Molecular insight on the altered membrane trafficking of TrkA kinase dead mutants

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Abstract

We address the contribution of kinase domain structure and catalytic activity to membrane trafficking of TrkA receptor tyrosine kinase. We conduct a systematic comparison between TrkA-wt, an ATP-binding defective mutant (TrkA-K544N) and other mutants displaying separate functional impairments of phosphorylation, ubiquitination, or recruitment of intracellular partners. We find that only K544N mutation endows TrkA with restricted membrane mobility and a substantial increase of cell surface pool already in the absence of ligand stimulation. This mutation is predicted to drive a structural destabilization of the αC helix in the N-lobe by molecular dynamics simulations, and enhances interactions with elements of the actin cytoskeleton. On the other hand, a different TrkA membrane immobilization is selectively observed after NGF stimulation, requires both phosphorylation and ubiquitination to occur, and is most probably related to the signaling abilities displayed by the wt but not mutated receptors. In conclusion, our results allow to distinguish two different TrkA membrane immobilization modes and demonstrate that not all kinase-inactive mutants display identical membrane trafficking.

Keywords

TrkA receptor, VEGFR2 receptor, tyrosine kinase domain, membrane dynamics, molecular dynamics, mutation.

1. Introduction

Receptor tyrosine kinases (RTKs) constitute a large superfamily of 58 known membrane receptors; these are activated by a wide array of growth factors, and mediate fundamental biological functions including cell growth and survival, cell-to-cell communication, differentiation, and metabolism [1], [2]. RTKs share an extracellular domain that interacts with the ligand, a single transmembrane α-helix and an intracellular domain that contains the catalytic tyrosine kinase domain (TKD). The TKD consists of two lobes, with antiparallel β-sheets and one single α-helix (denoted as αC helix) in the N lobe, and a mainly α-helical C lobe. RTKs activation is regulated by a specific orientation of the activation loop connecting the N to the C lobe, required for both catalysis and phosphotransfer reactions [3]. A number of auto-inhibitory mechanisms exist, based e.g. on the position of αC helix, or on the conformation of the activation loop, which prevent TKD activation in the unbound state [1]. These are released upon ligand binding, which results in efficient activation of the kinase activity. The catalyzed phosphotransfer reaction from ATP onto the hydroxyl group of Tyr represents an important posttranslational modification (PTM), evolutionarily conserved from prokaryotes to humans. Accordingly, the TKD of RTKs is highly conserved.

A growing number of mutations in RTKs are being identified, which crucially contribute to cancer, type 2 diabetes, cardiovascular, neurodegenerative and developmental disorders [4]–[7]. Most of these occur in the TKD key regulatory elements. Typically, kinase hyperactivating mutations are found in cancer, and kinase inactivating mutations in developmental and other genetic disorders [8], [9]. Furthermore, mutations of the residues coordinating ATP or performing catalytic activity are found in a subfamily of RTKs named pseudokinases [2], [10]. Although lacking kinase activity, these proteins do have signaling abilities and play important

physiological and pathological roles. However, the molecular basis underlying the functions of kinase-inactivating or pseudokinase mutations has been poorly investigated.

Here, we study the impact of specific mutations in the TKD of the Nerve Growth Factor (NGF) receptor TrkA on its membrane dynamics, intracellular trafficking and PTMs. TrkA plays fundamental roles in development of the nervous system [11], [12], and is also an important player in carcinogenesis [13]. Mutations of TrkA sequence are reported both in cancer [13] and in HSAN IV genetic disease [14]. In particular, we focus our attention on the mutation of lysine 544 (human numbering) in the β3 sheet of the TKD N lobe, which is crucial to allocate ATP and thus to kinase activity; noteworthy, this mutation resembles those displayed by pseudokinases [2]. ATP binding to Lys 544 is an upstream event during TrkA TKD activation [15], [16]. This drives phosphorylation of Tyr of the activation loop (Y676, Y680, Y681 [17], [18]), and of scaffolding Tyr (Y496, Y757, Y791 [19]–[21]). Furthermore, Lys 544 was reported to be important for TrkA ubiquitination [22], [23]. We provide evidence that mutation of this Lys to Asn slows down membrane dynamics in a manner that paradoxically resembles that of NGF-activated TrkA-wt [24]. However, the two membrane immobilization modes have distinct structural and functional determinants, which are here characterized. Our observations may possibly be extended to other RTKs, thus providing interesting cues to the study of their genetic or somatic mutations.

