Refined solution structure of a liganded type 2 wheat nonspecific lipid transfer protein

Jean-Luc Pons, Frédéric de Lamotte, Marie Francoise Gautier, Marc-André Delsuc

To cite this version:
Jean-Luc Pons, Frédéric de Lamotte, Marie Francoise Gautier, Marc-André Delsuc. Refined solution structure of a liganded type 2 wheat nonspecific lipid transfer protein. Journal of Biological Chemistry, American Society for Biochemistry and Molecular Biology, 2003, 278 (16), pp.14249-14256. 10.1074/jbc.M211683200 . hal-02675602

HAL Id: hal-02675602
https://hal.inrae.fr/hal-02675602
Submitted on 31 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
The refined structure of a wheat type 2 nonspecific lipid transfer protein (ns-LTP2) liganded with 1-α-palmitoylphosphatidylglycerol has been determined by NMR. The $^{15}$N-labeled protein was produced in Pichia pastoris. Physicochemical conditions and ligandation were intensively screened to obtain the best NMR spectra quality. This ns-LTP2 is a 67-residue globular protein with a diameter of about 30 Å. The structure is composed of five helices forming a right superhelix. The protein presents an inner cavity, which has been measured at 341 Å$^3$. All of the helices display hydrophobic side chains oriented toward the cavity. The phospholipid is found in this cavity. Its fatty acid chain is completely inserted in the phospholipid, while the glycerol moiety being located on a positively charged pocket on the surface of the protein. The superhelix structure of the protein is coiled around the fatty acid chain. The overall structure shows similarities with ns-LTP1. Nevertheless, large three-dimensional structural discrepancies are observed for the B3 and H4 α-helices, the C-terminal region, and the last turn of the H2 helix. The lipid is orthogonal to the orientation observed in ns-LTP1. The volume of the hydrophobic cavity appears to be in the same range as the one of ns-LTP1, despite the fact that ns-LTP2 is shorter by 24 residues.

Plant nonspecific lipid transfer proteins (ns-LTPs)$^3$ were first isolated from spinach leaves and named based on their ability to mediate in vitro the transfer of phospholipids between membranes (1). ns-LTPs are widely distributed and form a superfAMILY of related proteins subdivided into two families: the type 1 ns-LTPs (ns-LTP1) and the type 2 ns-LTPs (ns-LTP2) (see Refs. 2 and 3 for review). Both families are multigenic, and more than 150 sequences of plant ns-LTPs are listed in the GenBank database. This ns-LTP2 is a 67-residue globular protein of five helices forming a right superhelix. The protein presents an inner cavity, which has been measured at 341 Å$^3$. All of the helices display hydrophobic side chains oriented toward the cavity. The phospholipid is found in this cavity. Its fatty acid chain is completely inserted in the phospholipid, while the glycerol moiety being located on a positively charged pocket on the surface of the protein. The superhelix structure of the protein is coiled around the fatty acid chain. The overall structure shows similarities with ns-LTP1. Nevertheless, large three-dimensional structural discrepancies are observed for the B3 and H4 α-helices, the C-terminal region, and the last turn of the H2 helix. The lipid is orthogonal to the orientation observed in ns-LTP1. The volume of the hydrophobic cavity appears to be in the same range as the one of ns-LTP1, despite the fact that ns-LTP2 is shorter by 24 residues.

$^*$ The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked “advertisement” in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

$^\dagger$ To whom correspondence should be addressed. Fax: 33-467-52-96-29; E-mail: MA.Delsuc@cnrs.fr.

$^\ddagger$ The abbreviations used are: ns-LTP, nonspecific lipid transfer protein; LPG, 1-α-palmitoylphosphatidylglycerol; HSQC, heteronuclear single-quantum spectroscopy; NOE, nuclear Overhauser effect; NOESY, NOE-edited spectroscopy; TOCSY, total correlation spectroscopy; COSY, correlation spectroscopy; MALDI-TOF, matrix-assisted laser desorption/ionization-time-of-flight.
against H$_2$O, lyophilized, and analyzed by SDS-PAGE, MALDI-TOF, containing 0.1% trifluoroacetic acid. A 0.5-
proteins were eluted with 1 M NaCl. The purified protein was dialyzed
was mixed with 0.5
Tdltp18-tr5.2 (34) expressing a wheat ns-LTP2 was used for the pro-
entry 1L6H).

