Grana Formation and Protein Mobility

**Running Head:** Grana formation and protein mobility

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DIFFERENTIAL MOBILITY OF PIGMENT-PROTEIN COMPLEXES IN GRANAL AND AGRANAL THYLAKOID MEMBRANES OF C_3 AND C_4 PLANTS

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Grana Formation and Protein Mobility

Abstract

Photosynthetic performance of plants is crucially dependent on the mobility of the molecular complexes that catalyze conversion of sunlight to metabolic energy equivalents in the thylakoid membrane network inside chloroplasts. The role of the extensive folding of thylakoid membranes leading to structural differentiation into stacked grana regions and unstacked stroma lamellae for diffusion-based processes of the photosynthetic machinery is poorly understood. This study examines, for the first time, the mobility of photosynthetic pigment-protein complexes in unstacked thylakoid regions in the C₃ plant Arabidopsis thaliana and agranal bundle sheath chloroplasts of the C₄ plants Sorghum bicolor and Zea mays by the fluorescence recovery after photobleaching technique. In unstacked thylakoid membranes, more than 50% of the protein complexes are mobile whereas this number drops to about 20% in stacked grana regions. The higher molecular mobility in unstacked thylakoid regions is explained by a lower protein packing density compared to stacked grana regions. It is postulated that thylakoid membrane stacking to form grana leads to protein crowding that impedes lateral diffusion processes, but is required for efficient light-harvesting of the modular organized photosystem II and its light harvesting antenna system. In contrast, the arrangement of photosystem I – light-harvesting complex I in separate units in unstacked thylakoid membranes does not require dense protein packing which is advantageous for protein diffusion.
Introduction

In higher plants, the photosynthetic apparatus is compartmentalized in the specialized chloroplast organelle. The molecular machinery for the primary photosynthetic processes, the sunlight-driven generation of metabolic energy equivalents, is harbored in an intricate thylakoid membrane system within the chloroplasts. Recent improvements in electron tomography have led to 3D models of the complex architecture of thylakoids membranes (Kouril et al. 2011, Daum and Kühlbrandt 2011, Austin and Staehelin 2011, Nevo et al. 2009, Mustardy and Garab 2003). Although important details about the thylakoid structure are still highly controversial, consensus exists about the overall design of this membrane system. The thylakoid membrane consists of two morphologically distinct domains; strictly stacked cylindrical grana regions with a diameter of 300 to 600 nm are interconnected by unstacked stroma lamellae, thus, forming a continuous membrane system. The molecular complexes that catalyze energy transformation are distributed heterogeneously between the stacked and unstacked membrane regions. The majority of the photosystem II complex (PSII) and light-harvesting complex II (LHCII) are localized in stacked thylakoid regions, whereas photosystem I (PSI) and the ATP-synthase complex are lacking from stacked grana (Staehelin and van der Staay 1996, Albertsson 2001, Dekker and Boekema 2005). It is assumed that the fifth photosynthetic protein complex (cytochrome b$_{6}$f complex) is homogenously distributed.

An essential feature of the thylakoid membrane system is its high flexibility, which is required for adaptability and maintenance of the photosynthetic machinery in plants. Highly responsive to environmental conditions, both the overall thylakoid architecture (e.g. number of grana discs) and the molecular membrane composition can change remarkably to optimize, protect, and maintain the photosynthetic apparatus (Chuartzman et al. 2008, Walters 2005, Anderson et al. 2008, Dietzel et al. 2008, Betterle et al. 2009, Johnson et al. 2011). The underlying molecular processes require brisk protein traffic between stacked and unstacked thylakoid domains (Kirchhoff 2008). The role of grana in these transport-based processes is poorly understood.

Although photosynthetic energy conversion is possible without grana (Anderson et al. 2008), the fact that stacked thylakoids are ubiquitous in almost all land plants (with the exception of chloroplasts in bundle sheath [BS] cells in some C$_{4}$ plants, see below)
Grana Formation and Protein Mobility

highlights the evolutionary pressure to preserve this complex structural feature. Recently, the importance of grana formation was highlighted in *Arabidopsis* mutants, which lack the *GDC1* (*grana-deficient-chloroplast 1*) gene; they grow much slower than wildtype and exhibit seed lethargy due to missing grana formation (Cui et al. 2011). The functional advantages of grana formation have been discussed extensively (e.g. Anderson et al. 2008, Mullineaux 2005, Trissl and Wilhelm 1993). It was hypothesized that grana could (i) increase the thylakoid membrane area, and the pigment concentration, in chloroplasts, (ii) avoid energy spillover from PSII to PSI, (iii) regulate the balance of energy distribution between PSII and PSI by *state transition*, and (iv) enable transversal exciton energy transfer between adjacent grana discs. Although there are good arguments that these possibilities are important for photosynthetic energy conversion, the basis for the evolutionary development of grana has not been determined (Mullineaux 2005, Anderson et al. 2008).

A less considered aspect of grana formation is that it leads to a concentration of protein complexes (Murphy 1986, Kirchhoff 2008). The membrane area fraction that belongs to integral photosynthetic protein complexes is about 70%, making grana discs one of the most crowded biomembranes (Kirchhoff 2008). Light-harvesting by photosystem II benefits from a high protein packing density for two reasons. First, a concentration of PSII and LHCII in grana ensures a high concentration of light-absorbing pigments that increase the probability of capturing sunlight, which is a “dilute” energy source on the molecular scale (Blankenhship 2002). Second, it has been demonstrated that a high protein packing density in grana thylakoids is required for efficient intermolecular exciton energy transfer between LHCII and PSII (Haferkamp et al. 2010). Macromolecular crowding ensures that weakly interacting LHCII and PSII complexes come in close contact, allowing efficient Förster type energy transfer.