2. Materials and methods

2.1 Note on sequences

We performed our studies both on the rat and human TrkA sequences. The two sequences share a very high homology (86% in the entire protein sequence, 94.6 % in the TKD).

Throughout the text, we shall use *h*TrkA and *r*TrkA to specify the human and rat sequences, respectively. Analogously, for Vascular Endothelial Growth Factor receptor 2 (VEGFR2), we used both the mouse and human sequences, which are renamed *m*VEGFR2 and *h*VEGFR2, respectively. The correspondence between numbering of residues in the different sequences is listed in Table S1 for TrkA and S2 for VEGFR2.

2.2 Constructs

ACP-tagged *r*TrkA construct was previously described [25]. S6-tagged *h*TrkA construct was previously described [26]. These constructs were used to generate all TrkA mutants, using the QuikChange mutagenesis kit (Agilent) and a pair of specific oligonucleotides (Sigma) for each desired mutation. Multiple mutations in KM and RM were introduced sequentially in the template sequence. cDNAs of *h*TrkA-wt, *h*TrkA-K544N and *h*TrkA-K544R were also cloned in an "all-in-one" third generation Tet-on lentiviral pTRE vector [27]. S6-*m*VEGFR2 construct was obtained inserting the S6 tag after the signal peptide of *m*VEGFR2 cDNA by GeneArt Synthesis (Thermo Scientific) and cloning it into pTRE lentiviral vector. *m*VEGFR2-K866N and *m*VEGFR2-K866R were prepared starting from the wt sequence using the QuikChange Site-Directed mutagenesis kit (Agilent) and a pair of specific oligonucleotides (Sigma) for each desired mutation. All mutations and relative primer sequences are reported in Table S3.

2.3 Single molecule labeling of surface TrkA and VEGFR2 constructs

After 5 hours from transfection, SHSY5Y or GM7373 cells were trypsinized and transferred into glass-bottom chambers (at a density of 2-3*10^5 cells per 22-mm-diameter WillCo® dish). Next day, cells were serum starved for 2 hours. Then surface receptors were labeled with Qdot as described previously [24], [27]. Briefly, cells were first biotinylated with a 30-minute incubation

at 37°C with 0.5% BSA, 1 µM Sfp synthase, 10 mM $MgCl_2$ and 2 µM of coA-biotin in starvation medium. After two washes in PBS, cells were incubated for 2 minutes at room temperature (RT) with 2 nM Qdot® 655 streptavidin conjugate (Invitrogen) in borate buffer pH 8.3, 0.5% BSA and 215 mM sucrose. Cells were washed eight times with PBS and left in medium. For TrkA, cells were then both unstimulated and stimulated with 125 ng/mL NGF diluted in starvation medium. Ligand addition was performed directly on the dish at the microscope, by adding a 250 ng/mL NGF solution in starvation medium to an equal volume of medium in the dish. Unless otherwise stated, cells were always imaged for a maximum of 15 minutes upon ligand addition.

2.4 Total internal reflection fluorescence (TIRF) microscopy

Labelled cells were imaged at 37°C, 5% CO_2 with a Leica DM6000 microscope equipped with a TIRF-AM module, incubator chamber, electron multiplying charge-coupled-device (CCD) camera (ImagEM C9100-13, Hamamatsu), and 100× oil immersion objective (NA 1.47). For live cell imaging, time series were acquired on a region of interest (ROI) with constant size of 32.7×34.5 µm within the basal membrane of each cell; Qdot655 was imaged using the 488 nm laser line, FF01-655/15 Semrock emission filter and a penetration depth of 110 nm. For single step photobleaching assay, we used a ROI of 32.68 x 32.68 µm and Abberior635 was excited using the 635 nm laser line with a penetration depth of 90 nm. The integration time per frame, corresponding to the lag time between two consecutive frames, was set at 21 ms and typical time series lasted 3000 frames.

2.5 Single-molecule internalization assay

Transfected or transduced SHSY5Y cells seeded in glass-bottom WillCo dishes were starved for 2 hours, receptors labelled with Qdot and transferred at the TIRF microscope. The

automatized stage was used for saving the position of 4-5 fields in which a sizeable number of cells displayed Qdot moving particles. Then we added 125 ng/ml NGF to the medium and followed the cells in the selected fields in a time course of eight points (0, 5, 10, 15, 30, 40, 50 and 60 min); as control, we repeated a similar experiment without adding NGF. For each cell and time point, we quantified the membrane density as the number of labelled receptors within cell area (quantified from the relative DIC image), in order to measure enrichment or depletion of surface *r*TrkA-wt and -K547N receptors in the presence or absence of NGF stimulation. For comparing the internalization time-course of different cells, we normalized the spot density of each cell to its value at time 0. Cells with a similar (average) transgene expression levels were chosen, excluding those with a number of moving labelled receptors below 3.