In the final stages of preparation of this manuscript, the struc-
ture of a rice ns-LTP2 was reported (33) (Protein Data Bank
remained to be elucidated at the initiation of the present work.
This paper presents the refined solution structure of a recom-
binant wheat ns-LTP2 liganded with a C16 lyso-phospholipid.
This paper describes the Swiss-Prot accession number or
the Protein Data Bank accession number when available. The disulfide
remains to be elucidated at the initiation of the present work.
The primary sequence alignment of various ns-LTP1 and ns-LTP2.

**EXPERIMENTAL PROCEDURES**

**Production/Purification**—The *Pichia pastoris* transformant GS115-Tdltp18-tr5.2 (34) expressing a wheat ns-LTP2 was used for the production of the 15N-labeled protein. Production was carried out in an Applikon fermentor (400 ml of culture) with 99.4% 15N-labeled ammonium sulfate (Eurisotop) as nitrogen source. Labeled (15NH$_4$)$_2$SO$_4$ (0.9%

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**Lipid Screening**—NMR and Fluorescence ns-LTP2 Lipid Screening—Preliminary experiments revealed that NMR spectra could be significantly improved when ns-LTP2 interacts with a lipid. To find the best conditions for the

**Three-dimensional HSQC-NOESY** (200-ms mixing time, 64-h acquisition 305.2 K), and a

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Experimental Procedures**

**Production/Purification**—The *Pichia pastoris* transformant GS115-Tdltp18-tr5.2 (34) expressing a wheat ns-LTP2 was used for the production of the 15N-labeled protein. Production was carried out in an Applikon fermentor (400 ml of culture) with 99.4% 15N-labeled ammonium sulfate (Eurisotop) as nitrogen source. Labeled (15NH$_4$)$_2$SO$_4$ (0.9%

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

** Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Lipid Screening**—NMR and Fluorescence ns-LTP2 Lipid Screening—Preliminary experiments revealed that NMR spectra could be significantly improved when ns-LTP2 interacts with a lipid. To find the best conditions for the

**Three-dimensional HSQC-NOESY** (200-ms mixing time, 64-h acquisition 305.2 K), and a

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and

**NMR Spectroscopy**—All of the NMR samples were prepared by dis-

The protein was purified from culture supernatant by a single-step column was equilibrated in 30 mM sodium acetate, pH 5.5, and the

**Sequence Alignment and Model Prediction**—Primary sequence alignments were performed with the following software: CLUSTAL W (37) and PSI-BLAST (38). Early three-dimensional models of construction and
Refined Solution Structure of a Liganded Wheat ns-LTP2


The dynamical annealing protocol (anneal.imp) of the crystallography NMR (CNS) software (51) was used to generate the protein structure from the set of constraints. A first set of structures was obtained from the constraint list, without any constraint on the cysteine linkage and with no phospholipid in the topology. From this set of structures, the disulfide linkage could be unambiguously assigned, because all of the sulfur atoms were located in compatible distances. The observed disulfide bridges are: Cys-2/Cys-4, Cys-2/Cys-34, and Cys-36/Cys-67. Hj-Hj NOE contacts were further observed in the NOESY map, which confirmed this assignment.

The model of the liganded protein was constructed from the same set of constraints. Additional constraints were used, corresponding to the observed connectivity of the C16 terminal CH3 of the fatty acid chain with Hβ1 and Hβ2 of Tyr-44 and the middle of the lipid chain (C8) with Hj of Phe-35 with a long distance constraint. No additional constraint was used to force the exit of the phospholipid from the protein core. The distance constraints corresponding to the S-S bounds were then added to the constraint list. The dynamical annealing protocol was used for the calculation of 250 structures, from which the 10 structures with the lowest global energy were conserved. The obtained set of structures was deposited to the Protein Data Bank (code 1N89).