Besides these advantages, lateral protein traffic is challenged by macromolecular crowding (Mullineaux 2005, Kirchhoff 2008). The molecular mobility of proteins in grana thylakoids is reduced by numerous collisions of the diffusing object in the 2D reaction space of the membrane with obstacles, integral membrane proteins, that increase the apparent diffusion path and, consequently, the diffusion time. The strong impairment of a high protein density in grana thylakoids on protein mobility was demonstrated by
Grana Formation and Protein Mobility

computer simulations (Kirchhoff et al. 2004, Tremmel et al. 2003) and by diffusion measurement on isolated grana membranes (Kirchhoff et al. 2008) and intact chloroplasts (Goral et al. 2010) using the Fluorescence Recovery after Photobleaching (FRAP) technique. Processes that are expected to be affected by restricted protein mobility are regulation of energy distribution between PSII and PSI by state transitions (Lemeille and Rochaix 2010), the repair of photodamaged PSII (Mulo et al. 2008), membrane remodeling triggered by long-term environmental changes (Walters 2005, Anderson et al. 2008), and the biogenesis of the thylakoid membrane network (Adam et al. 2011). Recently, evidence has accumulated that photoprotective high-energy quenching also requires large-scale diffusion-based structural reorganization within grana thylakoids (Betterle et al. 2009, Johnson et al. 2011).

In contrast to our current understanding of diffusion-based processes in thylakoid membranes, knowledge about the factors that determine the mobility of photosynthetic protein complexes in different thylakoid domains is still fragmentary (Mullineaux 2008). The protein packing density is very likely a main element that determines protein mobility (Kirchhoff et al. 2008). However, other factors like electrostatic interactions between proteins by membrane surfaces charges (Tremmel et al. 2005) or the size and molecular shape of protein complexes (Tremmel et al. 2003) can contribute significantly. However, data only exists about protein mobility for isolated grana thylakoids (Kirchhoff et al. 2008) and for chloroplasts from the grana-containing C_3 plant Arabidopsis (Goral et al. 2010). The diffusion characteristics of the latter are almost completely determined by granal proteins. Limiting information on protein diffusion exists for stroma lamellae of C_3 plants (Consoli et al. 2005, Vladimirou et al. 2009) and no data is available for agranal thylakoids, which occur in BS cells of some C_4 species.

The current study fills this gap in the knowledge base by studying lateral protein diffusion in unstacked thylakoid membranes in BS chloroplasts of two NADP-ME type C_4 species, maize and sorghum, in comparison to the grana containing mesophyll chloroplasts. The analysis was also complemented by studies on isolated thylakoid sub-fragments (grana core, grana and stroma lamellae) from Arabidopsis. The protein mobility was measured by FRAP (Mullineaux and Kirchhoff 2007) which has been shown to be a straightforward method to analyze protein diffusion in photosynthetic
membranes by utilizing natural chlorophyll fluorescence (Kirchhoff et al. 2008, Goral et al. 2010). The comparison to diffusion characteristics in unstacked versus stacked membrane areas highlights the significance of grana formation on the lateral mobility of photosynthetic pigment-protein complexes.

**Results**

**Microscopic, spectroscopic and biochemical characterization of chloroplasts in isolated bundle sheath strands and mesophyll protoplasts of maize and sorghum**

In NADP-ME type C₄ plants, the BS chloroplasts are deficient in grana while the mesophyll (M) chloroplasts have well developed grana. The structural integrity of the BS cells was verified by confocal laser scanning microscopy (CLSM) for maize BS strands (Fig. 1A) and sorghum (not shown). Higher resolution CLSM micrographs show a lamellar membrane organization in BS chloroplasts of maize and sorghum (Fig. 1B and Fig. 1C) that confirms an agranal thylakoid organization in these chloroplasts (see Laetsch 1971; Metha et al. 1999). In contrast, CLSM images of grana containing M protoplasts from *Arabidopsis* (Figure 1D) and maize and sorghum (not shown) reveal particulate fluorescence spots of about 400 nm in diameter indicative of grana stacks in these cells.

Bundle sheath and M protoplast preparations of maize and sorghum were further characterized by room temperature chlorophyll fluorescence spectra and recorded with the same confocal microscope as used for FRAP (Fig. 2). For comparison, emission spectra of isolated grana core and stroma lamellae of *Arabidopsis* were measured (Fig. 2). Spectra of isolated grana core discs and stroma lamellae differ mainly in the far-red region. The broad shoulder in the far-red for stroma lamellae (Fig. 2, dashed line) is caused by the higher abundance of the PSI-LHCl complex, that has a peak emission around 725 nm and low emission at 680 nm at room temperature (Croce et al. 2000). It should be noted that the emission spectra of isolated stroma lamellae still have a maximum around 680 nm that originates from PSII and LHClII complexes (Krause and Weis 1991). On first thought, this is surprising because stroma lamellae have a much higher abundance of PSI relative to PSII (Albertsson 2001). The dominance of the PSII/LHClII emission in isolated stroma lamellae is explainable by their much higher
fluorescence yield compared to PSI-LHCI (Krause and Weis 1991). However, the far-red emission shoulder can be taken as an indicator of PSI/LHCI which is enriched in stroma lamellae and absent in grana core regions (Fig. 2).

The fluorescence spectrum for M cells (sorghum is shown as an example in Fig. 2A) is very similar to isolated grana core of Arabidopsis, indicating the presence of PSII/LHCII enriched grana. In contrast, the spectra of BS strands from maize and sorghum reveal clear far-red shoulders in accordance with the presence of agranal PSI-LHCI enriched chloroplasts (Fig. 2B). The higher amplitude of the far-red shoulder relative to the emission around 680 nm in sorghum BS cells is indicative of higher PSI/PSII ratios in sorghum thylakoid membranes compared to their counterparts in maize. For the FRAP measurements presented below, it is important to recognize that the dominance of the 680 nm emission in stroma lamellae and agranal BS chloroplasts implies that mainly PSII/LHCII diffusion was monitored.

