Determination of protein stoichiometries via dual-color colocalization with single molecule localization microscopy

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The stoichiometry of plasma membrane protein complexes is a result of the interactions between the individual proteins and an important determinant of their function. Most approaches used to address this question rely on extracting these complexes from their native environment, which may disrupt weaker interactions. Therefore, microscopy techniques have been increasingly used in recent years to determine protein stoichiometries *in situ*. Classical light microscopy suffers from insufficient resolution, but super-resolution methods such as single molecule localization microscopy (SMLM) can circumvent this problem. When using SMLM to determine protein stoichiometries, subunits are labeled with fluorescent proteins that only emit light following activation or conversion at different wavelengths. Typically, individual signals are counted based on a binomial distribution analysis of emission events detected within the same diffraction-limited volume. This strategy requires low background noise, a high detection efficiency for the fluorescent tag and intensive post-imaging data processing. To overcome these limitations, we developed a new method based on SMLM to determine the stoichiometry of plasma membraneproteins. Our dual-color colocalization (DCC) approach allows for accurate *in situ* counting even with low efficiencies of fluorescent protein detection. In addition, it is robust in the presence of background signals and does not require temporal clustering of signals from individual proteins within the same diffraction limited volume, which greatly simplifies data acquisition and processing. We used DCC-SMLM to resolve the controversy surrounding the stoichiometries of two SLC26 multifunctional anion exchangers and to determine the stoichiometries of four members of the SLC17 family of organic anion transporters.

single molecule localization microscopy | fluorescent protein | protein stoichiometry

Most membrane proteins form oligomeric assemblies, in which individual subunits cooperate to fulfill specialized functions. Some membrane proteins also form larger clusters, in which distinct classes of proteins interact with each other. The number of subunits within such protein structures is a crucial determinant of their function (Lussier et al., 2019). Native gel electrophoresis has been successfully used to determine subunit stoichiometries and the molecular determinants of oligomeric assemblies (Detro-Dassen et al., 2008; Gendreau et al., 2004; Schägger & von Jagow, 1991). However, this technique relies on isolating protein complexes from their native environment, which can disrupt some protein interactions. To overcome this limitation, *in situ* methods such as fluorescence correlation spectroscopy (Chen et al., 2003), stepwise photobleaching (Ulbrich & Isacoff, 2007) and single molecule localization microscopy (SMLM) (Annibale et al., 2011; Sengupta et al., 2011) have become increasingly popular in recent years.

Stepwise photobleaching relies on the irreversible and stochastic photobleaching of fluorescent tags linked to the subunit to be counted, and the resulting intensity steps depend on the number of subunits within the complex being tested. Such data can be acquired using comparatively inexpensive microscopes which has undoubtedly led to the widespread adoption of this method (Bartoi et al., 2014; Coste et al., 2012; Lussier et al., 2019; Ulbrich & Isacoff, 2007). However, this approach is only feasible for low expression densities as it is limited by the resolution of light microscopy. Therefore, *Xenopus laevis* oocytes, which are large in diameter and in which ectopic protein expression can be controlled by adjusting the amount of injected RNA, are most often used for this method (Ulbrich & Isacoff, 2007). However, some protein complexes exhibit a different stoichiometry when expressed in the *Xenopus* system compared with mammalian expression systems (Krashia et al., 2010). For mammalian cells, the resolution limit of light microscopy can be circumvented using super-resolution microscopy methods (Durisic et al., 2014; Hummer et al., 2016; Lee et al., 2012; Nan et al., 2013; Nicovich et al., 2017; Puchner et al., 2013; Sengupta et al., 2011). SMLM achieves a higher resolution by reconstructing the precise positions of isolated fluorophore emissions detected over thousands of individual frames (Betzig et al., 2006; Rust et al., 2006). The fluorophores used for quantitative SMLM

are usually photoactivatable or photoconvertible fluorescent proteins that are activated at wavelengths different from that of the excitation laser (H. Li & Vaughan, 2018). Their positions in each frame may then be assigned to individual proteins in post-processing, to produce accurate information about the number and position of proteins subunits (Sengupta et al., 2011).

Several problems have to be overcome during image acquisition and processing to determine protein stoichiometries: To increase the lateral resolution in SMLM, the simultaneous activation of multiple fluorophores within the same diffraction-limited volume must be avoided. To assign signals to individual subunits within the same protein complex, the activation of each fluorophore needs even greater separation in time. These criteria can only be achieved if the probability of activating a certain protein is kept minimal through a gradually increased activation laser intensity. Algorithms to optimize laser control have been developed, but they are not intended to temporally separate clusters of emissions from individual proteins (Lee et al., 2012). During the long recordings required for SMLM, inherent mechanical and thermal fluctuations, as well as sample drift, combine to reduce spatial resolution. The complex photophysics of fluorescent protein blinking may also result in over- or undercounting (Annibale et al., 2011; Lee et al., 2012). Another source of miscounting is the background noise, which cannot be easily distinguished from genuine signals at the single molecule level (Shivanandan et al., 2014; Zhao et al., 2018). Furthermore, it is impossible to detect all fluorophores in the sample because the probability of having a working fluorescent marker on an individual protein (also called the detection efficiency) is always less than one. This may be due to incomplete protein translation or folding, failure to activate into a fluorescent state, or pre-imaging bleaching (Durisic et al., 2014; Nicovich et al., 2017). Thus, the observed counts are not equal to the stoichiometry of interest but instead follow a binomial distribution that depends on both the real number of subunits per complex and the detection efficiency. Typically, only a detection efficiency of at least 0.5 ensures reasonable resolution between different stoichiometries (Durisic et al., 2014; Ulbrich & Isacoff, 2007).