2.6 Single step photobleaching assay

24 hours after doxycycline induction, SHSY5Y cells expressing *h*TrkA -wt, -K544N, -K544R were starved for 2 hours. Then all constructs were labelled for 30 minutes at 37°C with 20 nM CoA-Abberior635P, 1 µM Sfp synthase, 10 mM $MgCl_2$ in starvation medium. Cells were washed twice in PBS, fixed for 90 min at room temperature with 4% PFA/2% Sucrose/0.1% Glutaraldehyde in PBS (GA, Electron Microscopy Sciences), washed five times with PBS and imaged in PBS. Time series were then analyzed following the procedure reported in [28]: briefly, the background fluorescence was subtracted using the ImageJ software and then single spots were identified and detected as isolated fluorescent signals falling within a 3 x 3 pixels roi, so that the number of photobleach steps therein could be quantified.

2.7 Drug treatments

Cells were seeded in glass-bottom dishes, after 24 hours starved for 2 hours before or during the drug treatment, and finally fixed for 10 minutes at RT with 4% PFA. Cells were then washed twice with PBS, permeabilized for 4 minutes at RT with 0.1 % TritonX-100 in PBS (Sigma Aldrich), washed twice again and then blocked for 20 minutes at RT with 1% Bovine Serum Albumin (Sigma Aldrich) in PBS. After blocking, cells were incubated with Alexa Fluor 647-Phalloidin (Invitrogen) diluted 1:40 in blocking solution. Finally, cells were washed twice with PBS, once with water (Millipore), dried and mounted in Fluoroshield mounting medium (Sigma Aldrich). Samples were evaluated at the TIRF microscope, with penetration depth of 150 nm, using HCX PL APO 100X (NA 1.47) objective and a ROI of 58,4μm x58.4μm; excitation used the 488 nm laser line and emission was collected with a FF01-525/45-25 Semrock filter. Based on phalloidin staining, we defined as optimal the following incubations: i) 2h at 37°C with 1μM cytochalasin D (Sigma-Aldrich) during serum starvation before labelling; ii) 15 min at 37°C with 1 μM latrunculin B (Sigma-Aldrich) in the last half of labelling; iii) 30 min at 37°C with 100 nM jasplakinolide (Sigma-Aldrich) during labelling. Cells were then labelled as described previously, washed eight times with PBS, and then imaged in medium devoid of drugs.

2.8 Structural MD simulations

We performed Molecular Dynamics (MD) simulations of the *h*TrkA-wt TDK and of its K544N, K544R, K544P and K544A mutants, and of *h*VEGFR2 TKD and its K868N and K868R mutants. The structure of *h*TrkA TKD was taken from the X-ray structure with PDB code 4f0i (starting with Cys501 and ending with Val790; [29] and that of VEGFR2 from PDB code 6gqq (Leu814 to Asn1168; [30]). For TrkA, two protein chains are present in the PDB file and we chose chain B as the starting structure because residues 535 and 536 are missing in chain A. The Reduce

software [31] was used together with Whatif [32] to fix the orientation of Asn/Gln/His amino acids and detect the protonation of histidine residues. The two software packages gave the same results concerning the histidine buried inside the protein while they differed for some solvent exposed histidine. We considered an ε protonation for His 569, 594, 645, 648 and 772 in TrkA, and 816, 876, 879, 891, 895, 1004, 1026 and 1144 in VEGFR2, and δ protonation for all the other His residues. Mutations of Lys 544 (Lys868 in VEGFR2) to Asn, Arg, Pro and Ala were performed using the Rosetta software [33]. All proteins were solvated in a ~9 nm truncated octahedron box of ~17000 water molecules with a 0.1 M concentration of NaCl. The Amber ff99SB*-ILDN [34], [35] was used with TIP3P force field parameters for water. Within a periodic boundary condition set up, the system was subjected to geometry optimization by minimizing its total potential energy and then equilibrated with short MD simulations at constant temperature and pressure, applying restraints of decreasing strength to keep the non-hydrogen atoms of the protein close to the starting structure (20ps with 5000 kcal/mol $Å^{-2}$, 50ps with 3000 kcal/mol $Å^{-2}$ and 200ps with 1000 kcal/mol $Å^{-2}$). The equilibrated structures were used as starting points for 800ns-long production runs (600ns for VEGFR2). In the case of *h*TrkA-wt, -K544N and -K544R three different MD runs starting from the same geometry but different randomly assigned velocities were performed. Production runs employed a 2 fs time step (LINCS was used to constraint bonds involving H atoms), v-rescale thermostat (with a coupling of $\tau_T = 0.2$ ps) and Parrinello-Rahman barostat ($\tau_P = 5$ ps) to maintain a constant 300 K temperature and 1 bar pressure respectively. Snapshots were saved each 10 ps and the first 100 ns of each MD trajectory were discarded in the analysis. Simulations and analyses were performed with the Gromacs 5 package [36].