The composition of the thylakoid membranes in M and BS cells were characterized by determining their lipid and chlorophyll contents (Table 1). The chlorophyll a/b ratio of maize and sorghum is significantly higher in agranal BS tissues compared to grana containing M cells, as reported earlier (Ku et al. 1974, Pokarsaka and Romanowska 2007). The higher chlorophyll a/b ratio, and the higher ratios of chlorophyll fluorescence under liquid nitrogen temperature at 730nm/685nm for thylakoids of M than BS thylakoids (5 to 6 fold) is indicative of a much higher abundance of LHCl-PSI complexes in BS thylakoids of these C₄ plants (Mayne et al. 1974, Romanowska et al. 2008), in agreement with the room temperature chlorophyll fluorescence spectra (Fig. 2). The lipid composition was measured from total M and BS cells that include extrachloroplast lipids. Information about chloroplast lipids can be extracted from these data by quantification of the three lipid classes; monogalactosyldiacylglycerol (MGDG), digalactosyldiglyceride (DGDG), and sulfoquinovosyl diacylglycerol (SQDG), that are exclusively found in chloroplasts (Benning 2009). Since more than 80% of the chloroplast lipids are found in thylakoid membranes and less than 20% in envelope membranes (Kirchhoff et al. 2002), the quantification of MGDG, DGDG, and SQDG allows estimation of the lipid content in thylakoid membranes. We also quantified the fourth thylakoid lipid class, phosphatidylglycerol (PG) (Table 1) that is also found in
other cell membranes. Since the ratio of chloroplast to extrachloroplast lipids is high, the contamination with non-chloroplast PG is low. Both the relative abundance of the four lipid classes and the lipid/chlorophyll ratio for Arabidopsis (Table 1) are in good agreement with numbers determined for isolated thylakoid membranes from spinach (Kirchhoff et al. 2002). This indicates the validity of the approach to quantify the lipid content for thylakoid membranes from whole cell lipid extracts.

Since virtually all chlorophylls are bound to membrane-integral photosynthetic protein complexes, the chlorophyll content is a good measure of the protein content in thylakoid membranes. Consequently, the thylakoid-lipid/chlorophyll ratio is a good estimate for the protein packing density in thylakoids (Haferkamp and Kirchhoff 2008). From the lipid/chlorophyll ratios in Table 1, it follows that the protein packing density in agranal sorghum and maize BS strands is significantly lower (higher lipid/chlorophyll ratio) compared to grana containing M cells. The impact of these differences in protein packing on the mobility of photosynthetic pigment-protein complexes in thylakoid membranes is reported in the next sections.

**FRAP analysis with bundle sheath strands and mesophyll protoplasts of maize and sorghum**

For protein diffusion measurements by FRAP, the thylakoid membrane bound chlorophylls are irreversibly bleached in a small stripe by a short, intense laser excitation (Fig. 3). The time-dependent fluorescence recovery into the bleached line by unbleached pigments from the surrounding area is a direct measure of the diffusion of chlorophyll-protein complexes, e.g. the recovery is fast if the protein mobility is high.

Figure 3 shows FRAP examples for chloroplasts in grana-containing Arabidopsis protoplasts (upper panel Fig. 3A-3D) and in agranal sorghum BS chloroplasts (lower panel, Fig. 3E-3H). For easier comparison, the integrated fluorescence profiles along the x-axis of the chloroplasts are depicted on the right in each image. The recoveries of the bleach lines (triggered in B and F) are significantly different in both chloroplast types. After 40s, the intensity of the stripe is much fainter in sorghum BS chloroplasts (Fig. 3G) than in Arabidopsis (Fig. 3C); and after 130s, the line in Arabidopsis is still visible (Fig. 3D), but not visible in sorghum BS chloroplasts, indicating faster recovery (Fig. 3H).
This shows that the overall mobility of chlorophyll-protein complexes is higher in the agranal chloroplasts compared to their grana-containing counterparts in *Arabidopsis*.

Statistical analyses of the fluorescence recovery kinetics of grana-containing and agranal chloroplasts are depicted in Fig. 4. Two pieces of information can be extracted from FRAP kinetics: (i) the fraction of mobile molecules (in our case the chlorophyll-protein complexes) and (ii) the diffusion coefficient ($D_c$) of the mobile molecules. Reliable determination of $D_c$ is only possible if the membrane structure is simple, e.g. flat planar membranes (Mullineuax and Kirchhoff 2009). This precondition is not fulfilled for the complex structured thylakoid membranes system examined in this study. However, the mobile fraction can be accurately determined. In Fig. 4, this fraction is determined as the ratio of the fluorescence level at the end of the measuring window to the level before the bleach (the fluorescence level directly after the bleach at time point zero in Fig. 4 was set to zero). The calculated numbers for the mobile fraction (in percent) are indicated in Fig. 4. The analysis clearly shows differential protein mobility in grana-containing M chloroplasts of *Arabidopsis*, maize, and sorghum (Figs. 4A-C) and agranal BS tissues of maize and sorghum (Figs. 4D, 4E). While the mobile fraction in M cells is between 16% and 20%, this percentage increased to ~50% to 70% in agranal BS cells in sorghum and maize, respectively. The value of 20% mobile fraction for the C3 plant *Arabidopsis* (Fig. 4A) is in accordance with recently published numbers for isolated chloroplasts (Goral et al. 2010). The data indicate that the formation of grana leads to a decreased mobility of photosynthetic pigment-protein complexes.

