|  |  |
| --- | --- |
| **Fluorescence parameters** | **Physiological significance** |
| F0 ≡ F20µs | Minimal fluorescence when all the reaction centers are open |
| FK ≡ F300µs | Fluorescence intensity at 300 µs |
| FJ ≡ F2ms | Fluorescence intensity at the J-step (2 ms) of OJIP |
| FI ≡ F30ms | Fluorescence intensity at the I-step (30 ms) of OJIP |
| Fm (≡ FP) | Maximal recorded fluorescence intensity, at the peak P of OJIP when all PSII reaction centers are closed |
| Fv = (Fm-F0) | Variable chlorophyll fluorescence |
| tFm | Time to reach the maximal fluorescence intensity Fm |
| Vt = (Ft − F0)/(Fm − F0) | Relative variable fluorescence at time t |
| VI = (FI – F0)/(Fm – F0) | Relative variable fluorescence at the I-step |
| VJ = (FJ – F0)/(Fm – F0) | Relative variable fluorescence at the J-step |
| MO = (∆V/∆t)O = 4(F300µs – F0)/(Fm – F0)  | Approximated initial slope (in ms-1) of induction curve Vt (for F0 = F20µs) |
| Area  | Integrated area between the induction curve and the line F=Fm relates to the pool size of PSII electron transport acceptors |
| SM = Area/FV  | Normalized area (reflecting multiple turnover QA reduction events and representing energy necessary for the closure of all reaction centers |
| N = SM MO (1/VJ) | Number of QA redox turn over until Fm is reached |
| ABS/RC = MO (1/VJ) (1/ᵠPo)  | Absorption flux (for PSII antenna chlorophylls) per reaction center (RC)  |
| TRO/RC = MO (1/VJ)  | Trapped energy flux (leading to QA reduction) per reaction center RC |
| ETO/RC = MO (1/VJ) ψo  | Electron transport flux (further than QA–) per PSII RC(at t = 0) |
| DIO/RC = (ABS/RC) - (TRO/RC)  | Dissipated energy flux per reaction center RC (at t = 0) |
| ᵠPo = TRO/ABS = FV/Fm = [1 - (F0/Fm)]  | Maximum quantum yield of primary photochemistry (at t = 0) |
| ψo = ETO/TRO = (1 - VJ)  | Probability that a traped exciton moves an electron further than QA– |
| ᵠEo = ETO/ABS = [1 - (F0/Fm)] ψo  | Probability that an absorbed photon moves an electron further than QA– |
| ABS/CSm = Fm (at t = tFm)  | Absorption flux per excited cross section, approximated by Fm |
| TRO/CSm = ᵠPo (ABS/CSm) (at t = tFm)  | Trapped energy flux per excited cross section, approximated by Fm |
| DIO/CSm = (ABS/CSm) - (TRO/CSm) (at t = tFm)  | Dissipated energy flux per excited cross section, approximated by Fm |
| ETO/CSm = ᵠEo (ABS/CSm) (at t = tFm)  | Electron transport flux per excited cross section, approximated by Fm |
| RC/CSm = ψo (VJ/MO)(ABS/CSm) | Density of reaction centers per excited cross-section (at t = tFm) |
| RC/ABS = [(F2ms - F0)/4(F300µs - F0)](FV/Fm)  | Density of reaction centers per chlorophyll |
| PI(ABS) = (RC/ABS) (ᵠPo/(1-ᵠPo))-(ψo/(1-ψo))  | Performance index on absorption basis |
| PI(CSm) = (RC/CSm) (ᵠPo/(1-ᵠPo))-(ψo/(1-ψo))  | Performance index on cross section basis |

**Table S1:** Definitions and explanations of selected JIP-test parameters used in the present study (modified from Strasser et al., 2004)

**\* Sequences used for the synthesis of antibody raise against PTOX**

The synthesis of antibodies raised against PTOX in both species were designed using the protein sequence of PTOX for *Setaria viridis* and that of Maize for *Spartina alterniflora* based on the similarity degree of PTOX protein sequences (63%) between *Zea mays* and *Spartina alterniflora*, since the latter is not yet sequenced to date. So, we not have a complete available sequence for Spartina’s PTOX.

