A New F131V Mutation in Chlamydomonas Phytoene Desaturase Locates a Cluster of Norflurazon Resistance Mutations near the FAD-Binding Site in 3D Protein Models

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Abstract
The green alga Chlamydomonas reinhardtii provides a tractable genetic model to study herbicide mode of action using forward genetics. The herbicide norflurazon inhibits phytoene desaturase, which is required for carotenoid synthesis. Locating amino acid substitutions in mutant phytoene desaturases conferring norflurazon resistance provides a genetic approach to map the herbicide binding site. We isolated a UV-induced mutant able to grow in very high concentrations of norflurazon (150 μM). The phytoene desaturase gene in the mutant strain contained the first resistance mutation to be localised to the dinucleotide-binding Rossmann-like domain. A highly conserved phenylalanine amino acid at position 131 of the 564 amino acid precursor protein was changed to a valine in the mutant protein. F131, and two other amino acids whose substitution confers norflurazon resistance in homologous phytoene desaturase proteins, map to distant regions in the primary sequence of the C. reinhardtii protein (V472, L505) but in tertiary models these residues cluster together to a region close to the predicted FAD binding site. The mutant gene allowed direct 5 μM norflurazon based selection of transformants, which were tolerant to other bleaching herbicides including fluridone, flurtamone, and diflufenican but were more sensitive to beflubutamid than wild type cells. Norflurazon resistance and beflubutamid sensitivity allow either positive or negative selection against transformants expressing the mutant phytoene desaturase gene.

Introduction
Chlamydomonas reinhardtii provides an attractive model organism to dissect processes unique to photosynthetic eukaryotes [1]. Forward genetic screens for gain-of-function mutations that confer herbicide resistance provide a powerful approach to investigate herbicide mode of action [2]. These studies proceed rapidly using algal and plant models containing herbicide target sites, which are often absent in animals and fungi. Resistance resulting from a mutation in a target protein can identify an herbicide’s binding site, which is normally revealed by identifying and sequencing the corresponding mutant gene. Identifying genes responsible for herbicide resistance is facilitated by the availability of complete sequences of the C. reinhardtii nuclear and organelle genomes [3,4]. Forward genetics provided a powerful tool to locate the binding sites of triazine herbicides in the D1 protein of photosystem II by sequencing mutant phoA genes encoding D1 from herbicide tolerant C. reinhardtii strains [5,6,7]. The locations of the amino acid substitutions in the D1 protein identified the herbicide target site which overlapped with the Qb quinone binding site in photosystem II [8,9].

Norflurazon (CID 33775) is a bleaching herbicide that blocks the synthesis of carotenoids by inhibiting the activity of phytoene desaturase (PDS) [10]. The first committed step of the carotenoid synthesis pathway produces phytoene in a reaction catalysed by phytoene synthase. PDS catalyses the next step of the pathway involving the two-step dehydrogenation of phytoene to produce zeta-carotene via a phytofluene intermediate [11,12]. Carotenoids protect chloroplasts from excess light energy [13,14] and their absence results in chlorophyll bleaching and eventual cell death [15]. In C. reinhardtii, PDS is encoded by the single nuclear PDS1 gene (Cre12.g509650) located on chromosome 12 [4]. The C. reinhardtii and A. thaliana PDS3 (At4G14210.1) proteins are homologous and share 66% amino acid identity.
PDS mutations conferring norflurazon resistance have been described in algae, plants and cyanobacteria. A C. reinhardtii mutant tolerant to 2 μM norflurazon has been described [16] but the mutation responsible remains uncharacterised. Substitutions at arginine 304 (R304S, R304T, R304H, R304C) of the 580 amino acid PDS protein from the aquatic flowering plant *Hydrilla verticillata* conferred resistance to norflurazon and the related bleaching herbicide fluridone [17,18]. A L316F substitution in the 558 amino acid PDS protein of the green alga *Chlorella zofingiensis* prevented bleaching in media containing 0.25 μM norflurazon; wild type (WT) cells were bleached by 0.05 μM norflurazon [19]. In the cyanobacterium *Synechococcus* PCC 7942, mutant PDS proteins conferring resistance to norflurazon contain R195P, L320P, V403G and L436R substitutions [11]. The herbicide lethal dose was 40 μM and 70 μM for strains harbouring the R195P and L436R substitutions, respectively, and 0.5 μM for WT *Synechococcus* [11]. The 474 amino acid *Synechococcus* and C. reinhardtii PDS proteins share 62% identity over 448 amino acids. In *Synechocystis* PCC 6803, R195P and R195S substitutions in PDS gave higher levels of norflurazon resistance than a R195G substitution [20]. The relationship between these resistance mutations located at distant sites of the plant, algal and cyanobacterial PDS proteins and the norflurazon target site in the folded protein is not known.