**Protein mobility analysis in isolated grana and stroma thylakoid membranes of *Arabidopsis***

For further characterization of a differential protein mobility in stacked and unstacked thylakoid regions, FRAP measurements were performed on isolated stroma lamellae, grana (including grana margins), and grana core subfragments from *Arabidopsis* plants. In particular, the comparison of the mobile fractions in isolated stroma lamellae with agranal BS cells is interesting, since the protein organization in these unstacked membranes is different (see Discussion).
The identities of the three membrane domains were verified by their chl a/b ratios, and by their protein composition as analyzed by denaturative gel electrophoresis (SDS-PAGE) (Fig. 5). The chl a/b ratios of 4.92 for stroma lamellae, 2.56 for grana, and 2.34 for grana core are in accordance with literature values for these three thylakoid subdomains (Albertsson 2000). The identity of the three subdomains is further supported by the abundance of α-subunit (~54 kDa, *atpA* gene product) and β-subunit (~50 kDa, *atpB* gene product) of the CF₁ part of the ATP synthase complex in stroma lamellae and its depletion in grana and grana core as seen in SDS gels (Fig. 5D) since the ATPase complex is excluded from stacked thylakoid regions by steric hindrance (Albertsson 2001). In addition, densiometric analysis of the *AtpA* and *AtpB* bands reveals that the grana core membranes (16% *AtpA* and 14% *AtpB* abundance relative to thylakoids) are more depleted in these subunits than in grana preparations (24% and 27%). This indicates that the grana, compared to the grana core, contains a higher amount of ATPase-containing grana margins (Albertsson 2001), which is in line with the higher chl a/b ratio (Fig. 5). Finally, the depletion of the 25 kDa band in stroma lamellae is indicative of a low abundance of LHCII, as is expected for this thylakoid domain (Bassi et al. 1995).

FRAP studies on the three thylakoid subdomains show the highest mobile fraction in stroma lamellae. The value of about 55% is in the range found for agranal BS cells (Fig. 4). In contrast, the mobile fraction in grana and grana core preparations is much lower with the lowest values logged for grana core membranes. The recorded difference between the two grana preparations is statistically significant (t-test, P=0.010). This indicates that the additional margin contribution in grana increases the overall protein mobility.

**Discussion**

Chloroplasts in plants generally consist of grana and stromal lamellae, which are remarkably different in composition with primary functions of PSII in grana and PSI and ATP synthase in the stromal lamellae. Besides functioning cooperatively with PSII in the grana in linear electron flow for generating NADPH, PSI may function independently in the stroma lamellae in PSI mediated cyclic photophosphorylation (Johnson 2011). An unusual type of chloroplast exists in BS chloroplasts of NADP-ME type C₄ species
which, like the stromal lamellae, are deficient in grana and PSII but rich in PSI. The primary function of BS chloroplasts is the generation of ATP while the M chloroplasts have a major role in providing reductive power for CO$_2$ assimilation (Edwards and Walker 1983, Hatch 1987). Among the NADP-ME monocots, sorghum and sugarcane have extreme deficiency with agranal BS chloroplasts and PSII activity less than 1% of that of M cell chloroplasts, and maize having a few rudimentary grana in BS chloroplasts with PSII activity ~3% of that of M cell chloroplasts (see Laetsch 1971, microscopy; Ku et al. 1974). PSII activity was measured with p-benzoquinone as a Hill oxidant with intact isolated M protoplasts and bundle sheath strands. Low levels of PSII in the BS chloroplasts may provide redox poise for PSI dependent cyclic photophosphorylation to compensate for electrons lost from the cycle (Ivanov et al. 2007; Romanowska et al. 2008). Thus, the unstacked thylakoid membranes of BS chloroplasts of these species provide a good model for studying protein diffusion in relation to composition and function of the stromal lamellae in chloroplasts having grana.

In chloroplasts of C$_3$ plants, not only are the types of protein complexes and supercomplexes different between grana and stromal lamellae (Albertsson 2001); there is also a difference in the protein packing density. Both the biochemical data (Murphy 1986) as well as ultrastructural data (Staehelin and van der Staay 1996) indicate that stroma lamellae in C$_3$ plants are significantly less crowded by membrane integral proteins than are grana membranes. In the present study, the comparison of FRAP data of grana core, grana (with margins), and stroma lamellae in *Arabidopsis*, a C$_3$ plant (Fig. 5), revealed that the lower protein packing densities in grana margins and, in particular, in stroma lamellae correspond to higher protein mobility. The same pattern was observed between agranal BS cells and grana-containing M cell thylakoids from the C$_4$ plants maize and sorghum (Fig. 4), i.e. BS cells have a lower protein packing density and higher mobile fractions in thylakoid membranes than M cells. Two conclusions can be drawn from this data. First, grana formation leads to tighter packing of membrane embedded protein complexes. In this respect, the significantly lower protein packing density in agranal BS chloroplasts, as determined in this study, complements the existing data on stroma lamellae in C$_3$ chloroplasts (Murphy 1986, Staehelin and van der Staay 1996). Second, higher protein packing density in grana thylakoids decreases the mobility of
Grana Formation and Protein Mobility