The Procheck (52) program was used to check the quality of the obtained structures, as well as to compute the Ramachandran maps. The Vdoo (53–55) was used to compute the volume of the inner cavity, the solvent-accessible surface, and the radius of gyration of the protein.

RESULTS AND DISCUSSION

Production and Purification—The recombinant protein preparations were obtained as previously described (34–36). The N-terminal sequence (ACQASQLAVC) of the recombinant ns-LTP2, determined by mass spectroscopy, is identical to those of the wheat-purified ns-LTP2 (56), indicating that the recombinant protein was correctly processed by the P. pastoris KEX2 protease.

The mass spectroscopy was performed on the 15N-labeled protein. A 7055-Da average molecular mass was measured, confirming a 15N isotopic labeling over 95%. The mass spectrum also revealed that approximately 15% of the protein has been glycosylated with one to four C6 sugar moieties, assumed to be mannose (162 Da). This is consistent with the fact that P. pastoris adds O-glycans composed solely of mannose residues. Peptide mass fingerprinting of the digested protein revealed that only the first tryptic fragment at the N terminus of the protein (fragment 1–29) is glycosylated.

N-Glycosylation requires the Asn-Xaa-Ser/Thr consensus sequence, whereas O-glycosylation requires the presence of a Ser or Thr residue. The wheat ns-LTP2 does not contain the Asn-Ser/Thr sequence, whereas O-glycosylation (57). Of the four serine residues (at positions 5, 12, 16, and 21) and one threonine residue (at position 27), residues that are accessible for possible glycosylation. The presence of a proline residue in the vicinity of a serine or threonine residue can enhance O-mannosylation (57). Of the four serine residues available for O-linkage, residue 21 is the only one close to a proline residue. All of these results indicated that a small fraction of the wheat ns-LTP2 is expressed as a glycosylated protein. To our knowledge, no glycosylation has been reported for ns-LTP purified from plant.

Physicochemical Context Screening and Ligand Choice—Intensive screening of the physicochemical solution conditions was performed to find a set of conditions that provides NMR spectra of good quality. Ligand nature and ionic strength conditions were found to be critical.

Fluorescence screening experiments were performed on a series of phospholipids and fatty acids, highlighting a higher affinity for negatively charged phospholipids. We finally selected LPG with an average chain length (C16). The titration of the ns-LTP2 by LPG, monitored by NMR, shows that the ns-LTP2 becomes more structurally constrained in the presence of this ligand. A narrowing and a spreading out of the peaks are observed on the two-dimensional HSQC spectrum. This evolu-
tion is stabilized around 1 eq of LPG. The addition of 70 mM phosphate buffer was observed to also improve spectral quality (Fig. 2). On the other hand, we found that the protein could adapt a large range of pH (3.45 – 6.5) and temperatures (273 K to 323 K) without important modification of the HSQC spectra.

Under these conditions, a diffusion ordered spectroscopy experiment was used to determine the translational diffusion coefficient of the protein in the experimental conditions, found at 117 μm2/μs. Based on a calibration performed on a series of small globular proteins measured in the same conditions, this value confirms that the sample is monomeric. This result is in good agreement with the relaxation study, which has determined a rotational correlation time compatible with a monomeric form (58).

Under these optimized conditions, the 1H-15N HSQC spectrum of the 15N-labeled ns-LTP2 protein liganded with LPG displays more peaks than expected, considering the number of residues. A second step of purification designed to remove the glycosylated proteins was performed on the sample, and a 1H-15N HSQC was recorded. This spectrum displays a reduced number of peaks, but the peaks are still too numerous (labeled with question marks in Fig. 2).