*C. reinhardtii* mutants tolerant to norflurazon have been previously isolated [16,21] but the mutant genes responsible for herbicide tolerance have not been isolated and sequenced. Down regulation of PDS RNA levels by about 80% did not appear to affect carotenoid levels in *C. reinhardtii* [22]. Whilst there are no previous reports of using forward genetics to isolate and sequence mutant PDS alleles conferring norflurazon resistance in *C. reinhardtii*, substitutions that impair PDS function resulting in light-induced bleaching have been identified [23]. Selection with relatively high concentrations of herbicide has the potential to isolate a new *pds1* allele encoding an extremely resistant mutant protein that could act as a marker gene for nuclear transformation [24]. New missense mutations located in regions of the primary sequence not previously associated with herbicide resistance are particularly valuable for mapping the norflurazon binding site. Here we describe the isolation of a new mutant *pds1* allele containing the first herbicide-resistance mutation to be localised to the dinucleotide-binding Rossmann-like domain. The mutant allele confers resistance to 150 μM norflurazon allowing direct herbicide-based selection of nuclear transformants. We mapped this new mutation, and other amino acid substitutions conferring norflurazon resistance in homologous proteins, from algae, cyanobacteria and plants, on 3D models of *C. reinhardtii* PDS to identify the target site of norflurazon.

**Results**

**Isolation of a Mutant Strain Highly Resistant to Norflurazon**

After exposure of *C. reinhardtii nic7 arg7 yl1 mt+* cells to high energy UV light (254 nm), colonies were selected by their ability to grow on TAP medium containing 33 μM norflurazon. Norflurazon resistant mutant strain 1 (NFR1) was chosen for further analysis because it grew much more strongly under 33 μM herbicide selection. The parent *nic7 arg7 yl1 mt+* strain giving rise to NFR1 was sensitive to norflurazon and henceforth will be referred to as wild type (WT). The lowest concentration of norflurazon tested (1 μM) reduced WT cell densities by about 70% after four days of growth in liquid TAP medium (Fig. 1A). Growth of the WT strain was prevented by 5 μM norflurazon. The effective concentration of norflurazon inhibiting WT growth by 50% (Ec50) after a four day period was 0.7±0.1 μM. In contrast, strain NFR1 grew to similar densities in the presence or absence of 5 μM norflurazon after four days growth (Fig. 1B). The NFR1 culture densities were highest at four days when exposed to herbicide and then gradually declined. The Ec50 for the NFR1 strain was calculated to be 108 μM norflurazon at four days, which is over 150-fold higher than the WT Ec50. NFR1 grew in media containing 150 μM norflurazon, the highest concentration tested, and after four days reached cell densities that were about 30% of those reached in the absence of herbicide (Fig. 1B). Coloured carotenoid content was measured by absorbance at 470 nm. The coloured carotenoid content of WT cells was reduced by 79% and 99% following exposure to 2 μM and 10 μM norflurazon, respectively (Fig. 2A). By comparison 2 μM and 10 μM norflurazon reduced coloured carotenoids in NFR1 cells by 13% and 44%, respectively (Fig. 2B).

**Genetic Analysis of Norflurazon Resistance**

Segregation analysis of resistance to norflurazon was performed by crossing NFR1 mt+ with WT norflurazon-sensitive strains S1D2 mt- or CC621 mt- and scoring haploid progeny dissected from the meiotic products of diploid zygotes. Of the 179 colonies derived from random haploid spores dissected from tetrads, 81 were norflurazon resistant. This data fits a 1:1 segregation pattern for a single Mendelian locus better than the 3:1 segregation ratio predicted for a resistance trait encoded by two unlinked genes, where only 25% of progeny would be resistant to norflurazon. The mutation conferring herbicide resistance was localised to a *pds1-nfr1d* allele encoding a mutant PDS (see below).

![Figure 1. The influence of increasing norflurazon concentration on growth of *C. reinhardtii*. Cultures were inoculated to a density of 1×10⁶ cells/ml on day 0 and optical density at 750 nm used to estimate cell density. (A) WT progenitor *PDS1* strain. (B) NFR1 mutant *pds1-nfr1d* strain. The mean values of three experiments were plotted. Standard error bars are shown. doi:10.1371/journal.pone.0099894.g001](http://www.plosone.org/apply/images/10.1371%20journal.pone.0099894.g001.jpg)
Figure 2. Impact of norflurazon concentration on coloured carotenoid content. (A) WT progenitor PDS1 strain, (B) NFR1 mutant pds1-nfr1d strain. Data obtained after seven days of growth in a 12 h light/12 h dark cycle from a starting cell density of 10⁵ cells/ml. Norflurazon was added at day 0. Average values of three replicate cultures were plotted. Standard error bars are shown.

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Figure 3. DNA blot showing Gulliver transposon bands in Hind III digests of total DNA from parental NFR1a and PQR20 strains and a diploid strain. Letters on the left represent Gulliver transposons [26]. Arrowheads indicate bands unique to either parent strain.

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Diploid (2n) cells [25] were used to determine whether the mutant allele in the NFR1 strain was dominant or recessive to the corresponding WT gene. Norflurazon resistant strain NFR1a (pds1-nfr1d, arg7 mt-) was mated to a paraquat (PQR) resistant strain PQR20 (PDS1, nic7, pqr mt-) previously isolated in our laboratory (unpublished) to produce diploid cells. Complementation of the arg7 and nic7 loci in diploid cells resulted in prototrophic growth. All diploid colonies isolated were tolerant to norflurazon and paraquat. This indicated that the mutant genes responsible for norflurazon and paraquat resistance were dominant or semi-dominant to their corresponding WT alleles. Dominance or semi-dominance of the pds1-nfr1d allele over the WT PDS1 gene was confirmed by its use in transformation experiments (see below).