grana-hosted proteins. This is in agreement with *in vitro* studies on isolated grana membranes (‘BBY’ membranes) with different lipid/protein ratios, which show a strong dependency of the immobile fraction in FRAP experiments on the protein density (Kirchhoff et al. 2008). The protein mobility data on agranal and grana-containing chloroplasts in different cells is summarized in Fig. 6. To verify that the lipid/chlorophyll ratio (Fig. 6A) is an adequate measure for protein density in the different thylakoid types we compared the mobile fraction with the lipid/protein ratio in washed thylakoids (Fig. 6B). Washing with the chaotropic NaSCN removes extrinsic and attached proteins to thylakoid membranes (Fiedler et al. 1994). Thus, protein determination after NaSCN-treatment specifically measures only membrane integral complexes. Since both the lipid/chlorophyll (Fig. 6A) and the lipid/protein ratio (Fig. 6B) correlate linearly with the mobile fraction, the lipid/chlorophyll ratio provides a measure of the relative protein density in the examined thylakoid membranes. For comparison with literature data, we will focus on the lipid/chlorophyll ratio (Fig. 6A) in the further discussion. The good linear correlation (\(r^2 = 0.973\)) between mobile fraction and lipid/chlorophyll ratio for the different species having different thylakoid architectures (Fig. 6A) gives strong evidence that the dependency of protein mobility on protein density is a general principle realized in higher plant thylakoid membranes. This is supported by the fact that protein mobility in isolated stroma lamellae from *Arabidopsis* is similar to the mobility in agranal BS cells. Both have a lower protein density compared to grana thylakoids and have PSI, cytochrome *b*₆*f* complexes, and ATP synthase with low levels of PSII reaction centers. However, it was recently shown that agranal BS cells of maize contain dimeric LHCII/PSII supercomplexes (Romanowska et al. 2008), whereas the stromal lamellae of C₃ plants have monomeric PSII complexes (Danielsson et al. 2006). This indicates that the packing density of membrane complexes determines their mobility, rather than any difference in PSII centers. This does not exclude the possibility that protein mobility can be modulated by other factors like electrostatic effects and/or by the different shapes or sizes of the proteins. Rather, it highlights the dominant role of protein packing density.

From extrapolation of the regression line in Fig. 6A, the lipid/chlorophyll ratio where all proteins are immobile (intersection with x-axis) and where all proteins are mobile (at 100 % mobility), can be predicted. It follows that at a molar lipid/chlorophyll
ratio of ~0.8 all proteins in thylakoid membranes are expected to be immobile. It is interesting to compare this value with the number of 1.13 (Kirchhoff et al. 2002), which is the required lipid/chlorophyll ratio needed to encircle all thylakoid protein complexes with one layer of lipids (so-called boundary lipids). This comparison indicates that at lipid/chlorophyll ratio ~0.8, not enough lipids are available to avoid direct protein-protein contact between photosynthetic supercomplexes, and in consequence, all proteins are immobilized in thylakoid membranes. This may be realized by a homogenous depletion of boundary lipids between all protein complexes or a by heterogeneous depletion, i.e. many proteins are in direct contact creating free lipid space in other membrane areas. However, a critical lowest lipid amount in thylakoid membranes is obviously required to ensure minimal flexibility of the protein network which is required to adjust and maintain the photosynthetic machinery (see Introduction). How the lipid/protein ratio is adjusted in photosynthetic membranes remains an important point for future research.

The other extreme deduced from Fig. 6A is the lipid/chlorophyll ratio where all proteins are mobile. This is expected at ~6 lipids per chlorophyll, in accordance with the protein-density titration experiment with isolated grana (BBY) membranes (Kirchhoff et al. 2008). In the BBY study, the highest level of mobile proteins was found at a lipid/chlorophyll ratio of ~7. The original number of 10 added lipids per chlorophyll was corrected to the measured lipid/chlorophyll ratio in the final preparation (Haferkamp and Kirchhoff 2008), as this is equivalent to what is used in the present study. Furthermore, at a threshold value of ~6 lipids per chlorophyll (corrected as above), maximal functional uncoupling between LHCII and PSII in BBY membranes is reached (Haferkamp et al. 2010). This functional uncoupling was explained by protein-dilution induced separation of weakly interacting LHCII and PSII supercomplexes leading to disruption of Förster-type exciton energy transfer. In this context, it is interesting that a significant fraction of functional uncoupled LHCII was detected in BS cells of maize (Romanowska et al. 2008). In light of our findings, this can be explained by the lower protein packing density in BS thylakoid membranes, which leads to separation and functional uncoupling of LHCII from PSII.

This study demonstrates that the lower protein packing density in unstacked thylakoid membrane regions facilitates lateral protein mobility. In turn, concentrating...
proteins by grana formation impairs efficient protein transport. An example where this differential mobility could be relevant is the PSII repair cycle that reactivates photodamaged PSII (Tikkanen et al. 2011). In C₃ plants, PSII is photodamaged in stacked grana regions, whereas the main components of its repair machinery are localized in unstacked stroma lamellae (Tikkanen et al. 2011). Thus, repair of PSII depends on lateral protein traffic between grana thylakoids and stroma lamellae. Evidently, this structural separation is not present in agranal BS cells of C₄ plants. Interestingly, the degradation of photodamaged PSII in maize is significantly faster in agranal BS chloroplasts than in M cells (Pokorska and Romanowska 2007). This could be due to faster migration of damaged components of PSII in agranal membranes. It follows that formation of stacked grana could lead to a kinetic restriction of the PSII repair cycle in granal thylakoids of C₃ chloroplasts and mesophyll chloroplasts of C₄ plants. Our Monte Carlo computer simulations predicted that the PSII supercomplex localized in grana discs required about one hour to reach the unstacked stroma lamellae (Kirchhoff et al. 2004). The situation in native membranes of C₃ plants is more complex than in the computer simulations. For example, phosphorylation of damaged PSII subunits causes a slight overall increase in protein mobility (Goral et al. 2010), and disassembly of the supercomplex (Tikkanen et al. 2011, Pesaresi et al. 2011). Both could speed up lateral diffusion of damaged PSII out of the grana. However, the observation of faster PSII degradation in agranal BS thylakoids of a C₄ plant points to a significant contribution of lateral protein diffusion for PSII repair in grana-containing thylakoid membranes.