One-dimensional and exchange spectroscopy two-dimensional 31P spectra were recorded on this sample. Two phosphorous lines can be observed in the one-dimensional spectrum, corresponding to the bound phospholipid and to the slight excess of free phospholipid in solution. No additional peaks nor any exchange peak could be observed in the exchange spectroscopy spectra, even at very long mixing time. To observe eventual chemical exchange, a two-dimensional 1H rotating frame NOE-edited spectroscopy experiment was performed on the LPG-liganded protein. In this spectrum a strong exchange peak is visible in the Hα region, as well as several weaker peaks close to the diagonal in the aliphatic and amide regions. The same peaks are observed when the LPG ligand is replaced with a fully deuterated DPC phospholipid. An exchange between the holo and the apo states of the protein being excluded by the 31P experiments, this is an indication that a conformational equilibrium between a major and a minor form of the protein is taking place. This equilibrium is the source of the additional peaks observed in the HSQC spectra. It was taken into account during the assignment phase, and several peaks were assigned to the minor form. However, no effort was done to fully assign this minor form.

Assignments and Secondary Structure Elements—The assignment of the protein resonances was performed from the set of 15N-edited NOESY and TOCSY spectra. The sequential strategy was used, aided by the 15N and natural abundance 13C HSQC spectra (Fig. 3).

The solvent protection experiments indicate that the secondary structure is quite strongly established, because about 40% of the amide protons remain unexchanged during the first hours of the D2O exchange experiment at 1 °C, and eight remain unexchanged after 5 days at room temperature. The solvent protection patterns, as well as J-coupling and NOESY patterns, are indicative of a structure mostly helical. On the other hand, the secondary structure prediction program Jpred (59) anticipates two helical zones, ranging from residues 22 to 29 and from residues 33 to 39.

Chemical assays as well as mass spectroscopy have shown that all eight cysteines of the protein are engaged in disulfide bridges. We have not been able to unambiguously assign the Hβ-Hα NOE contacts characteristic of this structure because of the crowding of this spectral region. However, after the first run of structure generation, all of the obtained structures exhibited side chain proximities permitting the disulfide skeleton based on these prestructures to be assigned. The disulfide bridges thus found are: Cys-25/Cys-60, Cys-10/Cys-24, Cys-2/Cys-34, and Cys-36/Cys-67. This is in agreement with the chemically determined assignment (32).

The 1H assignments of the LPG in the complexed form were obtained from two-dimensional COSY homonuclear experiments on the free LPG and by comparing the homonuclear spectra obtained from the LPG-ns-LTP2 complex and from the DPC-ns-LTP2 complex. A few chemical shifts of the fatty acid chain were clearly identified: the terminal methyl group (C16), its vicinal methylene (C15), as well as the proximal methylene (C2); the glycerol moiety attached to the fatty acid chains was also assigned. Some intermolecular NOE contacts were observed.

Structure Determination—from the complete set of geometric constraints extracted from the NMR spectra, a set of 10 structures has been obtained. They do not display any important constraint violation, and all of the residues are localized in the allowed regions of the Ramachandran plot. The ensemble of the 10 best structures present a root mean square deviation computed on residues 2–67 of 0.9 Å for all of the heavy atoms and a root mean square deviation of 0.67 Å for the backbone atoms. All of the statistics of the geometrical constraints and the structure reconstruction are given in Table I. The set of solution structures of ns-LTP2 liganded with LPG as obtained from this experimental work is presented in Fig. 4.

The protein is observed as a globular protein with a diameter of about 30 Å. The structure is composed of five helices arranged in a superhelix tertiary structure. Helix 1 is a 3–10 helix, encompassing residues 7–15. All of the other helices are α-helices. Helix 2 includes residues 22–31, helix 3 includes residues 34–40, helix 4 includes residues 44–49, and helix 5 includes residues 51–60. The overall fold is a right superhelix. The localization of the helices is in good agreement with the proton exchange experiment, which has shown that there are five main zones in which the amide protons are protected against solvent exchange: residues 14 and 15, residues 26–31,
residues 38–41, residues 47–50, and residues 56–64. The LPG molecule is found partly embedded in the structure of the protein, with the superhelix structure of the protein coiled around the fatty acid chain, and with the phosphate group and the external glycerol moiety unstructured and located outside of the core of the protein.