A Base Substitution in the pds1-nfr1d Allele Results in a F131V Missense Mutation

The PDS enzyme is a well characterised target of norflurazon [10,11,18,27]. The PDS1 gene (Cre12.g509650) located on chromosome 12 is comprised of six exons (Fig. 4A) which are spliced together into a continuous coding region of 1692 nucleotides terminated by a TAA stop codon. All the pds1-nfr1d exons from strain NFR1 genomic DNA were amplified into PCR products and sequenced directly. Two mutations were found in the pds1-nfr1d allele compared to the C. reinhardtii WT PDS1 sequence in GenBank (Acc. No. XM_001690807). A guanine to adenine transition in exon three (base 987 of the CDS) was a silent mutation that does not change glycine 329 in the protein; base one is the adenine in the start ATG codon. A thymine to guanine transversion in exon 2, located at base 476 of the gene (base 391 of the coding region), changed the phenylalanine TTC codon at amino acid position 131 to a valine GTC codon (Fig. 4A). This F131V missense mutation resides within the Rossmann-like domain (see below) in a region showing a high degree of conservation between cyanobacterial, algal and plant PDS proteins (Fig. 4B).

Use of the Mutant pds1-nfr1d Allele as a Selectable Marker for Transformation

To show that the F131V mutation conferred norflurazon resistance, the mutant pds1-nfr1d gene was cloned in an E. coli plasmid vector and used to transform C. reinhardtii cw92, which is a norflurazon sensitive cell-wall deficient strain [28]. The 5' region of the pds1-nfr1d gene was isolated as a 3.2 kbp PCR product (Fig. 4A, primers 1017 and 1114) and joined to the 3' region of the WT gene amplified as a 3.0 kbp PCR product (Fig. 4A, primers 1113 and 1065). The two cloned PCR products were combined at a ClaI site inserted in the third intron and ligated to pBluescript to assemble the 9121 bp pNFR1 plasmid (Fig. 5A). The ClaI site was created by inserting an ATC before the GAT tri nucleotide at base 130 of the third 612 bp intron. In order to include 5' and 3' expression elements, the coding region was flanked by 1468 bp of upstream and 1390 bp of downstream sequences. As a control construct, the equivalent 5' region was cloned from the PDS1WT gene and fused to the 3' end of the PDS1WT gene to produce the pWTPDS1 plasmid. The only difference between the pNFR1 and pWTPDS1 vectors was the thymine to guanine transversion in exon 2 of the pds1-nfr1d gene (Fig. 4A) in the pNFR1 vector, which was confirmed by sequencing both plasmids.

pNFR1 and pWTPDS1 vectors were used to transform the cell wall deficient and norflurazon sensitive strain cw92 using the glass-bead vortexing method [29]. Herbicide resistant colonies were isolated by direct selection on 5 μM norflurazon medium, followed by several rounds of continued selection on 5 μM norflurazon media. We found selection on 2.5 μM norflurazon gave rise to a high
background of surviving non-transformed cells. For pNFR1, 45 to 60 herbicide resistant colonies were isolated using 2 μg of supercoiled plasmid with ~1.5×10^7 cells. Sixty percent of the colonies isolated on primary selection plates were PCR positive for the pNFR1 plasmid (not shown). In pWTPDS1 or control no-plasmid transformation experiments, typically 0–15 herbicide resistant colonies were obtained with ~1.5×10^7 cells on primary selection plates. PCR positive herbicide resistant colonies were only obtained following transformation with pNFR1 and none were isolated using pWTPDS1. The majority of PCR negative colonies from pNFR1 transformation experiments, and colonies from the pWTPDS1 and no plasmid DNA transformation experiments isolated on primary selection plates, grew relatively slowly and died following continued rounds of selection. Four norflurazon resistant colonies transformed with pNFR1 were chosen for further analysis.

Molecular Analyses of Transgenic pNFR1 Strains

DNA blots hybridized with a PDS1 cDNA probe are shown in Fig. 5C. The pNFR1 vector contains two Apa I sites and one Bam HI site (Fig. 5A). The Apa I site downstream of the Eco R1 site is located in the vector polylinker. Apa I digests of non-transformed cw92 DNA gave rise to a broad band comprised of closely migrating 3.6 and 3.8 kbp fragments (Fig. 5C lane 6, see map Fig. 5B). Transformant lanes 2–5 (Fig. 5C) contained additional Apa I bands consistent with integration of pNFR1 into the genome. A 3.3 kbp ApaI band common to three transformant lanes (Fig. 5C) represents a pNFR1 derived fragment (Fig. 5A). Additional Apa I bands in transformant lanes not corresponding to the pNFR1 bands of 3.8 kbp and 5.3 kbp are likely to represent junction fragments. Bam HI digests of DNA from all four transformants (Fig. 5C, lanes 7–10) contain the 5.8 kbp WT band (Fig. 5C, lane 11). The transformant lanes contained additional higher MW bands corresponding to integration of pNFR1 into their genomes. Three transformant lanes (A2, A10, 1A1) contained one additional higher MW Bam HI band of similar intensity to the 5.8 kbp BamHI band corresponding to the single copy endogenous PDS1 gene. This is consistent with single copy insertions. Transformant 2A1 appeared to contain multiple insertions giving rise to three additional bands in Bam HI digests (Fig. 5C, lane 10). Transforming DNA integrates by illegitimate recombination into the nucleus of C. reinhardtii and would account for differences in the banding pattern between lanes.