Here we developed a new strategy, dual-color colocalization SMLM (DCC-SMLM), which utilizes two spectrally different fluorescent proteins attached to the same protein of interest. DCC-SMLM is very tolerant of background noise and low detection efficiencies and does not require stringent control of the activation laser. We tested the new DCC-SMLM aproach on proteins of known stoichiometry and then used it to study proteins from two plasma membrane transporter families with controversial or previously unknown stoichiometries: the SLC26 and SLC17 families.

The human SLC26 family has 10 members that function as anion transporters or channels as well as the motor protein in cochlear outer hair cells. The physiological importance of these proteins is illustrated by the growth defects, chronic diarrhea or deafness associated with naturally occuring mutations. Biochemical and recent structural studies indicated that the proteins exist as dimers (Detro-Dassen et al., 2008; Geertsma et al., 2015; Walter et al., 2019), whereas other studies have proposed a tetrameric stoichiometry (Hallworth & Nichols, 2011; Sinha et al., 2010; Zheng et al., 2006). The SLC17 family includes proton-driven vesicular glutamate, aspartate, sialic acid, and nucleotide transporters, as well as Na^+-coupled phosphate transporters. Using DCC-SMLM, we determined the oligomeric states for two SLC26 proteins, the human epithelial chloride-bicarbonate exchanger SLC26A3 and the rat motor protein prestin (Slc26a5), and for four members of the SLC17 family: mouse vGlut1, 2, and 3 (Slc17a7, Slc17a6, and Slc17a8, respectively) and human sialin (SLC17A5).

Results

Dual-Color Colocalization SMLM for Determining Stoichiometry. A protein complex of *n* identical subunits, each labeled with a single indicator flurorescent protein (F) with a detection efficiency of *p* (the probability of being fluorescent and being detected), will be detected with a probability *P*:

$$P = 1 - (1 - p)^n \quad [1]$$

In theory, *P* is equal to the ratio of all proteins with visible fluorescence (N_F) by the number of labeled proteins in total (*N*):

$$P = \frac{N_F}{N} \quad [2]$$

However, direct determination of *P* from single-color microscopy images is impossible as the total number of proteins, including those not exhibiting fluorescence, is unknown. Therefore, in order to experimentally determine *P*, we additionally labeled each protein subunit with another fluorescent protein (M) as a baseline marker (Fig. 1A). As for F, the number of proteins observable by the fluorescence of M (N_M) will be smaller than *N*. Assuming that the fluorescence of F and M is independent, *P* can be determined from the number of proteins showing fluorescence of both proteins, M and F (N_{MF}), and N_M which can be counted from dual-color microscopy images (Fig 1B):

$$P = \frac{N_F}{N} = \frac{N_{MF}}{N_M} \quad [3]$$

The values of *P* obtained for proteins with known stoichiometries were used to solve Eq. 1 for *p*, which could then be used to determine unknown stoichiometries (Fig. 1C). Independence of both fluorescence signals was guaranteed by using proteins with separate emission and excitation spectra as well as performing sequential rather than simultaneous imaging of color channels.

We chose mVenus (Nagai et al., 2002) as the fluorescent marker protein M because of the very low background signal in its detection channel (Fig. 1D-F). mVenus is derived from yellow fluorescent protein with several improvements such as faster maturation, a monomeric structure, and a higher tolerance for cellular acidification and the surrounding halide concentration (Nagai et al., 2002). Like other GFP derivatives, it blinks by cycling between the fluorescent and dark states under continuous

illumination with the excitation laser (Dickson et al., 1997). PAmCherry was chosen as the indicator because it is quickly bleached by continuous excitation after activation (Durisic et al., 2014). However, this channel had considerably more background signals. PAmCherry fluorescence is stable for several frames after its activation (Durisic et al., 2014; Subach, Patterson, et al., 2009), resulting in small clusters of localizations per fluorescent protein. We partially corrected for the background by filtering out clusters with only a few signals (Supplementary information (SI) Fig. S1). However, some background signals were indistinguishable from genuine PAmCherry signals, which explains the higher background in that particular color channel (Fig. 1D-F). The order of mVenus and PAmCherry tags fused to the protein of interest did not significantly impact the probability of colocalization (SI Fig. S2).