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>GRMZM2G102349|GRMZM2G102349\_T0|maize: CDS

ATGGCGGTGGCTTCGACCTCGCCGCTATCCGCCACGGCCCCCTCGCCGCCCGCTCCGGTGTCCGGGTTCCTCGCTCTCCCCGCCCGCCGCGGCTGCGCAACGCGCCTCGGCTCCGCCGCCGCGTGGAGGAGGCTTCGCGTGGAGGCGATCTGGAAGCAGCAGGAGAAGCAGCGGGCAGAGGTGTCCGTCGAGGAACCCGCCCCCGTCAGGGAGGCCGCCGCGCCCCTGGACGGAGTCGGAGCTGACGACCCCATGGTTCCTTCCTCGGACGAGAGCTGGGTGGTCAGGCTCGAGCAGTCGGTCAACATTTTCCTCACGGAATCGGTGATTATACTACTCAATACCGTGTACCGTGATCGGAACTACGCCAGGTTTTTTGTGCTGGAGACGATTGCCAGGGTGCCGTATTTCGCGTTCATATCGGTGCTTCACATGTATGAAACCTTTGGCTGGTGGAGACGAGCTGATTATCTAAAAGTTCACTTTGCGCAGAGCTTGAACGAGTTTCATCATCTCTTGATCATGGAAGAATTGGGTGGCAACGCTATATGGATTGATTGTTTCCTTGCTCGATTTATGGCGTTTTTTTACTACTTCATGACTGTTGCGATGTACATGTTGAGCCCACGAATGGCATATCACTTCTCTGAATGTGTGGAGAGACATGCGTACTCCACCTATGATAAGTTCCTCAAGCTCCATGAAGAGGAATTGAAAACACTACCAGCTCCAGAGGCAGCATTGAACTATTACCTGAATGAGGACCTTTACTTATTTGATGAGTTTCAGACAACAAGAATTCCATGTTCTAGGAGGCCTAAAATAGATAACTTGTATGATGTATTCGTCAATATACGAGATGACGAGGCAGAGCACTGCAAGACAATGAAGGCATGTCAAACACATGGAACTCTTCGTTCTCCTCACTCAATGCCGAACTGCTTAGAAGCTGCTACAGAATGTGTAATACCTGAAAACGATTGTGAAGGTATTGTGGACTGTGTCAAAAAGTCCCTTACAAAGTAA

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>Spartina\_PTOX|Contig2: cDNA

CTCACATCTCATTTCCACCCCACAAACGCCCACGAAACCGCAGCATGGCGGTGGCAGCCTCCACCTCCTCCTCCCCCCTCCCGGTCGCGTGCTCGCACCGGCGGGGCCCTTCCGGGTTCCTCCCGCTCCACGGCCACCGCGCCGCCACCGCCGCCACATGGAGGAGGAGGAGGCTCCACGCGGGGGCGATGAAGACGCAGCAGGAGAAGGAGCAGGCGGAGGCGACCGTCGAGGAGTCCTTCCCCGTGAGAGAGGCCGCGCCTTTGGGCGGAGCGGACGACCAGGCGGTTCCCACGGACGACAGCAGCTGGGTGGTGAATCTCGAGCAGTCCGTGAACATCTTCCTCGTGGATTCGGTGGTGACGATACTCGACAGTCTCTACCGTGACCGCAGTTACGCCAGGTTCTTTGTGTTGGAGACGATTGCTAGGGTGCCGTATTTCGCATTTATTTCCGTGCTTCACTTGTACGAGACCTTTGGCTGGTCGAGAAGAGCTGATTATATAAAGGTTCACTTTGCTGAGAGCATGAACGAGTTCCATCACCTCATGATCATGGAAGAACTGGGCGGCAACTCTGTATGGAGTGATCGTTTTCTGGCACGGTTTCTGGGCGTTTTTTTACTATTTCATGACTGTTGGGATGTACATGCTGAGCCCAAGAATGGCTTATCACTTTTCTGAATGCGTAGAGAGACATGCATACTCAACATATGACAAGTTTCTCAAGCTCAATGAAGAGGAGTTGAAAGGACTACCAGCTCCGGAGGCAGCTATAAACTATTATCTGAATGAGGATCTTTACTTATTTGACGAGTTTCAGACAGCAAGAGTTCCATGTTCAAGGAGGCCTAAAATCGATAACTTATACGATGTATTTATCAATGTACGAGATGATGAGGCGGAACATTGCAAGACAATGAAGGCCTGTCAAACAGATGGGAATCTTCAATCCCCGCACTCCACGAAGAGCTTAGAAATTGATACATAATGTGTAATACCTGCAAGCGATTGTGAAGTGTTCGGACATATGACATTGACATCACAAATACAATGTCCAATGGCGAAGTCAACGAATTCTATGATCAGGAGGCACAATGCTATCCGTCACCAGAGCTGTAGCAATGAGAGCACTGTCACCATGTAATGTCTTTCCACACAACTAGTGTAGAGGCAATCACCATTTCAACAAGCCTTTACATTTTTACCAGCTATCATCGGAACTGTTGTCATACCACCGTACGATCGTGTAACGTTAAGACCATCTGTGAATGTACCTATCTAAGCATATGCAGAAGTGTTATGTAGCAGAATAGACCAATCTTTTN

