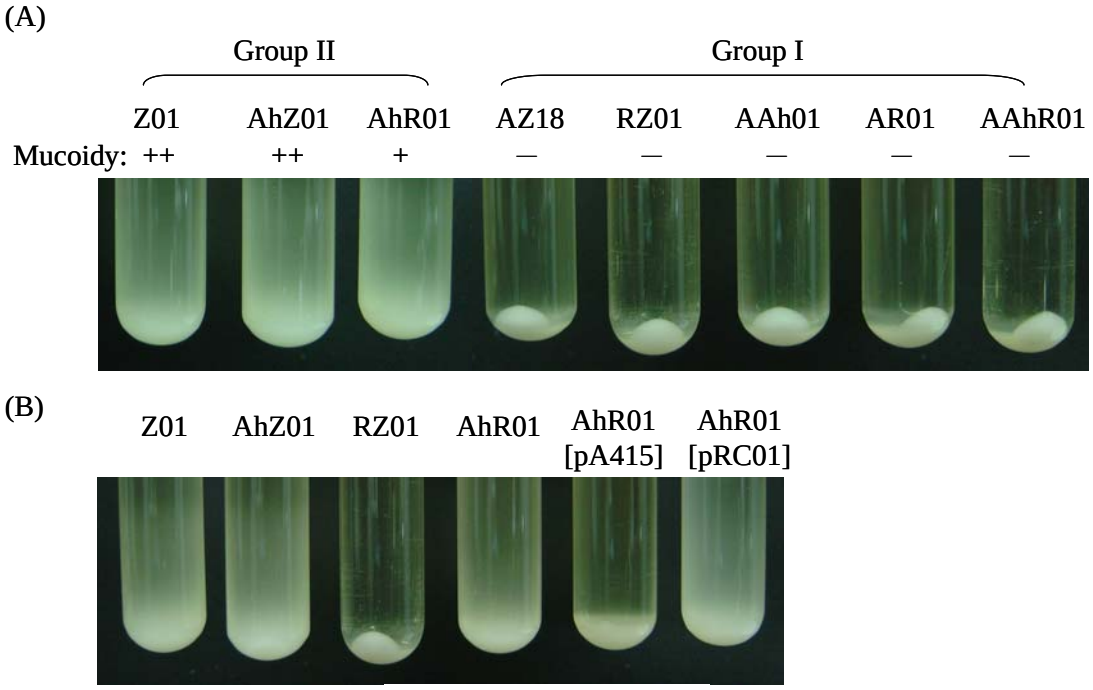

Fig. 2 Comparison of precipita s derived from *K. pneumoniae* CG43S3-Z01. (**A**) The strains night in LB broth at 37℃ and subjected to centrifugation a *g*) for 3 min. According to collective analysis of both ass lentified, in which the group I includes: AZ18, RZ01, AAh01, AR01, AAhR01, and the group II includes: Z01, AhZ01, AhR01. Bacterial mucoidy was assessed by string formation test after the bacteria grown on LB plates for 48 h. Symbols: —, negative; +, positive; ++, strong. (**B**) Effect of the complementation of AhR01 with either an intact *kvhA* or *kvhR*. The precipitation speed of the strains was also shown. AhR01 [pA415] indicated that AhR01 complementation with an intact *kvhA*. AhR01 [pRC01] indicated that AhR01 complementation with an intact *kvhR*.

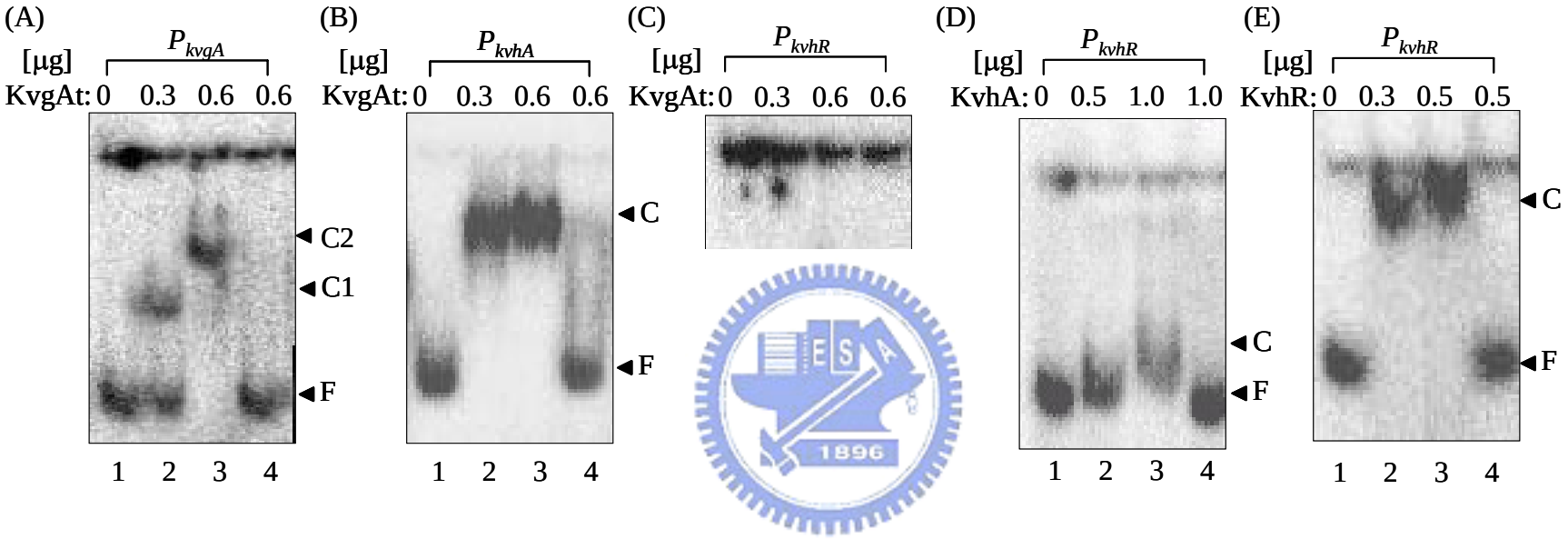

Fig. 3. EMSA of the specific DNA binding activity of KvgA, KvhA, and KvhR. DNA fragments of the P_{kvgA}, P_{kvhA}, and P_{kvhR} were labeled with [γ -^{32}P]ATP and used as probes. The recombinant KvgAt, KvhA, and KvhRt were added individually to the binding assay mixture. The amounts of protein used are indicated on each lane (lanes 1 to 3). Specific competition was performed by adding unlabelled DNA fragments into the mixture (lane 4). The DNA and protein complexes formed are indicated as C and the free probes are indicated as F.