Correction of Sample Drift, Chromatic Aberrations and Definition of Colocalization. The resolution of all SMLM data is compromised by sample drift and optical aberrations which affect the determination of colocalization. We recorded sample drift using TetraSpeck beads as fiducial markers and correcting for this during post-imaging data processing (SI methods) (Yi et al., 2016). This correction reduced the radius of clustered signals to ~30 nm (Fig. 2A and B). Since our approach relies on colocalization of the marker and indicator in two color channels, we also corrected chromatic aberrations resulting from different refractive indices at different emission light wavelengths. We confirmed earlier reports that lateral chromatic aberration can be described as a set of linear functions centered on the optical axis of the microscope (Erdelyi et al., 2013; Kozubek & Matula, 2000). Values from a linear fit of the measured inter-color distances of individual beads to their coordinates were used for correction (Fig. 2C). This way, lateral chromatic aberration could be reduced to 13.8 ± 8.9 nm for bead samples (Fig. 2D and E). Chromatic aberrations may also be corrected by determining regional averages with similar results (SI Fig. S3) (Churchman & Spudich, 2012; Georgieva et al., 2016). The axial chromatic aberration as determined by the focus offset between colors was less than 100 nm and thus considered irrelevant for SMLM signal registration in only two dimensions (Fig. 2F).

Unlike FPs in cellular samples, beads show an intense and long-lasting fluorescent signal. To determine the improvement in fixed cell samples, and to determine the threshold for colocalization, we applied the correction to recordings of samples expressing monomeric barttin (17 cells, 1 preparation) or

tetrameric $K_{ir}2.1$ (35 cells, 3 preparations), each subunit tagged with mVenus and PAmCherry (Fig. 2G). We determined the distances between each individual mVenus cluster and the surrounding PAmCherry clusters.–These include the distances from mVenus to (I) PAmCherry signals within the same protein complex, (II) neighboring clusters in the absence of any active PAmCherry in the same complex and (III) background signals (which are random and widely spread). We then calculated radial distributions (RDF) for PAmCherry signals around each mVenus cluster for two different constructs, the monomeric barttin and the tetrameric $K_{ir}2.1$ (Fig. 2H). Prior to the correction of chromatic abberations, the RDF shows high densities centered on a distance of about 100 nm but reaching up to 250 nm. Following correction, the majority of PAmCherry signals are distributed in a radius of below 100 nm around mVenus clusters so this value was chosen as threshold distance for colocalization.

Fixation Conditions. A critical prerequisite for DCC studies is to sufficiently immobilize the studied proteins while preserving the function of fluorescent proteins. A large proportion of membrane proteins remain mobile after fixation with paraformaldehyde (PFA) alone, requiring the addition of glutaraldehyde (GA) or the use of cold methanol (MeOH) for adequate immobilization (Stanly et al., 2016; Tanaka et al., 2010). To test whether these fixation methods affect mVenus and PAmCherry fluorescence in SMLM we stably expressed the chloride channel β-subunit barttin(Estévez et al., 2001) C-terminally tagged with both PAmCherry and mVenus. Both fixation methods led to comparable correlation distances between the two colors (Fig. 3A and B). However, upon MeOH fixation a significantly higher signal density, a higher ratio of PamCherry clusters to mVenus clusters and a higher colocalization ratio were observed (Fig. 3 A', B' and C-F). Similar results were obtained for many of the other proteins used in this study (SI Table S1). Therefore, we concluded that fixation with cold methanol better preserved the function of the fluorescent proteins used in this study compared with PFA/GA fixation and, therefore, chose cold methanol as our routine fixation method.

Calibration of the Dual-Color Colocalization Model. Given that the detection efficiency p of fluorescent proteins may differ between experimental setups (Durisic et al., 2014; Wang et al., 2014), we first calibrated the DCC model (Eqs. 1 and 3) using standards of known stoichiometry: the

monomeric ClC-K chloride channel β-subunit barttin (Scholl et al., 2006), the dimeric chloride channels ClC-2 and ClC-K (Park et al., 2017; Stölting et al., 2014; Thiemann et al., 1992), the trimeric glutamate transporter EAAT2 (Canul-Tec et al., 2017; Nothmann et al., 2011) and the tetrameric potassium channel $K_{ir}2.1$ (Doyle et al., 1998). All proteins were C-terminally tagged with PAmCherry and mVenus via two short peptide linkers (SI Table S2).

As an independent confirmation of the reported stoichiometries from the literature as well as to confirm the function of our constructs, we used high-resolution clear native electrophoresis (hrCNE) (SI Fig. S4). Our results also demonstrate that the use of a two fluorescent proteins linked to the proteins in our analysis did not interfere with their reported quarternary structure.

After correction for drift and chromatic aberration, signals were assigned to clusters using the DBSCAN algorithm (Ester et al., 1996). Colocalization ratios (P) for mVenus and PAmCherry clusters were then calculated (Eq. 3, Fig. 4A) and used with the known oligomeric states (n) to obtain p from Eq. 1 of the DCC model. The fit suggested a low detection efficiency (p) of 0.12 for PAmCherry. However, the fit did not describe the data very well (R^2 = 0.68; red dots in Fig. 4A), especially for the monomer and the trimer.