Helices 1 and 2 are organized in a near anti-parallel conformation. The contact between helices 1 and 2 is tightened by the Cys-10/Cys-24 disulfide bridge. They are linked by an extended strand from Ser-16 to Gly-22. Lys-19 appears to be oriented toward the solvent and does not display any NOE contact with other residue. It should be noted that in a previous dynamic study, it has been observed that the H-N vector of Lys-19 is highly mobile in the ns range (58). Helices 3–5 form a square configuration. Helix 3 contains a characteristic Cys-34, Phe-35, Cys-36 pattern, with Phe-35 buried into the structure and contributing to the hydrophobic core of the structure. Cys-34 and Cys-36 are respectively engaged in disulfide bridges with Cys-2 and Cys-67, forming two diametrically opposed bonds relative to the helix axis. All of the prolines are observed in trans conformation, as confirmed by the Hα(i)–Hα(i+1) contacts observed in the NOESY spectra, for all of the proline residues (Pro-20, Pro-42, Pro-51, and Pro-65).

Several additional secondary structure elements can be observed in the structure. The C-terminal of helix 1 presents an unusual hydrogen bond pattern, with the carboxyl moiety of Ser-12 being engaged with the HN of Ala-18. This structure is found in the 10 structures generated, and the HN of residue Ala-18 is found to be protected against solvent exchange, thus confirming this result. A type-1 γ turn is observed between helices 2 and 3, corresponding to residues Gln-31, Gln-32, and Gly-33. A type-1 β turn is observed between helices 3 and 4, corresponding to residues Asp-41, Pro-42, Thr-43, and Tyr-44, with the acidic head of Asp-41 engaged in a hydrogen bond with the HN of Thr-43. Three classic helix cappings can also be observed: the N-capping of helix 2 with the OH of Ser-21 hydrogen-bonded to the HN of Glu-23; the C-capping of helix 2 with the side chain of Gln-32 bonded to the CO of Arg-29; and the N-capping of helix 5, with the OH of Ser-50 bonded to the HN of His-52. Finally, a transient slat bridge between the amide moiety of Lys-40 and the C terminus of the backbone can be observed in several structures of the NMR ensemble.

The protein presents an inner cavity, which has been measured at 341 Å³. All of the helices present hydrophobic side chains directed toward the cavity. The phospholipid is found in this cavity. Only one unique phospholipid position is observed in the cavity for all 10 retained structures. The fatty acid chain is completely embedded in the protein structure. Its axis is aligned with the axis of the tertiary superhelix and is orthogonal to the α-helix axes (Fig. 4c). The terminal methyl group is positioned between the H1 and H4 helices. The fatty acid chain is inserted in the cavity constituted by the hydrophobic residues (Leu-7, Leu-28, Phe-35, Tyr-38, Tyr-44, Tyr-47, Ile-48, Ala-53, Leu-57, Val-64, and Pro-65). The chain presents a turn near carbon 8 and exits the cavity in a cleft between helices H4 and H5 and the C-terminal residue. The inner glycerol moiety
is located on a pocket on the surface of the protein. This pocket presents a basic environment constituted by the Arg-49, Arg-54, and His-66 side chains. These basic residues are observed in close proximity with the phosphate moiety, equilibrating the phosphate charge (Fig. 5). The cavity of ns-LTP2 is asymmetric. The proximal entrance of the cavity, where the phosphate group is found, presents several hydrophilic and basic groups: Arg-49, Arg-54, Thr-58, and His 66. The distal opening of the cavity is characterized with hydrophobic residues, such as Leu-7, Tyr-38, Tyr-44, and Tyr-47.

This location is in good agreement with the following spectroscopic observations: In the fatty acid chain only three unambiguous NOE intermolecular contacts have been identified. Four NOE contacts connect the LPG-terminal methyl groups (C16) with the Tyr-44 and Tyr-47 aromatic part. The other NOE connects the one of the methylenes of the fatty acid chain with the Hβ of Phe-35. All of these residues are found in the hydrophobic cavity. No NOE contacts were found between the protein and LPG glycerol moiety. The chemical shifts of the phospholipid glycerol moiety do not present much shift upon complexation with the protein. On the other hand, the fatty acyl chain chemical shift differences between isolated and liganded LPG are important.

