

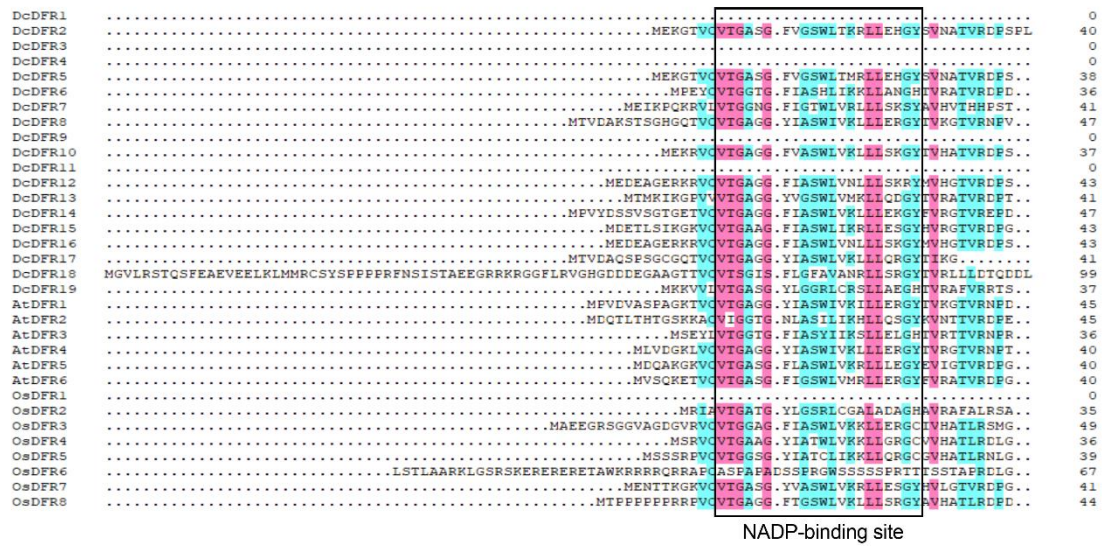


Figure S1 Amino acid sequences alignment of DcDFR with AtDFR and OsDFR protein. The putative NADP-binding site was marked by black box.

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DcDFR1 .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD 0
DcDFR2 .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD 100
DcDFR3 .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD 0
DcDFR4 .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD 0
DcDFR5 .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD 70
Consensus .....MEKGTVCVTGASGFVGSWLTMRLLLEHGYSVNATVRDPSPLPLAHSFPMNSITQLTYNESNIIETCAGNMKRVQHLLDLFRAESKRLRLWKADLVDEGSYD

DcDFR1 .....MPEIMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ 78
DcDFR2 .....GPISGIGVFHVGPIDFQTTDPENEMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ 200
DcDFR3 .....MPEIMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ 74
DcDFR4 .....MPEIMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ 78
DcDFR5 .....GPISGIGVFHVGPIDFQTTDPENEMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ 170
Consensus .....MPEIMIKPTVGGMLNVLRSCKAGTVRRVVFSSGAVIAPERRRQVYLESCWSDVEFCRATKMTGMYFVKTLAEQ

DcDFR1 .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP 178
DcDFR2 .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP 300
DcDFR3 .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP 174
DcDFR4 .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP 178
DcDFR5 .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP 270
Consensus .....AFKKEEERLDFISIVSTLVNGPFIMSMETHTLTAALITRSTPHYILKQCHVHLLDLCMAHIFLFEHPQAKGRYICSSHMTIYGLAKMLKEYP

DcDFR1 .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR 242
DcDFR2 .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR 364
DcDFR3 .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR 238
DcDFR4 .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR 242
DcDFR5 .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR 334
Consensus .....EFDIPTDFGIDPSIDVVFSSKKLLDLGFEFFYSVEEMDGEIECCRKKGLLPLANGGKPNR

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Figure S2 Amino acid sequences alignment of DcDFR1–5.