We suspected that misfolding or truncation of both the marker and indicator in fusion proteins might have led to a loss of fluorescence for some protein subunits. This would especially affect proteins with smaller stoichiometries where the relative contribution of fluorescence is greater for each subunit. Therefore, we introduced an additional factor, m, to describe the probability of this phenomenon occuring. For a protein complex comprising n identical subunits, each C-terminally labeled with mVenus and PamCherry, having been detected via mVenus, the probability of it also being detected via a PAmCherry signal is:

$$P(n)=\sum_{k=1}^{n}\left\{\binom{n}{k}\frac{(1-m)^k m^{n-k}}{1-m^n}\left[1-(1-p)^k\right]\right\} \quad [4]$$

Fitting Eq. 4 to the observed colocalization ratios of mVenus and PAmCherry clusters for the protein standards, gave values of 0.24 for m and 0.16 for p. This new model better aligns with the data (R^2 = 0.87) compared with the original DCC model, especially for the monomer (blue dots in Fig. 4A), and was therefore used to analyze proteins with contradictory or unknown stoichiometries.

Using DCC-SMLM to Determine the Subunit Stoichiometry of SLC26 and SLC17 Proteins. We next used DCC-SMLM to resolve the subunit stoichiometries of several SLC26 and SLC17 transporters. The colocalization ratios of mVenus and PAmCherry clusters for these proteins were determined (Fig. 4B) and compared with those expected for different oligomeric states using the DCC model (Eq. 4). To quantify the difference between expected and observed values, we introduced the coefficient of mismatch M^2 (SI). A M^2 value of 0 indicates a perfect match, with larger values indicating larger differences. As shown in Fig. 4 C-H, M^2 values are lowest for a dimeric assembly of SLC26A3 and prestin and a monomeric state for all of the SLC17 transporters. These results are also consistent with the results of native gel electrophoresis (SI Fig. S4). Our M^2 analysis was further validated by a two-sample Kolmogorov-Smirnov (KS) test to compare the distribution of values from each protein of interest to those of the protein standards (Fig. 4I–N). Moreover, we independently confirmed our results for the SLC26 and SLC17 proteins with high-resolution clear native electrophoresis utilizing the same constructs and expression system as in our DCC-SMLM experiments (SI Fig. S4).

Discussion

We have developed a novel DCC-SMLM technique to determine the stoichiometries of plasma membrane protein complexes *in situ* in mammalian cells. Using mVenus as the marker fluorescent protein and PAmCherry as the indicator fluorescent protein for counting, we established a dimeric state for two representatives of the SLC26 family, the epithelial anion exchanger SLC26A3 and the motor protein prestin (Slc26a5); and a monomeric state for four representatives of the SLC17 family, the vesicular glutamate transporters vGlut1, 2, and 3 and the lysosomal sialic acid transporter sialin.

Our DCC-SMLM approach (SI Fig. S8) overcomes several limitations of methods commonly used to determine protein stoichiometries: unlike for biochemical methods, no solubilization or purification of proteins is necessary as DCC-SMLM works with proteins *in situ*. In comparison to photo-bleaching experiments, DCC-SMLM can be applied reliably even in small mammalian cells where the high densities of protein expression are problematic. In contrast to previously reported quantitative SMLM methods, DCC-SMLM holds several advantages that result in a simplification of the procedure and offers greater reliability of counting. Binomial SMLM counting strategies require clustering of signals in at least three dimensions (*x*, *y* and time) to identify individual protein subunits. This demands stringent control of the activation laser and intensive post-imaging data processing (Lee et al., 2012). Another recently published SMLM-based quantification strategy also foregoes the need for temporal clustering as it utilizes the blinking behavior of some fluorescent proteins (Fricke et al., 2015; Hummer et al., 2016). This, however, requires fluorescent proteins that show blinking behavior (multiple on ↔ off sequences) which is not guaranteed for all fluorescence proteins or dyes(Durisic et al., 2014; Subach, Malashkevich, et al., 2009). Additionally, all previously published SMLM quantification and photobleching step analysis methods require large photoefficiency values ($p \geq 0.5$) as they are otherwise unable do resolve the small oligomeric stoichiometries typically observed for most membrane proteins. In contrast, DCC-SMLM only relies on the relationship between the total detection probability for a protein complex and the number of fluorophores within the complex. This relationship is determined by the detection efficiency of the individual fluorophores (Eq. 1) and is independent of temporal separation or specific fluorophore behavior. In fact, while we use the x- and y-coordinates

provided by SMLM, DCC itself is not even reliant on SMLM and the algorithm may also be used with other microscopy modalities given enough spatial resolution. Examples may include structured illumination (Kner et al., 2009) and super-resolution radial fluctuations (Gustafsson et al., 2016) which are otherwise difficult to quantify at the single molecule level because they rely on the mathematical processing of multiple raw images to yield super-resolution images thereby removing much of the information required by other algorithms.