The structure of the minor form present in solution has not been studied, even though it appears to be structured. About one-third of the amino acids seem to be involved in the conformation equilibrium; no attempt was made to assign the residues involved in this equilibrium. Previous dynamic study (58) has shown that the major form is predominantly rigid, with $S^2$ ranging from 0.8 to 0.9, except for Lys-19, exposed to the solvent.

**ns-LTP2 versus ns-LTP1 Comparison**—The three-dimensional structure is known for several ns-LTP1 from different species (19–29). They are very similar among plant and consist in four $\alpha$-helices organized in a superhelix structure and connected by four disulfide bridges. We compared the structure we present here with wheat ns-LTP1 (Protein Data Bank code 1gh1) (19) using the Visual Molecular Dynamics software (46) (Fig. 6).

The best superposition is obtained when the H1, H2, and H5 (residues 3–16, 22–32, and 50–63) helices in ns-LTP2 are superimposed with the H1, H2, and H4 helices (residues 5–8,10–
The presence of an hydrophobic cavity is a characteristic of ns-LTPs; the hydrophobic ligands are bound in this cavity in a rather nonspecific manner. No major differences have been observed between the structure of the free and palmitate complexed maize (21) and barley (25) ns-LTP1 and free and prostaglandin B2-ligated wheat ns-LTP1 (29), whereas large conformational changes have been seen for barley ns-LTP1 when it complexes with palmitoyl CoA (25). Orientation of the lipid within the hydrophobic cavity was found to be opposite in maize (21) and barley (26) liganded structures, whereas wheat ns-LTP1 is able to bind two monoacylated lipids insert head to tail in the hydrophobic cavity (28).

Measured volumes of this hydrophobic cavity are highly variable in ns-LTP1 (23), with typical values ranging from 150 to 580 Å³. However, barley ns-LTP1 exhibits a large volume change upon palmitoyl-CoA binding, with a measured cavity volume increasing from 39 to 620 Å³. The volume observed for the wheat ns-LTP2 appears to be in the same range, even though the protein is smaller by 24 amino acids.

The orientation of the phospholipid main chain, observed in ns-LTP2, is roughly orthogonal to the α-helix axes, and the chain runs from helices H1 to H5. This is in contrast with most described ns-LTP1 cavities found with a main axis parallel to the α-helix axes.

**Conclusion**—The present work presents the refined structure of the wheat ns-LTP2 protein, liganded with 1-α-palmitoylphosphatidylglycerol, as determined by NMR spectroscopy. The protein was observed as being composed of five helices, structured as a right superhelix, surrounding the phospholipid. This structure presents some homologies with other lipid transfer proteins such as ns-LTP1; however, the phospholipid was found in a quite different location than in most LTP1s. An hydrophobic cavity was also observed, with a volume equivalent to the one found in ns-LTP1 but with a different geometry.

The ns-LTP2 protein structure also presents homology with the one soybean hydrophobic protein that does not exhibit any lipid transfer activity. This permits us to devise a protein family encompassing ns-LTP1 and ns-LTP2 but also soybean hydrophobic protein and other related vegetal proteins, based on structural homologies, rather than on the function of primary sequence homologies.

Extensive ligand screening had to be undertaken to find a set of conditions allowing structural study. This indicates that even if the ns-LTP2 is able to adapt a large number of hydrophobic ligands in its hydrophobic pocket, it certainly presents varying affinities depending on the nature of the ligand. The better affinity for single chain phospholipid, negatively charged,
can be explained a posteriori, by the size of the pocket and by the patch of positively charged residues located around its entrance. Further comparative studies on this protein and on homologous proteins will have to be undertaken to improve the understanding on the phospholipid binding affinity and of the phospholipid transfer activity.

Finally it remains to be explained how the structural differences observed in the plant LTP family might be related to the various in vivo activities putatively assigned to its members. Comparative structural and dynamical studies on several isoforms of wheat ns-LTPs are currently in progress in our group. This complementary work should permit us to draw stronger links between structural features and biological functions.

Acknowledgments—We acknowledge N. Sommerer for mass spectrometry analysis; C. Royer, C. Blanchard, and F. Vagner for helping in the fluorescence and HSQC screening experiments; and the VMD team for efficient support.

REFERENCES