Accumulation of the PDS protein in transformants was compared to non-transgenic strains cw92 and cc621 by protein blot analysis (Fig. 5D). A PDS-specific antibody showed variable accumulation of a PDS band in the four transgenic lines. Transgenic strains A10 and 2A1 accumulated over two-fold higher levels of PDS protein (Fig. 5D, lanes 3, 5 and 6) than the untransformed cw92 and cc621 strains (Fig. 5D, lanes 7–8). Transgenic strains A2 and 1A1 (Fig. 5D, lanes 2 and 4) accumulated similar levels of PDS compared to the non-transgenic cw92 and cc621 strains. A~50 kDa band present in all lanes serves as a loading control and indicates similar amounts of protein were loaded per lane. Differences in PDS levels between transformants can be explained by position effects resulting from random integration of foreign genes into the C. reinhardtii nuclear genome by illegitimate recombination.

Transgenic pNFR1 Strains were Highly Resistant to Norflurazon

Growth of pNFR1 transformants and the recipient non-transgenic cw92 strain were compared in TAP media containing increasing concentrations of norflurazon (Fig. 6A). Growth of cw92 was severely reduced by 1 μM norflurazon (67% reduction) and prevented by 5 μM norflurazon after seven days growth. The growth of all transformants showed marked resistance to norflurazon. The highest levels of resistance were shown by strains 2A1 and 1A10 (Fig. 6A), which accumulated more PDS protein (Fig. 5D). All transgenic strains grew in media containing 150 μM norflurazon. When grown in TAP media without herbicide, the transformants grew at similar rates to WT (Fig. 6B). This indicates that the expression of pds1-nfr1d in transgenic strains does not have a marked impact on cell growth. Growth of transformant A2 plateaued earlier than the other strains and reached a final density that was 70% of the WT density at day six. The reduced cell density observed for one transformant...
(transformant A2) relative to cw92 is likely to reflect factors that are not directly related to the presence of transgenic DNA containing \( pds1-nfr1 \), such as the transgene integration site. In the presence of 150 \( \mu \)M norflurazon, transformant 2A1 grew to the highest densities (Fig. 6C).

**Figure 5.** Nuclear transformation vector and analysis of pNFR1 transformants. (A) pNFR1 and pWTPDS1 transformation vectors. The two vectors are distinguished by a single base substitution conferring norflurazon resistance in pNFR1. Shown are coding regions (black boxes), pBluescript vector backbone (thin grey line), extent of cDNA probe used for DNA hybridization and restriction enzyme sites. (B) Map of the \( PDS1 \) gene (white box) located on chromosome 12 (Chr12). Restriction sites and overlap region of the cDNA probe are shown. (C) Blots of digested DNA from pNFR1 transformants and untransformed cw92 strain hybridized with a \( PDS1 \) cDNA probe. Restriction enzyme used, band sizes and MW standards are indicated. (D) Protein blot of fractionated total cell protein from pNFR1 cw92 transformants, the cc621 WT strain and the non-transformed cw92 strain incubated with an affinity-purified polyclonal antibody raised against a PDS peptide. The PDS band is arrowed.

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**Figure 6.** Resistance levels of pNFR1 transformants to norflurazon. Cells were inoculated at an initial OD750 of 0.05 and were grown in TAP media with varying concentrations of norflurazon. (A) Norflurazon resistance of cw92 (norflurazon sensitive non-transformed strain) and pNFR1 A2, A10, 1A1 and 2A1 transformants. Optical density was measured after 7 days of growth. (B–C) Growth curves of NFR1 cw92 transformants and non-transformed cw92 strain in liquid TAP media without norflurazon (B) or with 150 \( \mu \)M norflurazon (C). Green line: cw92; blue line: A2; yellow line: A10; purple line 1A1; red line: 2A1. The mean values of three cultures were plotted. Standard error bars are shown.

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F131 Maps to a Rossmann-like Domain and Clusters with other Norflurazon-resistant Mutations in 3D Protein Models

A linear scheme of the 564 amino acid precursor PDS protein from C. reinhardtii containing the chloroplast transit peptide is shown in Figure 7A. F131V and previously described resistance mutations in homologous PDS proteins identify amino acids that are likely to affect norflurazon binding. The high conservation amongst PDS proteins allowed us to map substitutions conferring norflurazon resistance in homologous proteins (Fig. 8) onto the C. reinhardtii PDS sequence (Fig. 7A). The F131V mutation reported here lies in the N-terminal quarter, whereas previously reported amino acids substitutions conferring norflurazon-resistant mutations map closer to the middle (R268, L388) or C-terminus (V472, L505, L517) of the 564 amino acid protein (Fig. 7A). The F131V is the first herbicide resistance mutation localising to the dinucleotide binding Rossmann-like domain [30,31,32] spanning amino acids Y91 to L144 (Fig. 7A). This organisation of Rossmann-like domain amino acids contributing to a FAD-binding domain is characteristic of pyridine nucleotide-disulphide oxidoreductases [31]. A previously described substitution (E143K) in this domain reduces function and is suppressed by intragenic suppressor mutation K90M [23].