At the single molecule level, noise and genuine signals become hard to distinguish, especially for photoactivatable fluorescent proteins with low brightness such as PAmCherry (Subach, Patterson, et al., 2009). Since DCC considers the overlap of two colors, the effect of background signals on the indicator is greatly reduced. The probability of noise signals falling within the colocalization threshold radius of a given mVenus cluster follows a Poisson distribution. Our measured background signal density in the PAmCherry channel of ~0.8 clusters/μm^2 inside cells (Fig. 1E) suggests that only 2.6% of all mVenus molecules erroneously colocalize with noise (SI Eq. S13). Compared with the colocalization ratios of > 0.2 for dimers and higher oligomeric forms, this results in a signal-to-noise ratio of > 10. This estimate compares favorably with single-color experiments: transfected cells showed a mean density of ~2.2 PAmCherry clusters/μm^2 consistent with a signal-to-noise ratio of < 4 for this FP alone. However, higher background noise levels in the marker detection channel would lead to the over-counting of marker clusters, resulting in a decreased colocalization ratio (Eq. 3), and should be avoided. Our use of the much brighter mVenus tag as the marker allowed us to use a narrow detection window, resulting in very low levels of background noise (Fig. 1D and SI Table S3).

For data processing, filtering of noise signals is important for determining the detection efficiency accurately. The higher tolerance to background noise enabled us to use only a simple filter based on an empirical threshold of the minimal number of signals for a single PAmCherry protein (SI Fig. S1). This is confirmed by our observation that signal clusters recorded from background regions showed mostly only small clusters (SI Fig. S1A).

While data on the stoichiometry in large protein clusters and macro-structures can be relevant, DCC-SMLM was developed to only resolve smaller oligomeric structures *in situ* as they are typically the smallest functional units of proteins. We therefore removed larger structures from further analysis (SI methods). The number of clusters removed, however, was very low with typically more than 98% remaining (SI Fig. S7).

The use of two fluorescent proteins linked sequentially to our reference proteins and proteins of interest did not interfere with their structure as indicated by our hrCNE results (SI Fig. S4). This may not be surprising as similar results have been reported previously for similar constructs in other contexts (Leeman et al., 2018; Liang et al., 2018; Murata et al., 2005; Ranade et al., 2014).

In conventional binomial analyses of SMLM data, a low detection efficiency ($p < 0.5$) is a significant limitation when determining stoichiometries (Durisic et al., 2014). Theoretically, DCC-SMLM can optimally distinguish oligomeric states from monomer to pentamer if p is between 0.2 and 0.4 (Fig. 1C). However, even lower values of p may be tolerated, as seen in our study. This makes PAmCherry and other fluorescent proteins with low detection efficiencies viable for determining stoichiometries with DCC-SMLM (Fig. 4). The original DCC model (Eqs. 1 and 3) suggested a p value of 0.12 for PAmCherry, but did not result in an acceptable fit for our experimental data from reference proteins (Fig. 4A). We reasoned that the function of the two fluorescent proteins may somehow become impaired in the context of fusion proteins. Therefore, we introduced a modification factor, m, to describe the probability of both fluorescent proteins becoming dysfunctional. Fitting this modified DCC model to our reference data suggested a slightly higher p value of 0.16 for PAmCherry which resulted in a fit that aligned well with the experimental data (Fig. 4A). Previously reported detection efficiencies for PAmCherry range from 0.04 when expressed in *E. coli* (Wang et al., 2014) to about 0.5 in *Xenopus* oocytes (Durisic et al., 2014). This variability suggests that the expression system influences the functionality of fluorescent proteins, but may also reflect differences in image acquisition and data processing. It should be considered that many fluorescent proteins and dyes are sensitive to their specific microenvironment and it may not be taken for granted that the same values of

p and *m* can be used in every circumstance. However, in our case, the same values gave reasonable results that matched the stoichiometries as determined by high-resolution clear native electrophoresis (SI Fig. S4).

To achieve the necessary spatial resolution across two colors, we implemented and compared simple methods of cell fixation of cells and post-imaging correction of common artifacts such as drift and chromatic aberrations. While our implementation is based on SMLM, it could also be adapted for other types of microscopy as stated above. In our experiments, there was no difference between a linear fit of chromatic aberrations and local average correction (Fig. 2 and SI Fig. S3); however, this may depend on the quality of the optical setup and should be carefully evaluated for every instrument.

It should be emphasized that DCC-SMLM does not consider the behavior of individual protein complexes; instead, it is based on statistical information from a large number of protein complexes. Therefore, if the protein complex of interest does not exist in a single oligomeric state, DCC-SMLM counting can only report an average stoichiometry. We simulated many such cases but there was no clear pattern that allowed users to determine whether such averaging occurs based on a single experiment only (SI Fig. S5). Although this is a limitation, similar caveats apply to most other methods that rely on the aggregation of information from multiple protein complexes. To exclude an effect of expression density on the stoichiometry of our observed proteins, we used cells which covered a wide range of expression densities. A plot of the colocalization ratio versus the density of expressed clusters (SI Fig. S6) did not reveal any significant correlation between the two values, effectively ruling out aggregation at higher expression densities. Future efforts should aim to explore whether additional information obtained from DCC-SMLM experiments or other experimental designs could be used to increase its usefulness in analyzing proteins that adopt a mixture of oligomeric states.

