~~WHAT IS CLAIMED IS~~CLAIMS:

1. A DNA construct comprising an isolated nucleotide sequence selected from SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or 11 or promoter portion thereof operatively linked to a polypeptide-encoding sequence operatively linked to a transcriptional terminator, wherein the DNA construct enables efficient expression of the polypeptide in a fungal species selected from *Pucciniomycotina* and *Ustilaginomycotina* subphyla, and wherein the isolated nucleotide sequence contains at least one GAGGAG sequence motif, or its reverse complement sequence.

2. The DNA construct of claim 1, wherein the promoter portion is about 400 base pairs up to about 1100 base pairs in length starting from the -1 position from the ATG codon.

3. The DNA construct of claim 1 or 2, wherein the DNA construct is inserted in a T-DNA vector, a shuttle vector, or in a fungal chromosome.

4. The DNA construct of claim 1 or 2, wherein the fungal species is selected from *Rhodosporidium*, *Rhodoturula*, *Pseudozyma, Ustilago* or *Sporobolomyces* genus, wherein the genome contains at least 50% C and G.

5. The DNA construct of claim 1 or 2, wherein the polypeptide-encoding sequence contains at least 50% CG, preferably 60% CG and most preferably more than 70% CG.

~~6. The DNA construct of claim 1 or 2, wherein the isolated nucleotide sequence contains at least one GAGGAG sequence motif, or it reverse complement sequence.~~

~~7~~6. A fungal cell containing at least one DNA construct of any one of claims 1 to ~~6~~5.

~~8~~7. The fungal cell of claim ~~7~~6, wherein the cell preferably contains no more than 3 identical copies of a nucleotide sequence set forth in SEQ ID NO:1-11 or promoter portion thereof, preferably not more than 2 identical copies of a nucleotide sequence set forth in SEQ ID NO:1-11 or promoter portion thereof.

~~9~~8. The fungal cell of claim ~~8~~7, wherein the promoter portion is about 400 base pairs up to about 1100 base pairs in length starting from the -1 position from the ATG codon.

~~10~~9. The fungal cell of claim ~~7~~6, ~~8~~ 7 or ~~9~~8, wherein the fungal cell is species selected from *Pucciniomycotina* and *Ustilaginomycotina* subphyla, preferably selected from *Rhodosporidium*, *Rhodoturula*, *Pseudozyma, Ustilago* or *Sporobolomyces* genus.

~~11~~10. An isolated promoter selected from the group consisting of:

(i) a promoter comprising the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(ii) a promoter comprising a nucleotide sequence having at least 50% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(iii) a promoter comprising a nucleotide sequence having at least 60% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(iv) a promoter comprising a nucleotide sequence having at least 70% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(v) a promoter comprising a nucleotide sequence having at least 80% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(vi) a promoter comprising a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof;

(vii) a promoter comprising a nucleotide sequence having at least 95% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof; and

(viii) a promoter comprising a nucleotide sequence having at least 98% identity with the nucleotide sequence of SEQ ID NO:1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 or promoter portion thereof,

wherein the promoter enables efficient expression of the polypeptide in a fungal species selected from *Pucciniomycotina* and *Ustilaginomycotina* subphyla.

~~12~~11. The isolated promoter of claim ~~11~~10, wherein the promoter portion is about 400 base pairs up to about 1100 base pairs in length starting from the -1 position from the ATG codon.

~~13~~12. The isolated promoter of claim ~~11~~ 10 or ~~12~~11, wherein the isolated promoter is inserted in a T-DNA vector, a shuttle vector, or in a fungal chromosome.

~~14~~13. The isolated promoter of claim ~~11~~10, ~~12~~ 11 or ~~13~~12, wherein the fungal species is selected from *Rhodosporidium*, *Rhodoturula*, *Pseudozyma, Ustilago* or *Sporobolomyces* genus, wherein the genome contains at least 50% C and G.