The crystal structure of a plant PDS has not been determined. Whilst the structure of a CRTI-type PDS enzyme present in bacteria and fungi is available [33], it is distantly related to the plant PDS enzyme and may have an independent evolutionary origin [34]. In order to map the F131V mutation and the positions of other norflurazon resistance mutations onto the structure of PDS, 3D models of the C. reinhardtii protein were constructed using four programs: 3DLigandSite [35] which uses the Phyre prediction system [36], MODELLER [37,38] via the BioSerf service [39], SwissModel [40] (Fig. 7B), and 3D-Jigsaw [41]. The predicted PDS structures are shown in Figure 7B and Figure S1. Each program used the crystal structures of different proteins to predict the folded structure of PDS. Phyre used human monoamine oxidase type B [42], MODELLER used an oxidoreductase from Methanosaeta mazei [43] and SwissModel used putrescine oxidase from Arthrobacter aurescens [44]. C. reinhardtii PDS shares: 15% identity (32% similarity) with human monoamine oxidase chain B over aligned PDS amino acids 76–537; 16% identity (30% similarity) with M. mazei oxidoreductase for PDS amino acids 76–526; 18% identity (32% similarity) with A. aurescens putrescine oxidase for PDS amino acids 76–553.

In all four models of the folded protein, three amino acids implicated in norflurazon resistance F131 (red), V472 (pink) and L505 (green), cluster together in the protein (Fig. 7B, Fig. S1). R268 (blue), whose substitution confers norflurazon resistance in cyanobacteria and Hydrilla (Fig. 8), is also part of the cluster in the 3D structures predicted by MODELLER, SwissModel (Fig. 7B) and 3D-Jigsaw (Fig. S1). In the 3D structure predicted by Phyre, R268 lies outside the cluster in close proximity to F131 (Figs. 7B and 7D). Mutations of amino acids L388 (purple) and L517 (orange) also confer norflurazon resistance (Fig. 8). L388 and L517 are located on opposite sides of the cluster (Fig. 7B). Previous work using 3D-LigandSite has suggested E143 (black) and K90 (cyan) are juxtaposed in the folded protein [23]. Consistent results were obtained with Bioserf/MODELLER, SwissModel (Fig. 7B) and 3D-Jigsaw [41,45] (Fig. S1), where E143 and K90 lie close to each other in the predicted protein structures. Amino acids in the Rossmann-like domain (Y91-L144) are shown as a yellow ribbon in Figure 7B. Whilst both F131 (red) and E143 (black) are located in the Rossmann-like domain (Fig. 7A), they are separated in the folded protein models (Fig. 7B).

Norflurazon inhibits PDS activity by competing with the enzyme’s co-factors rather than the phytoene substrate [46]. The purified plant enzyme is a flavoprotein containing FAD [47]. In bacterial CRT-I type PDS, FAD appears to be the only co-factor required for phytoene desaturation [33]. Following the desaturation reaction the reduced FADH2 produced is re-oxidised to FAD by plastocinoline either directly or indirectly [48]. The 3D-LigandSite program [33] predicts the location of the FAD binding domain [32,49,50] in PDS. The amino acids contributing to the predicted FAD binding domain in the C. reinhardtii PDS enzyme are shown in Fig. 7C. These include amino acids that are also part of the Rossmann-like domain (Fig. 7C, shaded yellow). Of the amino acids whose substitution confers norflurazon resistance, V472 (pink) is part of the predicted FAD-binding domain, whilst F131 (red) and L505 (green) lie adjacent to FAD-binding domain residues F131 and L505 (Fig. 7C). A magnified view of the relative positions of F131, V472 and L505 and FAD in the 3D-model of PDS is shown in Figure 7D. The close proximity of F131, V472 and L505 to the predicted FAD binding site is consistent with norflurazon inhibiting the function of this co-factor.

Cross-tolerance Conferred by the PDS1-nfr1d Gene to other Bleaching Herbicides

The highest levels of norflurazon resistance were exhibited by pNFR1 transformants 2A1 and A10. Four different bleaching
Synechococcus PCC7942 and Synechocystis PCC 6803 are listed. Colour coding of amino acids is the same as in Figure 7.

Discussion

We used forward genetics to isolate a new F131V substitution in the C. reinhardtii PDS protein that confers a high level of resistance to norflurazon. Whilst growth of WT cells was prevented by 5 μM norflurazon, cells containing the mutant pds1-nfr1d gene were able to grow in media containing 150 μM norflurazon. The EC50 values to norflurazon were 0.7 mM and around 100 mM for WT and mutant NFR1 cells, respectively. The norflurazon-resistance mutation conferred cross-tolerance to the bleaching herbicides fluridone, flurtamone, and diflufenican but enhanced sensitivity to beflubutamid relative to WT cells. The mutant pds1-nfr1d allele is dominant or semi-dominant to the WT gene allowing the cloned pds1-nfr1d gene to be used as a marker for nuclear transformation with direct norflurazon selection for resistant transgenic cells.