Using DCC-SMLM, we determined the stoichiometries of proteins from the SLC26 and SLC17 families. Studies using Blue native electrophoresis (Detro-Dassen et al., 2008) and X-ray and cryo-EM (Geertsma et al., 2015; Walter et al., 2019) previously reported a dimeric assembly for SLC26, whereas

microscopy approaches supported a tetrameric assembly (Hallworth & Nichols, 2011; Sinha et al., 2010). This discrepancy might indicate that SLC26 forms stable dimers that survive protein purification and solubilization as well as weakly associated “dimer-of-dimer” tetramers in native membranes that may only be visible in intact cells. Although we cannot exclude the possibility that a minor fraction of prestin forms tetrameric structures, our results show that both prestin and SLC26A3 predominantly form dimers in intact HEK293T cells (Fig. 4B-D).

We also studied the oligomeric state of vGlut1, 2, and 3 (Slc17a7, Slc17a6 and Slc17a8, respectively), and sialin (SLC17A5) and found that they are likely to be monomeric. Again, these results are consistent with native gel electrophoresis (SI Fig. S4). An earlier report suggested dimeric organization for SLC17 transporters based on SDS-PAGE results (Andersen, 2004) but a recent cryo-EM study reported a monomeric structure (F. Li et al., 2020). Functional expression studies have also demonstrated that vesicular glutamate transporters and sialin can function without accessory subunits (Eriksen et al., 2016; Morin et al., 2004), which, when considered alongside our results, confirms that SLC17 proteins are functional monomers.

Our study provides a new approach to determine the stoichiometries of membrane proteins *in situ*. DCC-SMLM overcomes many of the drawbacks and requirements of previous methods, making stoichiometry determination more reliable and much easier to perform.

Materials and Methods

Cell Culture and DNA Constructs. HEK293T cells and Flp-In T-REx 293 cells were grown in DMEM supplemented with 50 U/mL penicillin-streptomycin and 10% FBS at 37 °C and 5% CO_2 (Tan et al., 2017). For Flp-In T-REx 293 cells, the medium was additionally supplemented with 10 µg/mL blasticidin S HCl and 100 µg/mL hygromycin B. cDNAs encoding the fusion proteins were inserted into the cloning site of the pcDNA5/FRT/TO or pcDNA3 vector plasmid via overlap extension PCR, restriction digestion and DNA ligation.

Sample Preparation for SMLM Imaging. For SMLM imaging, HEK293T cells were sparsely seeded onto clean 25-mm coverslips in 1.5 mL DH10 in 3.5 cm petri dishes 3 h before transfection. Cells were transfected with 0.5-1.0 µg plasmid DNA plus 1.0 µL Lipofectamine 2000 (Life Technologies) and cultured overnight (12-16 h) before fixation. Flp-In T-REx 293 cells were seeded on coverslips in the same way and 0.01 µg/mL tetracycline was added to the culture medium 14.5 h before fixation. For details, see SI.

SMLM Imaging and Data Processing. SMLM imaging started 16–24 h after fixation. All SMLM imaging was performed on a custom-built wide field and TIRF microscope (Stölting et al., 2015). The fixed cells were imaged in PBS and diluted TetraSpeck beads were added to track sample drift. Raw images were first loaded into SNSMIL (Tang et al., 2015) to extract the precise location of fluorescent signals. The resulting datasets were processed with custom python scripts to correct of lateral chromatic aberrations and sample drift and for DCC analysis based on python v3.6.8. For details, see SI.

Acknowledgements This research was supported by the Deutsche Forschungsgemeinschaft (FA 301/15-1 to Ch.F.) as part of Research Unit FOR 5046, project P4. We are grateful to Dr. Iman Abdollahzadeh, Dr. Johnny Hendriks and Dr. Thomas Gensch for their generous support with the imaging setup. Many thanks also go to Cora Hannack, Dr. Raul E. Guzman and Arne Franzen for

providing plasmids encoding vGlut and sialin. We also thank Ashley Craig of Alchemy Editorial Services Ltd for language editing.

Author contributions: H.L.T., G.S. and Ch.F. designed the project. H.L.T. was responsible for molecular cloning, the mathematical model and SMLM experiments. S.B.-P. performed the clear native PAGE and the relevant data processing. H.L.T., G.S. and D.K. were responsible for processing and analyzing SMLM data. H.L.T. wrote the first draft and all authors contributed to revising this manuscript.

The authors declare no conflict of interest.

