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RFLP Reports

Chromosomal location of the genes for ferredoxin in wheat, barley and rye

C. N. Chinoy, K. M. Devos, D. Bringloe [1], J. C. Gray [1], M. D. Gale * and T. A. Dyer

Cambridge Laboratory, Colney Lane, Norwich NR4 7UJ, UK
[1] Botany School, University of Cambridge, Downing Street, Cambridge CB2 3EA, UK

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Ferredoxin is the terminal acceptor of electrons from photosystem I. It is an iron-sulphur protein of relatively low molecular mass (about 10 kDa) and has a key role in the distribution of photosynthetically generated reducing power to most metabolic processes.

Source of the probe

cDNA derived from poly(A^+) RNA extracted from young wheat leaves (*Triticum aestivum*) was used in the construction of a λ gt 11 expression library (Raines et al. 1988). The library was screened using a polyclonal antibody that had been raised against the ferredoxin of pea (*Pisum sativum*). An insert of 0.5 kbp from a plaque that reacted positively with the antibody was subcloned and used as a probe, to isolate a gene from a wheat genomic library in λ Charon 35 (Lloyd et al. 1991), and its complete coding sequence was determined (D. Bringloe, unpublished results). A 1.3-kbp HindIII genomic fragment was used as a probe for gene localization.

Chromosomal localization

The hybridization patterns obtained with the ferredoxin probe in three restriction digests consist of three bands in wheat cv Chinese Spring, one band in barley cv Betzes and one band in rye cv Imperial. This indicates that the genes, designated *Fed*, are present in a single copy per genome. Nullisomic, ditelosomic and alien-wheat chromosome addition analysis showed these copies to be located on the long arms of *7A*, *7B* and *7D* and on chromosome *7R* and *7H* (barley chromosome 1).

* To whom correspondence should be addressed

Locus symbol(s)

XFed (*XFed-7A*, *-7B*, *-7D*, *-7R*, *-7H*).

Polymorphisms

Among the 15 wheat varieties screened, no RFLP was found at the *7A* locus. *XFed-7B* was extremely polymorphic with three alleles and a potential heterozygosity value, *H* (Crow 1986), of 55% with EcoRV. *XFed-7D* was mildly polymorphic with two alleles and 23% heterozygosity with EcoRV and HindIII.

The probe hybridizes strongly to barley but, of the 13 varieties screened, only 1 showed a fragment length polymorphism, with EcoRI. For rye, two varieties were examined, with three restriction enzymes. In all three cases, the varieties differed in pattern.

Table 1 shows the fragment sizes for the A, B and D genomes of Chinese Spring and that of Betzes, obtained with three restriction digests. As a further indication of the degree of RFLP at the various loci, the numbers of alleles found among 15 diverse wheat varieties and among 13 barley varieties are shown in parentheses.

Table 1. Hybridizing fragment sizes (kbp) in the A, B, and D genomes of Chinese Spring and the H genome of Betzes with different restriction digests of genomic DNA

XFed-	EcoRI	EcoRV	HindIII
7A	7.7 (1)	18.6 (1)	14.8 (1)
7B	5.4 (1)	21.6 (3)	5.4 (1)
7D	17.0 (2)	10.4 (2)	1.6 (2)
7H	7.2 (2)	2.9 (1)	10.1 (1)

Other studies of ferredoxin genes

Reports of characterization of *Fed* genes are available for *Silene pratensis* (Smeekens et al. 1985), *Spinacia oleracea* (Wedel et al. 1988), *Pisum sativum* (Elliott et al. 1989) and *Arabidopsis thaliana* (Somers et al. 1990; Vorst et al. 1990).

Probe availability

Contact D. Bringloe.

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