An open question remains as to why the protein packing densities of stacked and unstacked thylakoid subdomains are different. A possible explanation is that the different light-harvesting antenna organizations of PSII and PSI play an important role. In higher plants, PSI occurs as individual units which bind up to four or five LHCI (Busch and Hippler 2011). In contrast, the organization of PSII and LHCII in stacked grana is more complex. The structural and functional PSII building block is a dimeric supercomplex that includes two strongly bound LHCII trimers. In addition, up to six more loosely bound LHCII are connected to the supercomplex (Anderson 1986, Kirchhoff et al. 2007). Furthermore, on the supramolecular level, PSII and LHCII complexes form a connected light-harvesting network manifested by an exchange of excitonic energy between several
Grana Formation and Protein Mobility

PSII centers (Joliot and Joliot 1964, Kramer et al. 2004), a phenomenon called connectivity. Recently, we could demonstrate that this functional interaction in grana between numerous protein complexes requires a tight interaction between PSII supercomplexes and LHCII (Haferkamp et al. 2010). This is accomplished by high packing density in grana discs. Thus, macromolecular crowding is a prerequisite for efficient conversion of sunlight by PSII and its antenna system. On the contrary, the light-harvesting interaction with PSI in unstacked stroma lamellae does not require intermolecular energy transfer between different LHCI-PSI supercomplexes. So, the protein packing density can be lower. As shown in this study, this is an advantage for lateral protein traffic. Since BS thylakoids in NADP-ME type C₄ plants are optimized to produce mainly ATP by cyclic electron transport, and are depleted in PSII but enriched in PSI, their thylakoid membranes have a protein packing density similar to stroma lamellae, which consequently allows for higher protein mobility.

CONCLUSION
Grana formation leads to a macromolecular crowding that is required for efficient light harvesting by the modularly organized PSII/LHCII system. Optimizing this function seems to be a higher evolutionary priority than allowing a high mobility of grana-hosted protein complexes. It is important to note that although 70% to 80% of the protein complexes in grana are virtually immobile, the remaining protein complexes are very mobile (Kirchhoff et al. 2008). It is likely that the mobile fraction increases under environmental conditions that require brisk lateral protein transport through the crowded grana. In unstacked thylakoid membranes, the need to pack protein complexes tightly is not required because of the non-modular organization of the PSI/LHCI system. Thus, the physicochemical forces that govern tight protein packing in grana stacks are not operative in unstacked regions, leading to a lower protein packing density and higher protein mobility. Obviously, high protein packing densities are only formed if required, e.g. for efficient light-harvesting, but high packing densities do not occur if not needed due to interference in the mobility of membrane constituents.

Material and Methods
Mesophyll protoplast and Bundle sheath Preparations

Zea mays inbred T43 and Sorghum bicolor leaves were harvested from 1-month-old plants grown in computer-controlled growth chambers (Econair GC-16; Bio Chambers) under 14 h light/10 h dark photoperiod and a 32°C/18°C temperature regime. A maximum of 900 PPFD (μmol quanta m⁻² s⁻¹, photosynthetic photon flux density,) at the mid-day light period was obtained in a stepwise manner by regulating the lights in two hours increments. Plants of Arabidopsis thaliana (ecotype Columbia) were grown in the same type of chamber, with a mid-day maximum of 400 PPFD, a 12 h/12 h photoperiod and day/night temperature of 25°C/18°C. Mature leaves were harvested from 1-month-old plants.

Bundle sheath (BS) strands were isolated mechanically and M protoplasts enzymatically from maize and sorghum, following a process similar to that described in Sheen (1995) and modified by Markelz et al. (2003) and Sharpe et al. 2011. For preparation of BS strands, the 8th emergent leaf was divided into 5 equal sectors; the distal 4th sector was sampled and cut into 2 mm square segments. Segments were submerged in BS buffer I (0.33 M sorbitol, 0.3 M NaCl, 0.001 M EDTA, 0.001 dithiothreitol, and 0.2 M Tris [pH 9.0]) and processed with several 10-s pulses in a polytron blender. BS strands were collected via filtration through a 60 μm mesh and then reprocessed with 30-s pulses in a polytron blender with BS buffer II (0.35 M sorbitol, 0.005 M EDTA, 0.1% [v/v] β-mercaptoethanol, and 0.05 M Tris [pH 8.0]). BS strands were re-filtered and microscopically observed. Processing by blending in BS buffer II was repeated until BS strands, free of all attached M cells, were collected. Mesophyll protoplasts were prepared from leaf samples of maize and sorghum (the 4th sector as described above) and from mature leaves of Arabidopsis. Transverse sections (1 to 2 mm) were prepared and incubated in enzymatic digestion media including 5 mm MES-NaOH, pH 5.8, 10 mm CaCl₂, 0.6 M sorbitol, 2% [w/v] Sumizyme C [Shin-Nihon Chemical], and 0.1% Macerase [Calbiochem], and gently rocked on a shaker for 2.5–3 h. At the end of the incubation, M protoplasts were filtered from the tissue strips using a 60 μm mesh. Protoplasts were pelleted at 15g for 5 min, washed once with 5 mm MES-NaOH, pH 5.8, 10 mm CaCl₂, 0.6 M sorbitol), re-pelleted, and resuspended in the same media.
Membrane preparations