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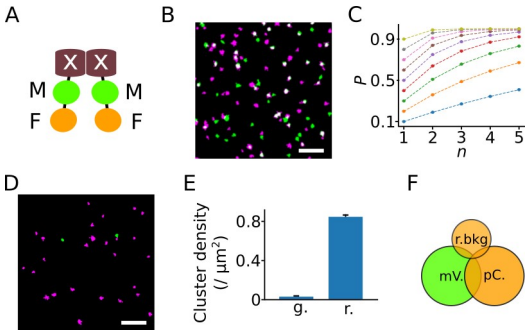

Fig. 1. The DCC strategy to determine protein stoichiometry. (*A*) Model of a dimeric fusion protein used for DCC-SMLM. The protein of interest is marked with a white "X", whereas the marker and indicator fluorescent proteins are labeled "M" and "F", respectively. (*B*) A reconstructed SMLM image from an HEK293T cell expressing K_{ir} 2.1 labeled with both mVenus (green) and PAmCherry (magenta). White indicates colocalization of the two color signals. Scale bar: 1 μm. (*C*) The probability *P* of detecting a protein complex changes with the number (*n*) and detection efficiency (*p*) of the fluorescent proteins it contains. Each color indicates a different *p* value from 0.1 to 0.9 in steps of 0.1. (*D*) A representative image reconstructed from a recording of a bare coverslip suface showing background signals in the PAmCherry (magenta) and mVenus channels (green). Scale bar: 1 μm. (*E*) The mean background cluster densities in the mVenus (green, g.) and the PAmCherry (red, r.) recording channels. A cluster comprises a series of fluorescent signals that are spatially close and clustered with the DBSCAN algorithm. *N* = 283 recordings. (*F*) As the background signals in the green channel are negligible, only three types of signals are considered: signals from mVenus (mV.), signals from PAmCherry (pC.) and background signals in the red channel (r.bkg).

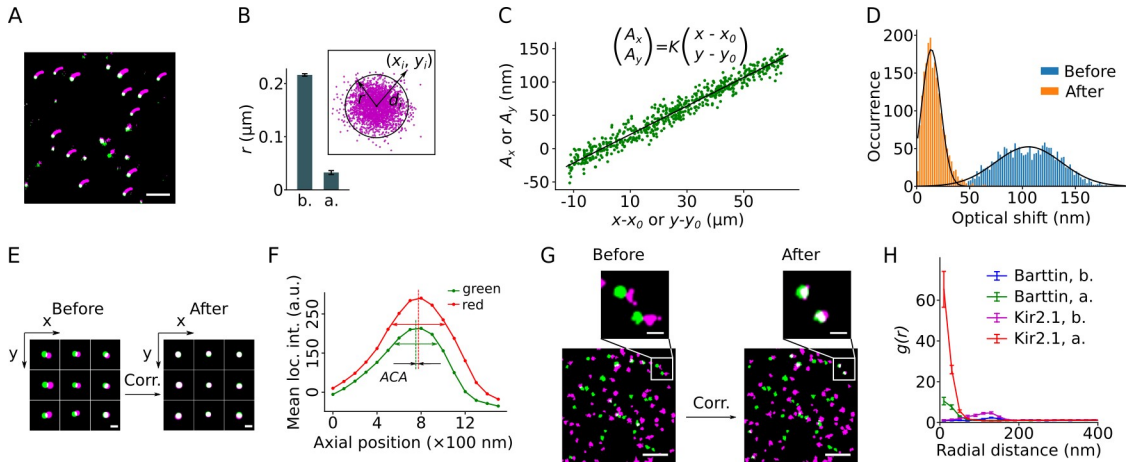

Fig. 2.Correction of sample drift and chromatic aberration.

(*A*) An SMLM image of a bead sample reconstructed from 13,000 frames recorded over ~18.5 minutes. The small magenta smears indicate sample drift. The corrected positions are displayed in green or, when overlapping, in white. Scale bar: 1 μm. (*B*) The mean cluster radius of positions extracted from 41 beads before (b.) and after (a.) drift correction, with error bars indicating the SEM. The cluster radius is defined as $\mu + 2\sigma$ of the Euclidean distances (d_i) of all signals (with coordinates (x_i, y_i)) to the center of the cluster, as shown in the inset. (*C*) Plot of the lateral chromatic aberration between the red and green channels, (A_x, A_y), versus the distance of the beads from a center point (x_0, y_0). Data from both dimensions are included in the graph. Linear regression (black line) yielded the values of the slope K, x_0 and y_0. The fitting was from a single recording of a bead sample.

(*D*) Lateral chromatic aberrations (blue) from nine recordings of a bead sample with a total of 1980 beads were corrected with the values obtained in *C*, as shown in orange. Black lines show Gaussian fitting. (*E*) Reconstructed images of nine representative beads from different areas before and after drift & chromatic aberration corrections. The green and magenta indicate signals from the mVenus and PAmCherry channels, respectively. Scale bar: 200 nm.

(*F*) The mean intensities of the beads recorded at the green and the red channels change along the axial position of the sample. The axial distance between the two peaks indicates the axial chromatic aberration (ACA). (*G*) Representative reconstructed images showing the mVenus (green) and PAmCherry clusters recorded from HEK293T cells expressing barttin-mVenus-PAmCherry before and after drift & chromatic aberration corrections. Un-clustered signals were omitted from the images. Scale bars indicate 1 μm and 200 nm respectively in the bottom and the zoomed-in images. (*H*) Radial distribution of PAmCherry clusters (Clst.) and localizations (Loc.) around mVenus clusters and localizations, respectively, before (b.) and after (a.) drift & chromatic aberration corrections. Un-clustered signals were excluded from the analysis.