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>Sevir.3G032600|Sevir.3G032600.1|seteria\_viridis: CDS

ATGGCGGTGGCCTCCACCTCCATCCCGCCCCTCCCCGTGGCGCTGCCCGCCGCCGCCGCCGCCCGCTTCCTCCCGCTCCGCGGCCGCCGCGCCGCAGACCCGCGCCTCGGTCCCGTCGCCACGTGGAGGAGGTTCCGCGCGGAGGCGATTAAGACGCAGCGGGAGAAGCAGCAGACGGAGGTGCCCGTCGAGGAGTCCTTCCCCGCGAGGGAGGCCGCGCCGCTGGACGGAGCGGACGACCCGATGGTTCCATCGGATGAGGGCTGGGTGGTGAAGCTCGAGCAGTCGGTCAACATTTTGCTCACGGATTCGGTGATCATGGTACTCAATGGTGTTTACCGTGACCGGAGCTACGCCAGATTTTTTGTGCTGGAGACGATTGCTAGGGTGCCGTATTTTGCATTTATATCGGTGCTTCACTTGTATGAGACCTTTGGCTGGTCGAGGAGAGCTGATTATATAAAGGTTCACTTCGCTGAAAGCTGGAACGAGTTCCATCACCTCTTGATCATGGAAGAATTGGGTGGCAACGCTTTATTTTTTGATCGTTTCCTTGCTCGGTTCATGGCATTTTTTTACTACTTCATGACTGTTGGGATGTACATGCTGAGCCCAAGAATGGCATATCATTTTTCTGAATGTGTGGAGAGACATGCGTATTCAACTTATGACAAGTTTCTCAAGCTCCATGAAGAGGAGTTGAAAAGACTACCAGCTCCAGAGGCAGCTCTAAACTATTACCTGAACGAGGACCTTTACTTATTTGATGAGTTTCAGACAGCAAGAGTTCCATGTTCTAGGAGGCCTAAAATAGATAACTTGTATGATGTGTTTGTCAATATAAGAGACGATGAGGCAGAGCACTGCAAGACAATGAAGGCCTGTCAAACGCATGGAAGTCTTCGCTCTCCTCACTCAACACAGAACTGCTTAGAAGCTGATACGGAAGGTGTAATACCCGAAAAATGA
###
>GRMZM2G102349|GRMZM2G102349\_T01

MAVASTSPLSATAPSPPAPVSGFLALPARRGCATRLGSAAAWRRLRVEAIWKQQEKQRAE
VSVEEPAPVREAAAPLDGVGADDPMVPSSDESWVVRLEQSVNIFLTESVIILLNTVYRDR
NYARFFVLETIARVPYFAFISVLHMYETFGWWRRADYLKVHFAQSLNEFHHLLIMEELGG
NAIWIDCFLARFMAFFYYFMTVAMYMLSPRMAYHFSECVERHAYSTYDKFLKLHEEELKT
LPAPEAALNYYLNEDLYLFDEFQTTRIPCSRRPKIDNLYDVFVNIRDDEAEHCKTMKACQ
THGTLRSPHSMPNCLEAATECVIPENDCEGIVDCVKKSLTK
###