The F131V substitution is the first norflurazon resistance mutation to be mapped to the dinucleotide binding Rossmann-like domain of PDS. F131V and three other resistance mutations, which correspond to substitutions at R268, V472 or L505 in the C. reinhardtii protein (Fig. 8), are located at distant sites of the primary sequence but cluster together in the predicted tertiary structure. Moreover, three of these amino acids lie adjacent to (F131, L505) or part of (V472) the predicted FAD binding domain (Fig. 7C).

These results, based on locating amino acid substitutions conferring norflurazon resistance on 3D-models of PDS, predict the herbicide’s target region on the protein and suggest the herbicide’s mode of action involves inhibition of FAD function. Substitutions of amino acids L388 and L517 also confer norflurazon resistance but these residues do not map close to the F131-R268-V472-L505 cluster of resistance mutations on 3D models. To resolve whether L388 and L517 interact with norflurazon directly or affect binding of norflurazon indirectly by affecting the folding of the protein will become clearer if a crystal structure becomes available.

Use of the pds1-nfr1d allele as a positive selection marker for nuclear transformation of C. reinhardtii avoids the use of antibiotic resistance genes [51,52,53,54,55], which may raise regulatory concerns for commercial applications of transgenic algae. The transformation procedure used the mutant pds1-nfr1d allele with its own promoter and terminator and 5 μM norflurazon, which was substantially higher than the concentration required to kill the majority of non-transformed cells (EC50 of 0.7 μM). In a recent study, 0.5 μM norflurazon was used to select C. reinhardtii transformants expressing a cDNA encoding a mutant PDS protein in which the L505F substitution was introduced by site-directed mutagenesis [24]. The RbcS2 promoter [52] was used to express the L505F mutant gene resulting in elevated PDS transcripts [24]. Here we found that 5 μM norflurazon was required for effective selection of transformants in the light regimes used. Use of 2.5 μM norflurazon on selection plates led to a high background of non-transformed colonies. Previous herbicide resistant marker genes [24,56] and a mutant CRY1 gene providing resistance to the translational inhibitors emetine and cryptopleurine [57] have used 5’ and 3’ regulatory elements from the RbcS2 gene to allow the isolation of nuclear C. reinhardtii transformants [24,56,57]. The use of herbicide resistance genes with native regulatory elements [58] including the mutant pds1-nfr1d gene (this work) as marker genes overcomes the possibility of RbcS gene silencing and titration of
transcription or translation factors needed to express the native \(\text{RbcS}\) genes [59] in \(C.\ Reinhardtii\).

Transformants containing the \(\text{pds1-nfr1d}\) gene were 4.8 fold less resistant to beflubutamid than WT cells. By comparison, transformation of the WT \(\text{Hydilla PDS}\) protein into Arabidopsis increased seedling sensitivity to diflufenican [18]. Arabidopsis seedlings expressing a \(\text{Hydilla}\) norflurazon resistant PDS protein with a R304C (corresponds to position R268 in the \(C.\ Reinhardtii\) protein) mutation, were more sensitive to both diflufenican and beflubutamid [10]. These results show that changes in the region identified by the cluster of amino acid substitutions conferring norflurazon resistance (Figs. 7A, 7D) are critical in determining the action of herbicides and provide a step towards the rational design of new herbicides targeting this protein. The enhanced susceptibility of \(\text{pds1-nfr1d}\) transformants to beflubutamid allows negative selection. This enables \(\text{pds1-nfr1d}\), which is a native algal gene, to be used for either positive or negative selection, which is conditional on the selection agent used. Norflurazon enables positive selection whereas beflubutamid allows negative selection. Because the transformants contain both the WT and norflurazon-resistant PDS enzymes, this suggests that beflubutamid sensitivity is dominant or semi-dominant to resistance conferred by the WT enzyme. Raised PDS levels in the A10 and 2A1 transformants relative to WT cells was consistent with higher levels of the beflubutamid-sensitive mutant PDS enzyme in transgenic cells. Dual and conditional positive/negative selection markers are powerful tools for manipulating genomes and controlling the growth of transgenic cells [60,61,62]. The high norflurazon resistance levels exhibited by \(\text{pds1-nfr1d}\) transformants suggests the coding region flanked by appropriate regulatory elements may serve as a marker for transformation of a wide range of algae and plants susceptible to norflurazon and related bleaching herbicides. The PDS protein is localised to chloroplasts, which raises the possibility of using a modified coding sequence with chloroplast regulatory elements as a new marker gene for the chloroplast transformation toolbox [63]. Negative selection can be used to restrict the spread of transgenic cells, influence recombination events such as marker excision, and in mutant screens. The \(\text{pds1-nfr1d}\) allele confers sensitivity to beflutamid and is a candidate for a new negatively selectable marker for algal genetics.

Conclusions

A phenylalanine to valine substitution at position 131 in the dinucleotide binding Rossmann-like domain of phytoene desaturase increased the 5 \(\mu\)M norflurazon concentration needed to restrict growth of WT \(C.\ Reinhardtii\) cells to over 150 \(\mu\)M in mutant cells. The F131V substitution clusters with two other substitutions conferring norflurazon resistance close to the predicted FAD-binding site in 3D-protein models.