*Arabidopsis thaliana* plants were grown in soil under short-day conditions (9 h light/15 h dark) cycles with 100 PPFD at a constant temperature of 20°C in a growth chamber. Leaves of 4- to 6-week-old plants were harvested at the end of the dark period and isolation procedures were carried out in darkness under dim green light in a cold room. Washed leaves were briefly ground in a blender (3 – 10 s) with ice-cold media containing 50 mM Hepes (pH 7.5), 0.33 M sorbitol, 1 mM EDTA, 15 mM NaCl, 5 mM MgCl₂, 5 mM CaCl₂, 0.15% (w/v) BSA, and 1 mM sodium ascorbate. The homogenate was immediately filtered through four layers of cotton gauze and one layer of Miracloth and centrifuged for 5 min at 3,200 × g. The chloroplast pellet was suspended with a brush in a hypotonic media containing 50 mM Hepes (pH 7.5), 15 mM NaCl, and 10 mM MgCl₂ and allowed to stand for 10 min in the dark on ice in order to lyse chloroplasts. To remove unbroken material, the solution was shortly centrifuged for 1 min at 200 × g. The supernatant was then subjected to subsequent centrifugation for 10 min at 3,200 × g to pellet thylakoid membranes which were suspended in a storage buffer containing 50 mM Hepes (pH 7.5) 0.1 M sorbitol, 15 mM NaCl, and 10 mM MgCl₂. Thylakoids were subfractionated into grana and stroma lamellae by digitonin treatment followed by differential centrifugations as described by Fristedt et al. (2009). Grana core membranes were isolated by mechanical fractionation of isolated thylakoids followed by aqueous two-phase partition according to Svensson and Albertsson (1989).

Lipid analysis

BS strands or protoplasts from maize and sorghum or *Arabidopsis* leaves were ground in liquid nitrogen. The organic components were extracted with chloroform/methanol (2:1, v/v) and separated from aqueous components by a two-phase system established by addition of a 1 M KCl solution. The green organic phase was harvested, dried completely with nitrogen gas, and dissolved in chloroform (lipid extract). Lipids were separated by two-dimensional thin layer chromatography (TLC) and stained by bathing the TLC plates in 10% copper sulphate and 7.5% phosphoric acid followed by heating at 170°C as described in Haferkamp and Kirchhoff (2008). The four types of thylakoid lipids were quantified by comparing their staining intensity with the staining of reference lipid (Lipid
Grana Formation and Protein Mobility

Products, UK) (Haferkamp and Kirchhoff 2008). The chlorophyll concentration of the lipid extract was determined spectroscopically according to Porra et al. (1989) and the lipid to chlorophyll ratio calculated.

**Protein Analysis**

BS strands or mesophyll protoplasts from maize, sorghum, or Arabidopsis leaves were homogenized in a protoplast buffer (without enzymes) with a Brinkman homogenizer then ground in liquid nitrogen. The extract was pottered for 12 plunges then filtered through an 80 μm followed by a 20 μm mesh. The eluate was centrifuged at max speed with Eppendorf 5417R table centrifuge (25000 x g). The pellet was then resuspended in dH2O and subjected to a membrane pretreatment (exposure to 5M NaSCN to bind extrinsic proteins) according to (Fiedler et al 1994). Protein concentration is then determined using a standard Lowry assay via. Folin–Ciocalteu Reagent. We determined that the lipid/protein ratio increases with increasing amounts of membranes used for protein determination. Therefore, all protein determinations were performed at chlorophyll concentrations between 100 to 150 μg/mL. In this concentration, range the lipid/chlorophyll ratio levels off.

**Gel electrophoresis**

Protein composition was determined by SDS-denaturing gel electrophoresis (SDS-PAGE) on 12.5% polyacrylamide gel (Laemmli 1970) containing 6 M urea using Coomassie staining.

**FRAP measurements**

Mesophyll protoplast or bundle sheath samples were directly placed on a glass slide and covered with a cover slip. For measurements with isolated grana core, grana and stroma lamellae of Arabidopsis the glass slide was covered with a bilayer of phosphatidylcholine (PC) to avoid artificial glass-membrane interactions (Kirchhoff et al. 2008). For isolated stroma lamellae, the mobile fraction with and without the PC-support system was 55% and 33.5%, respectively. This indicates that the glass membrane interactions impede protein mobility and it highlights the importance of using a fluid support system to
analyze protein mobility in isolated membranes. Furthermore, the measurements with isolated thylakoid subdomains were performed under anaerobic conditions (Kirchhoff et al. 2008). For fluorescence spectra and FRAP experiments, a Leica SP5 confocal laser scanning microscope with AOBS system was used. Chlorophyll fluorescence was excited at 488 nm (Argon line) and detected between 650 and 720 nm. The FRAP series includes 8 pre-bleaches, the bleach, 10 post-bleaches with 3 s separation, and 10 post-bleaches with 10 s separation.

A critical assumption for application of FRAP is the irreversibility of the bleached pigments, i.e. the recovery should be dependent on diffusion of unbleached pigments from neighboring regions into the bleached stripe only. We verified this by bleaching whole chloroplasts or whole sub-thylakoid patches. The recovery of these totally bleached samples is very low. The data presented in Figs. 4 and 5 are corrected against the total bleach recovery.

**Mathematical analysis**

FRAP images were analyzed with ImagePro and SigmaPlot (v.11) software. From the CLMS time series, one-dimensional fluorescence profiles were extracted from each image by summing the fluorescence in the x-direction (see Fig. 3). Because the sample size is small, bleaching results in a significant decrease in the total fluorescence from the sample (FRAP analysis assumes an infinite reservoir of unbleached pigments). To correct for this, the profiles were normalized to the same total fluorescence of each image. The pre-bleach fluorescence profile was then subtracted from the post-bleach fluorescence profiles to generate differential bleach profiles. From these bleach profiles the maximum level was plotted versus time (Fig. 4 and 5). The mobile fraction was estimated by comparing the first post-bleach profile with the profiles obtained at the longest time-points.