> Spartina. Alterni protein seq-

MAVAASTSSSPLPVACSHRRGPSGFLPLHGHRAATAATWRRRRLHAGAMKTQQEKEQAEATVEESFPVREAAPLGGADDQAVPTDDSSWVVNLEQSVNIFLVDSVVTILDSLYRDRSYARFFVLETIARVPYFAFISVLHLYETFGWSRRADYIKVHFAESMNEFHHLMIMEELGGNSVWSDRFLARFLGVFLLFHDCWDVHAEPKNGLSLF

###

>Sevir.3G032600|Sevir.3G032600.1
MAVASTSIPPLPVALPAAAAARFLPLRGRRAADPRLGPVATWRRFRAEAIKTQREKQQTE
VPVEESFPAREAAPLDGADDPMVPSDEGWVVKLEQSVNILLTDSVIMVLNGVYRDRSYAR
FFVLETIARVPYFAFISVLHLYETFGWSRRADYIKVHFAESWNEFHHLLIMEELGGNALF
FDRFLARFMAFFYYFMTVGMYMLSPRMAYHFSECVERHAYSTYDKFLKLHEEELKRLPAP
EAALNYYLNEDLYLFDEFQTARVPCSRRPKIDNLYDVFVNIRDDEAEHCKTMKACQTHGS
LRSPHSTQNCLEADTEGVIPEK

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\* To design the RT-qPCR primers, we have used the PTOX Contig 6 of Spartina with degree of similarity was higher between protein sequences of maize and Spartina. It was around 74%. Results will be more accurate than using contig2 with 63% similarity.

**\* Sequences used for the gene expression level of PTOX (q-RT-PCR)**

>Spartina\_PTOX| Contig 2: CDS

Atggcggtggcagcctccacctcctcctcccccctcccggtcgcgtgctcgcaccggcggggcccttccgggttcctcccgctccacggccaccgcgccgccaccgccgccacatggaggaggaggaggctccacgcgggggcgatgaagacgcagcaggagaaggagcaggcggaggcgaccgtcgaggagtccttccccgtgagagaggccgcgcctttgggcggagcggacgaccaggcggttcccacggacgacagcagctgggtggtgaatctcgagcagtccgtgaacatcttcctcgtggattcggtggtgacgatactcgacagtctctaccgtgaccgcagttacgccaggttctttgtgttggagacgattgctagggtgccgtatttcgcatttatttccgtgcttcacttgtacgagacctttggctggtcgagaagagctgattatataaaggttcactttgctgagagcatgaacgagttccatcacctcatgatcatggaagaactgggcggcaactctgtatggagtgatcgttttctggcacggtttctgggcgtttttttactatttcatgactgttgggatgtacatgctgagcccaagaatggcttatcacttttc

###

>Spartina\_PTOX| Contig6\_protein-seq

MAVAASITSPLPSTLSANPTAARSHARAPPRSLPLHGHRVRAPRLGTVATWRRFRAEAMRTQQEKEQTEVAVEESFPAREAAPLDGADDQMVPTDDSWAVKLEQSVNVFLVDSVVTILDSFYRDRSYARFFVLETIARVPYFAFISVLHLYETFGWSRRADYIKVHFAESMNEFHHLLIMEELGGNSVWIDRFLARFLAFFYYFMTVGMYMLSPRMAYHFSECVERHAYSTYDKFLKLNEEELKGLPAPEVAINYYLNEDLYLFDEFQTARAPCSRRPKIDNLYDVFVNVRDDEAEHCKTMKACQTHGTLRSPHATKNNLETDT
###