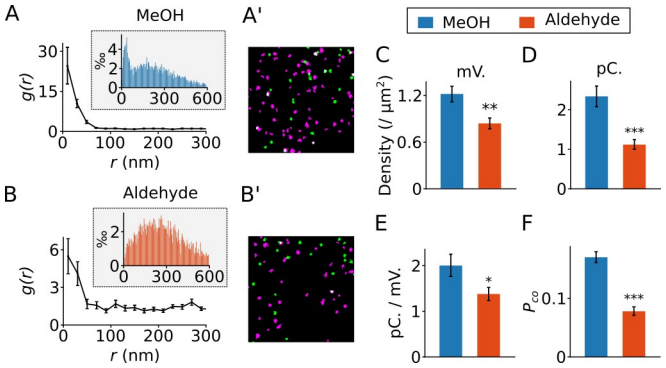

Fig. 3. Effect of different fixation methods on the number of clusters. (*A* and *B*) Results from the radial distribution function *g(r)* for PAmCherry clusters around mVenus clusters recorded in Flp-In T-REx 293 cells expressing barttin-mVenus-PAmCherry and fixed with cold methanol (*A*, MeOH, 24 cells) or para-formaldehyde plus glutaraldehyde (*B*, Aldehyde, 29 cells). The inset shows the histograms of the nearest neighbor distances. (*A'* and *B'*) Reconstructed images from recordings of cells expressing barttin-mVenus-PAmCherry fixed with cold methanol (*A'*) or the aldehyde (*B'*), with green indicating mVenus clusters and magenta for PAmCherry clusters. (*C* and *D*) The densities of mVenus (*C*, p = 0.0028) and PAmCherry (*D*, $p = 4.9\times10^{-5}$) clusters in samples prepared using the two fixation methods. (*E*) The relative density of PAmCherry (pC.) clusters to mVenus (mV.) clusters, p = 0.02. (*F*) The measured colocalization ratio of mVenus with PAmCherry, $p = 1.6\times10^{-10}$. *: $0.05 > p > 0.01$, **: $0.01 > p > 0.001$, ***: $p < 0.001$, Student t-test.

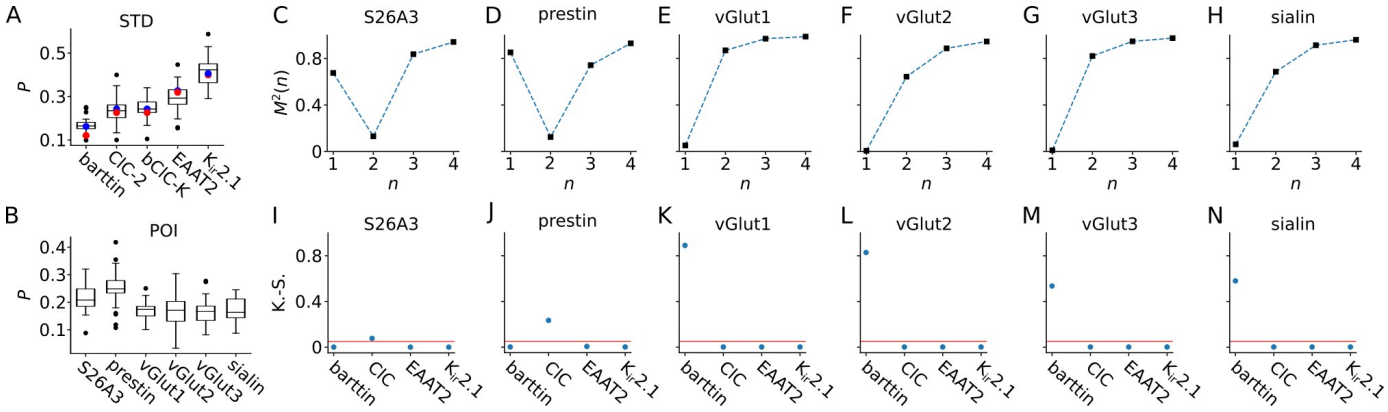

Fig. 4. Calibration and determination of stoichiometry through analyzing the colocalization ratios with DCC-SMLM. (*A*) The colocalization ratios (*P*) for mVenus and PAmCherry linked to proteins with known stoichiometries (STD). Red dots show the fit with Eq. 1 and blue dots show the fit with Eq. 3 including the modification factor *m*. The number of cells included in the analysis are (in brackets): barttin (13), ClC-2 (30), bClC-K (14), EAAT2 (19) and $K_{ir}2.1$ (34). (*B*) Colocalization ratios for mVenus and PAmCherry linked to the indicated proteins of interest (POI). The number of cells included are 24, 27, 22, 25, 30 and 22, respectively. (*C-H*) The coefficient of mismatch (M^2) calculated for all the proteins of interest at assumed stoichiometries (*n)* of 1, 2, 3 and 4. (*I–N*): Two-sample Kolmogorov-Smirnov tests of the observed colocalization ratios from each protein of interest compared with the protein standards in (*A*). The orange horizontal line indicates the Bonferroni-corrected threshold for the α-level (0.0125).