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Figure Legends

Figure 1 CLSM images of BS strands and M protoplasts of maize and sorghum. The images show natural chlorophyll fluorescence. A. Low resolution images of an isolated
Grana Formation and Protein Mobility

bundle sheath strand from maize. B. Close-up CLSM of a BS cell from maize. C. Chloroplasts within bundle sheath strand of sorghum. D. Chloroplasts within a protoplast isolated from *Arabidopsis*. Note the small bright spots representing grana discs. Scale bars, A, 50 μm, B-D, 10 μm.

**Figure 2** Fluorescence spectra of chloroplasts of M and BS cells from maize and sorghum and of isolated grana core and stroma lamellae from *Arabidopsis*. Samples were excited at 488 nm. Spectral bandwidth was 10 nm. The spectra for M and BS cell chloroplasts were recorded with similar material as shown in Fig. 1. A. Spectrum of M chloroplasts of sorghum. In addition, spectra of grana core and stroma lamellae of *Arabidopsis* are shown. Spectra of maize and *Arabidopsis* mesophyll chloroplasts are very similar (not shown). B. Chlorophyll fluorescence spectra of BS cells from maize and sorghum compared to grana core and stromal lamellae of *Arabidopsis*.

**Figure 3** FRAP measurements on *Arabidopsis* protoplasts (A-D) and sorghum BS cells (E-H). The images show individual chloroplasts before the bleach (A, E), directly after the bleach (B, F), and post-bleach images at two different time points (C, G and D, H). For a better comparison between *Arabidopsis* and sorghum, fluorescence profiles are shown at the right for each bleach image. Scale bars 2 μm.

**Figure 4** Fluorescence recovery kinetics. From the fluorescence profiles (see Fig. 3), the maximum fluorescence intensity for the bleach line is extracted for each time point and plotted versus time. The first image after bleaching was set to zero seconds. The fluorescence intensities were normalized to the pre-bleach values. Data represent mean values with standard deviations from 8 up to 29 measurements from two preparations. The mobile fractions (with standard deviations) deduced from the fluorescence recovery kinetics are indicated.

**Figure 5** Fluorescence recovery kinetics for grana core (A), grana including margins (B), and stroma lamellae (C) isolated from *Arabidopsis*. D. SDS-PAGE analysis showing protein composition of the thylakoids (T), grana core (G.c.), grana (G) and stroma.
Grana Formation and Protein Mobility

lamellae (S.L.) preparations. An amount of sample corresponding to 5 μg of chlorophyll per lane was loaded into each well. Apparent molecular weights were estimated by co-electrophoresis of a low molecular weight protein standard (MW) (Invitrogen). Bands for the ATPase subunits (AtpA and AtpB protein) as an indicator of unstacked stroma lamellae are depicted. In addition, the LHCII band is boxed as an indicator of stacked grana. MW is given in kDa. Data in Figures (A) to (C) represent mean values with standard deviations of 14 to 19 measurements collected from one preparation.

Figure 6 Dependency of the mobile fraction determined from FRAP measurements on the lipid to chlorophyll ratio (A) or the lipid to protein ratio (B). Data represent the mean with standard deviation. Further statistical information for the mobile fraction is given in Fig. 4 and for the lipid/chlorophyll data in Table 1. The lipid/protein data was collected from two to four independent measurements. The regression line for A is \( y = -17.3 + 20.8x \) \( (r^2 = 0.973) \). For B the regression equation is is \( y = -6.9 + 663.1x \) \( (r^2 = 0.973) \).
Table 1: Chlorophyll a/b ratios and lipid compositions in grana containing and agranal tissues, and mole percentage of chloroplast lipids.

|          | Chl. a/b (mol / mol) | Lipid / chl. (mol / mol) | MGDG / DGDG / SQDG / PG (mol%) |
|----------|---------------------|--------------------------|---------------------------------|
| Arabidopsis leaves | 2.8±0.3          | 1.66±0.12                | 46±5 / 24±2 / 8±1 / 24±3          |
| maize M      | 3.5±0.4          | 1.51±0.13                | 45±5 / 36±3 / 14±2 / 5±1          |
| maize BS     | 5.7±0.7          | 3.93±0.19                | 46±7 / 42±2 / 5±2 / 8±4          |
| sorghum M    | 2.9±0.4          | 2.01±0.17                | 43±10 / 35±3 / 10±7 / 13±4        |
| sorghum BS   | 7.8±2.0          | 3.36±0.24                | 44±2 / 37±3 / 7±2 / 12±2          |

Chlorophyll content was determined spectroscopically according to Porra et al. (1989). Lipid content was quantified by 2D-thin layer chromatography. Data represent the mean with standard deviation from three to six independent measurements. M, mesophyll cell protoplasts, BS, bundle sheath strands.
**Figure 1** CLSM images of BS strands and M protoplasts of maize and sorghum. The images show natural chlorophyll fluorescence.  
**A.** Low resolution images of an isolated bundle sheath strand from maize.  
**B.** Close-up CLSM of a BS cell from maize.  
**C.** Chloroplasts within bundle sheath strand of sorghum.  
**D.** Chloroplasts within a protoplast isolated from *Arabidopsis*. Note the small bright spots representing grana discs. Scale bars, A, 50 μm, B-D, 10 μm.
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Figure 5 Fluorescence recovery kinetics for grana core (A), grana including margins (B) and stroma lamellae (C) isolated from Arabidopsis. D. SDS-PAGE analysis showing protein composition of the thylakoids (T), grana core (G.c.), grana (G) and stroma lamellae (S.l.) preparations. An amount of sample corresponding to 5 μg of chlorophyll per lane was loaded into each well. Apparent molecular weights were estimated by co-electrophoresis of a low molecular weight protein standard (MW) (Invitrogen). Bands for the ATPase subunits (AtpA and AtpB protein) as an indicator of unstacked stroma lamellae are depicted. In addition, the LHCII band is boxed as an indicator of stacked grana. MW is given in kDa.
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