>Spartina\_PTOX| Contig6\_CDS

atggcggtggcagcctccatcacctcccccctcccgtcgacgctctccgccaaccccaccgcggcgcgctcgcacgcgcgggcacctccccgatccctcccgctccacggccaccgcgtccgcgccccgcgcctcggcaccgtcgccacatggaggaggttccgcgcggaggcgatgaggacgcagcaggagaaggagcagacggaggtggccgtcgaggagtccttccccgcgagggaggccgcgcctttggacggagcggacgaccagatggttcccacggatgacagctgggcggtgaagctcgagcagtccgtgaacgttttccttgtggattcggtggtgacgatattagacagtttctaccgtgaccgcagttacgccaggttttttgtattggagacgattgccagggtgccgtatttcgcatttatatcggtgcttcacttgtatgagaccttcggctggtccagaagagctgattatataaaggttcacttcgctgagagcatgaacgagttccatcacctcttgatcatggaagaattgggcggcaactctgtatggatcgatcgttttcttgcacgatttctggcgtttttttactatttcatgactgttgggatgtacatgctgagcccaagaatggcttatcacttttctgaatgcgtagagagacacgcatactcaacttatgacaagtttctcaagctcaatgaagaggagttgaaagggctaccagctccagaggtagctataaactattatttgaatgaagatctttacttatttgacgagtttcagacagcaagagctccatgctcaagaaggcctaaaattgataacttatacgatgtatttgtcaatgtacgagatgacgaggcggaacactgcaagacaatgaaggcctgtcaaacacatggaacacttcgctcccctcacgccacaaagaacaacttagagaccgataca

**Reference gene (housekeeping) for Spartina and Setaria: Tubulin alpha**

CDS sequence

>Sevir.9G071900|Sevir.9G071900.1; Setaria\_tubulin\_alpha

ATGAGGGAGTGCATCTCGATCCACATCGGGCAGGCCGGCATCCAGGTCGGCAACGCGTGCTGGGAGCTCTACTGCCTCGAGCACGGCATCCAGCCTGATGGCCACATGCCCGGAGACAAGTCTGCAGGACACTACGATGATGCCTTCACCACCTTCTTCAGCCAGACCGGCGCAGGGAAGTATGTGCCCCGTGCAATCTTCGTTGATCTTGAGCCCACTGTGATTGATGAGGTGCGCACCGGCATATACCGTCAGCTCTTCCACCCTGAGCAGCTCATCAGCGGCAAGGAGGATGCAGCCAACAACTTTGCTCGTGGCCACTACACAATTGGCAAGGAGATTGTTGATCTGTGCCTTGACCGCATCCGCAAGCTTGCTGACAACTGCACTGGCCTTCAGGGCTTTCTGGTCTTCAATGCTGTTGGTGGTGGCACCGGTTCTGGCCTTGGTTCACTCCTCCTTGAGCGCCTGTCTGTGGACTACGGCAAGAAATCCAAACTGGGCTTCACTGTGTACCCATCTCCCCAGGTGTCAACCTCTGTTGTTGAGCCCTACAACAGCGTGCTCTCCACCCACTCTCTTCTGGAGCATACTGATGTCTCCATCCTGCTCGACAACGAGGCCATCTATGACATCTGCAGGCGCTCTCTGGACATTGAGAGGCCCAACTACTCCAATCTGAATCGCCTTGTGTCTCAGGTTATCTCATCGCTGACTGCTTCCCTGAGGTTTGATGGTGCCCTCAATGTGGATGTGAATGAGTTCCAGACCAACCTGGTTCCTTACCCAAGGATCCACTTCATGCTGTCCTCGTATGCGCCGGTGATCTCTTCAGAGAAGGCCTACCATGAGCAGCTGTCGGTGTCGGAGATCACCAACAGCGCGTTCGAGCCGGCGAACATGATGGTCAAGTGTGACCCCCGCCACGGCAAGTACATGGCGTGCTGCCTGATGTACCGCGGCGATGTGGTGCCCAAGGATGTGAACGCGGCGGTGGCCACCATCAAGACGAAGCGCACGATCCAGTTTGTGGACTGGTGCCCAACAGGGTTCAAGTGCGGCATCAACTACCAGGCACCGACAGTGGTGCCGGGTGGTGACCTCGCCAAGGTGCAGCGCGCTGTGTGCATGATCTCCAACTCCACCAGCGTCGCTGAGGTGTTCTCCCGCATCGACCGCAAGTTCGACCTCATGTATGCCAAGCGCGCCTTTGTGCACTGGTATGTCGGCGAGGGCATGGAGGAGGGGGAGTTCTCCGAGGCCCGTGAGGACCTGGCGGCCCTGGAGAAGGACTACGAGGAGGTCGGCGCTGAGGGCGGTGGTGACGATGATGAGGAGGACGAGGAGTACTGA