Materials and Methods

\(C.\ Reinhardtii\) Strains, Media, Mutagenesis and Genetic Crosses

All \(C.\ Reinhardtii\) strains were from the Chlamydomonas Center (University of Minnesota). Strains were maintained at 20°C to 25°C on TAP medium [1]. Transformants were propagated on TAP medium with 5 \(\mu\)M norflurazon (Sigma-Aldrich, Poole, UK). Large 25 ml–200 ml liquid cultures were grown at 25°C in a New Brunswick Scientific Innova 4340 illuminated orbital shaker at 120 rpm. Arginine (Sigma-Aldrich) was used at a final concentration of 50 mg L\(^{-1}\) and nicotinic acid (Sigma-Aldrich) at 25 mg L\(^{-1}\).

For mutagenesis 5 ml of 1 \(\times\) 10\(^7\) cells ml\(^{-1}\) of \(C.\ Reinhardtii\) strain \(\text{mc87 arg7 y1 m+}\) were irradiated for 20 seconds with a 254 nm XX-15 BlackRay germicidal UV lamp (UVP, Upland, California) at 2.42 mW cm\(^{-2}\) in 9 cm petri dishes with gentle rocking.
Irradiated cells were kept in the dark for 12 h, and then concentrated by centrifugation at 600 x g at room temperature. Three norflurazon resistant cell lines (NFR1-3) were selected on media containing 33 μM norflurazon at 25°C with a light intensity of 60 μmol m⁻² s⁻¹ in a 12 h light cycle. Only NFR1 survived several rounds of serial propagation on 33 μM norflurazon selective plates. Two additional resistant mutants were isolated using UV irradiation of 2.86 and 3.62 mW cm⁻² for 20 seconds but these grew very slowly and could not be propagated.

Genetic crosses to isolate vegetative diploid cells or zoogametes giving rise to meiotic tetrads for segregation analyses were performed as described [1,64]. Norflurazon resistant strain NFR1a (arg7, nic7, pds1-nfr1d, mt+) was isolated from a meiotic product of the cross NFR1 (nix7, arg7, pds1-nfr1d, mt+) with an arg7 mt− strain. NFR1a was sensitive to paraquat. Diploids were made by crossing paraquat-resistant strain PQR20 (ARG7, nix7, PDS1, pqr mt−) with NFR1a; the pqr locus responsible for paraquat resistance has not been identified. PQR20 was sensitive to norflurazon. Eighty one diploid colonies capable of growing on media without arginine or nicotinic acid were resistant to both norflurazon (33 μM) and paraquat (39 μM). NFR1 (nix7, arg7, pds1-nfr1d, y1 mt+) was crossed with either S1D2 mt− [65] or CC621 mt− to provide tetrads for segregation analysis.

Nucleic Acid Methods

Total DNA from C. reinhardtii was prepared according to Day et al 1988 [66], except an additional DNA precipitation was included by adding 0.6 volumes of 20% PEG 8000, 1.5 M NaCl (Sigma-Aldrich) to the total DNA solution. RNA was purified using the RNaseasy plant mini kit (Qiagen) according to the manufacturer’s instructions. Genomic DNA for PCR screening was isolated according to Cao et al. [67]. Hybridisation probes were comprised of a Gulliver [26] internal fragment and a 1.5 kbp PDS1 cDNA from C. reinhardtii strain CC-503 cw92 mt+ prepared using nested RT-PCR with primers 1297 and 1298 followed by primers 1328 and 1329. Probes were labelled with [γ-32P] dCTP (Promega, Madison, USA). Direct sequencing was on: (i) a 3235 bp PCR product containing exons 1–3 was amplified with primers 1017+1114, cloned into pGEM-T and sequenced.

Construction of pNFR1 and pWTPDS1

The pWTPDS1 plasmid was constructed by joining 5’ (3235 bp; primers 1017+1114) and 3’ (2965 bp; 1113+1065) PCR products (cloned in pGEM-T Easy) amplified from CC503 cw92 mt+ total DNA via a Cla I site located in primers 1113 and 1114. The WTPDS1 sequences in pGEM-T Easy were excised with Not I and Cla I (3235 bp sequence) and Cla I and EcoR1 (2965 bp sequence) and cloned into pBluescript KS+ [68]. To construct pNFR1, the 3.2 kbp 5’ WT PDS1 Not I - Cla I fragment was replaced with the equivalent 5’ pds1-nfr1d fragment. The complete inserts in both plasmids were sequenced to exclude PCR errors.

Nuclear Transformation of C. reinhardtii

Chlamydomonas cell wall deficient strain CC-503 cw92 mt+ was transformed according to Kindle, 1990 [29].25 ml of cell culture (~5x10⁷ cells/ml) was sedimented at 500 x g. The cell pellet was resuspended in 2.5 ml of TAP media and 300 μl mixed with 0.3 g of sterile 0.4 nm glass beads (BDH, Poole, UK), 2 μg circular (mainly supercoiled) plasmid DNA and 100 μl of 20% (W/V) polyethylene glycol (MW 8000). The mixture was vortex-mixed (Rotamix, Hook and Tucker Instruments Ltd., Croydon, UK) at maximum setting for 30 seconds. 700 μl of TAP media was added, and the cells spread onto three 9 cm selection plates containing solid (1% W/V agar) TAP media with 5 μM norflurazon. Cells were allowed to recover for 36 h in dim light (10 μmol m⁻² s⁻¹) and then transferred to high-light (250 μmol m⁻² s⁻¹). Colonies became visible after 21 days and were transferred to fresh selection media.

The Effects of herbicides on Cell Cultures

Growth curves for the NFR1 strain were prepared by inoculating cells to a concentration of 1x10⁵ cells ml⁻¹, growing them for 7 days in 50 ml of TAP media in a 12 h light cycle (60 μmol m⁻² s⁻¹) at 25°C with shaking (120 rpm) with increasing concentrations of norflurazon and measuring optical density (OD) at 750 nm. Transformant herbicide growth assays were carried out in continuous light (250 μmol m⁻² s⁻¹) at 25°C without shaking and culture ODs measured daily in a microplate reader (Biotek Synergy, Potton, UK). Transformant cells were inoculated in 1 ml of TAP media to an OD of 0.05 containing increasing concentrations of norflurazon in 24-well plates and grown for 7 days. Resistance curves for other herbicides were obtained by growing cells in 200 μl TAP media with increasing concentrations of herbicides in 96-well plates. Fluridine was used at 5, 10, 50 and 150 nM concentrations. Beflubatimid and flurtamone were utilised at 25, 50, 75 and 100 nM concentrations. Diflufenican was used at 25, 50, 100 and 300 nM concentrations. All experiments were performed in triplicate. Herbicides were from Sigma-Aldrich.

For estimation of coloured carotenoids, cultures were grown for 7 days in TAP media in a 12 h day (60 μmol m⁻² s⁻¹) with shaking (120 rpm) at a starting density of 1x10⁵ cells ml⁻¹. Carotenoids in sedimented cells (~5x10⁷ cells/ml) were extracted twice with 4 ml of 80% acetone for 20 minutes. Carotenoids were partitioned into 8 ml of 50% diethyl ether with the addition of 2 M NaCl to promote phase separation. The organic phase was washed twice with 5 ml of 4 M NaCl and then dried under nitrogen. The dried carotenoids were dissolved in diethyl ether and coloured carotenoids were estimated from the absorbance at 470 nm [1].
Protein Blot Analyses

Cells were sedimented from 50 ml cultures at 1 x 10^7 cells ml^{-1}, frozen, resuspended in 300 µl of 1 x SSC (0.15 M NaCl, 0.015 M Trisodium citrate) and 100 µl 4x gel sample loading buffer added (0.25 M Tris- HCl, pH 6.8, 40% V/V glycerol, 12% W/V SDS, 20% V/V β-mercaptoethanol, 0.4% W/V bromophenol blue). The mixture was placed in a boiling water bath for 5 minutes and then sedimented for 2 min (2000 rpm, in an Eppendorf 5415C microfuge). For SDS-PAGE, 6 µl of the supernatant was loaded per lane on 10 well, 12% W/V polyacrylamide gels with 4% stacking gels and electrophoresed in Tris-Glycine SDS buffer using the MiniProtein II system (BioRad, Hemel Hempsted, UK). Proteins were electroblotted onto Hybond ECL nitrocellulose (GE Healthcare) and incubated with antibody as previously described [69]. An affinity-purified polyclonal antibody raised in rabbits against peptide VAAWKEDGDWYETG (Eurogentec, Belgium) was used to detect PDS. The primary antibody was detected with an anti-rabbit IgG-alkaline phosphatase conjugate (Sigma-Aldrich, Poole, UK) and visualised using 5-bromo-4-chloro-3-indolyl phosphate/nitro blue tetrazolium (NBT/BCIP) reagent (Sigma-Aldrich).

Models of Protein Tertiary Structure

The C. reinhardtii PDS sequence (GI 158279545) was submitted for structural prediction using default parameters to the 3DLigandSite [35], BioSerf [39], SWISS MODEL [40] and 3D-JIGSAW [41,45]. Protein structure files were visualised and annotated using UCSF Chimera [70]. Images were rendered using POV-Ray within UCSF Chimera.

Supporting Information

Figure S1 Space-filling model of C. reinhardtii phytoene desaturase predicted by 3D JigSaw [41,45]. Amino acids F131, R268, L388, V472, L505 and L517 whose substitution are associated with norflurazon resistance are shown (see Figs. 7 and 8). Also shown are E143 and K90. Mutation of E143 impairs function and this is suppressed by a mutation at K90 [23]. The F131, R268, V472 and L505 cluster of amino acids associated with norflurazon resistance is magnified on the right. (TIF)

Table S1 Sequences of oligonucleotides used as primers for PCR and sequencing reactions. (DOCX)

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Author Contributions

Conceived and designed the experiments: PGT SB JVS AD. Performed the experiments: SB JVS. Analyzed the data: SB PGT AD JVS. Contributed reagents/materials/analysis tools: JVS SB AD. Wrote the paper: JVS AD.

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