>Contig15\_spartina\_tubulin\_alpha

atgagggagtgcatctcgatccacatcggccaggccggtatccaggtcggaaacgcgtgctgggagctgtactgcctcgaacatggcattcaggctgacggtcagatgcctggtgacaagaccattggaggaggtgatgatgctttcaacaccttcttcagtgagactggcgctggcaagcatgtgccccgtgccgtgtttgttgaccttgagcccactgtgattgatgaggtgaggactggcacttaccgccagctcttccaccctgagcagctcatcagtggtaaggaggatgcagccaacaactttgcccgtggtcactacaccattggcaaggagattgttgacctgtgccttgaccgcatcaggaagcttgccgacaactgtactggtctccagggtttccttgtcttcaatgctgtcggtggaggaactggctctggtcttggttccctcctccttgagcgtctgtctgttgactatggcaagaagtccaagctcgggttcactgtgtacccatcaccccaggtctccacctcggtggttgagccatacaacagtgtcctgtccactcactcgctcctcgagcacactgatgttgctgtgctgcttgacaatgaggccatctacgacatctgccgccgctccctcgacattgagcgcccaacctacaccaatctcaacaggcttgtatctcaggtcatctcatctctgacagcctccctgaggtttgatggtgctctgaacgtggatgtgaacgagttccagaccaacctggtgccctaccccaggatccacttcatgctttcgtcctacgcgccagtgatctctgccgagaaggcctaccacgagcagctgtctgttgctgagatcaccaacagtgccttcgaaccttcctccatgatggctaagtgtgacccccgccatggcaagtacatggcttgctgcctcatgtaccgtggtgatgttgtgcccaaggacgtgaacgctgctgtggccaccatcaagaccaagcgcaccattcagttcgtggactggtgccccactggcttcaagtgcggtatcaactaccagccacccagcgttgtccctggtggcgacctggccaaggtgcagagggccgtgtgcatgatctccaactccaccagtgttgtggaggtgttctcacgcatcgaccacaagttcgacctcatgtacgccaagcgtgcctttgccacgtggtacgtgggtgagggcagtgggaggagggcg

Tubulin alpha gene

Tub-F 5' AGGGAGTGCATCTCGATCCAC 3'

Tub-R 5' ACCTCATCAATCACAGTGGGCTC 3'

Product 230bp

Similarity 85%

**PTOX sequence similarity: 73%**

**>Sevir.3G032600|Sevir.3G032600.1|Seteria\_viridis: CDS**

ATGGCGGTGGCCTCCACCTCCATCCCGCCCCTCCCCGTGGCGCTGCCCGCCGCCGCCGCCGCCCGCTTCCTCCCGCTCCGCGGCCGCCGCGCCGCAGACCCGCGCCTCGGTCCCGTCGCCACGTGGAGGAGGTTCCGCGCGGAGGCGATTAAGACGCAGCGGGAGAAGCAGCAGACGGAGGTGCCCGTCGAGGAGTCCTTCCCCGCGAGGGAGGCCGCGCCGCTGGACGGAGCGGACGACCCGATGGTTCCATCGGATGAGGGCTGGGTGGTGAAGCTCGAGCAGTCGGTCAACATTTTGCTCACGGATTCGGTGATCATGGTACTCAATGGTGTTTACCGTGACCGGAGCTACGCCAGATTTTTTGTGCTGGAGACGATTGCTAGGGTGCCGTATTTTGCATTTATATCGGTGCTTCACTTGTATGAGACCTTTGGCTGGTCGAGGAGAGCTGATTATATAAAGGTTCACTTCGCTGAAAGCTGGAACGAGTTCCATCACCTCTTGATCATGGAAGAATTGGGTGGCAACGCTTTATTTTTTGATCGTTTCCTTGCTCGGTTCATGGCATTTTTTTACTACTTCATGACTGTTGGGATGTACATGCTGAGCCCAAGAATGGCATATCATTTTTCTGAATGTGTGGAGAGACATGCGTATTCAACTTATGACAAGTTTCTCAAGCTCCATGAAGAGGAGTTGAAAAGACTACCAGCTCCAGAGGCAGCTCTAAACTATTACCTGAACGAGGACCTTTACTTATTTGATGAGTTTCAGACAGCAAGAGTTCCATGTTCTAGGAGGCCTAAAATAGATAACTTGTATGATGTGTTTGTCAATATAAGAGACGATGAGGCAGAGCACTGCAAGACAATGAAGGCCTGTCAAACGCATGGAAGTCTTCGCTCTCCTCACTCAACACAGAACTGCTTAGAAGCTGATACGGAAGGTGTAATACCCGAAAAATGA

**PTOXSV-F** 5' CGATTGCTAGGGTGCCGTAT 3'

**PTOXSV-R** 5' AAAGCGTTGCCACCCAATTC 3'

**Product length: 211**

**>Spartina\_PTOX| Contig 6\_CDS**

atggcggtggcagcctccatcacctcccccctcccgtcgacgctctccgccaaccccaccgcggcgcgctcgcacgcgcgggcacctccccgatccctcccgctccacggccaccgcgtccgcgccccgcgcctcggcaccgtcgccacatggaggaggttccgcgcggaggcgatgaggacgcagcaggagaaggagcagacggaggtggccgtcgaggagtccttccccgcgagggaggccgcgcctttggacggagcggacgaccagatggttcccacggatgacagctgggcggtgaagctcgagcagtccgtgaacgttttccttgtggattcggtggtgacgatattagacagtttctaccgtgaccgcagttacgccaggttttttgtattggagacgattgccagggtgccgtatttcgcatttatatcggtgcttcacttgtatgagaccttcggctggtccagaagagctgattatataaaggttcacttcgctgagagcatgaacgagttccatcacctcttgatcatggaagaattgggcggcaactctgtatggatcgatcgttttcttgcacgatttctggcgtttttttactatttcatgactgttgggatgtacatgctgagcccaagaatggcttatcacttttctgaatgcgtagagagacacgcatactcaacttatgacaagtttctcaagctcaatgaagaggagttgaaagggctaccagctccagaggtagctataaactattatttgaatgaagatctttacttatttgacgagtttcagacagcaagagctccatgctcaagaaggcctaaaattgataacttatacgatgtatttgtcaatgtacgagatgacgaggcggaacactgcaagacaatgaaggcctgtcaaacacatggaacacttcgctcccctcacgccacaaagaacaacttagagaccgataca

**PTOXSA F** 5’ CCTTGTGGATTCGGTGGTGA 3’

**PTOXSA R** 5’ GCTCTCAGCGAAGTGAACCT 3’

**Product length 184**

**Table S2:** Primers list used to determine the PTOX expression level with qPCR analysis relative to the reference gene Tubuline-alpha (Tub) according to Livak and Schmittgen (2001) formula: 2−ΔΔCT (ΔCT = CT, gene of interest−CT, Tubulin-alpha).

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Gene name** | **Primers** | **Product size** |
| Tub-F | Tubulin alpha | AGGGAGTGCATCTCGATCCAC | 230 |
| Tub-R | Tubulin alpha | ACCTCATCAATCACAGTGGGCTC | - |
| PTOXSV-F | PTOX | CGATTGCTAGGGTGCCGTAT | 211 |
| PTOXSV-R | PTOX | AAAGCGTTGCCACCCAATTC | - |
| PTOXSA-F | PTOX | CCTTGTGGATTCGGTGGTGA | 184 |
| PTOXSA-R | PTOX | GCTCTCAGCGAAGTGAACCT | - |