2.9 Statistical analysis

Statistical analysis was performed with OriginPro v8.50 and GraphPad Prism 6 softwares, or with algorithms implemented in MatLAB. For most of experiments, we used a one-way ANOVA, with Bonferroni's means comparison. The time course of *r*TrkA-wt versus *r*TrkA-K547N internalization was analyzed with a two-way ANOVA. Non-parametric tests for analysis of two samples were performed with Mann–Whitney test, of more than two samples with Kruskal-Wallis test followed by Dunn's means comparison. Significance was set at α=0.05. For testing differences in D and L distributions we evaluated the error in each bin j considering the different weight w_{ji} in it for each trajectory i: the frequency f_j and its variance $\sigma_{f_j}^2$ was calculated as $f_j = \sum_{i=1}^{n} w_{ji}$, $\sigma_{f_j}^2 = \frac{n}{n-1}\left(\sum_{i=1}^{n} w_{ji}^2 - \frac{\left(\sum_{i=1}^{n} w_{ji}\right)^2}{n}\right)$ as in [37], where n is the total number of trajectories. Normalized frequencies and their error bars where calculated dividing f_j and σ_{f_j} by $\Delta \sum_j f_j$, where Δ is the bin width and the sum is over all bins. Differences in frequency counts in single-step photobleaching assay and in L distributions were analyzed using χ^2 tests, in D distributions were analyzed as described [28]. Each experiment was independently repeated at least twice, as indicated in detail in each figure caption along with the p values obtained.

3. Results

3.1 Membrane accumulation and immobilization of TrkA-K547N mutant

We previously performed single particle tracking (SPT) measurements of *r*TrkA and *h*TrkA membrane diffusion, thanks to the insertion of the acyl carrier protein (ACP) tag (or its shortened version S6 tag) at the extracellular receptor portion (Fig. 1A) and its specific conjugation to

quantum dots (Qdots) [25], [27], [38]. We unveiled that NGF elicits a strong immobilization and clustering of membrane TrkA [24]. In order to unequivocally validate the relationship between membrane immobilization and receptor activation, we engineered an ACP-tagged construct in which Lys 547 (rat numbering, corresponding to human 544; Table S1) of *r*TrkA ATP-binding pocket was point-mutated to Asn (Fig. 1A). This substitution occurs in a conserved residue of the TKD N-lobe (Fig. 1A), and is a commonly adopted TrkA kinase-inactive variant (Table S1), while completely preserving NGF binding ability (Fig. S1). Both *r*TrkA-wt and -K547N were transfected in SHSY5Y cells, their membrane pool labelled with Qdots and imaged by TIRF with single-molecule resolution. Visual inspection of the moving spots (Video S1-S2) and relative trajectories (Fig.1B) suggested that *r*TrkA-K547N moves slower and explores smaller regions of the membrane compared to *r*TrkA-wt. This was confirmed by quantitative analysis of the diffusion coefficient (D) of mobile trajectories: *r*TrkA-K547N displays a bimodal distribution of D values similar to *r*TrkA-wt, but the faster population is slowed (peaked at 0.2 $\mu m^2/s$ versus 0.3 $\mu m^2/s$) and significantly decreased (Fig. S2A), matching with the rise of receptors moving at lower D (peaked at 0.005 $\mu m^2/s$ versus 0.013 $\mu m^2/s$, Fig. 1C). Furthermore, we classified the receptor modes of motion in immobile, confined and diffusive categories. We observed that the diffusive population of *r*TrkA-K547N is reduced by about 43% with respect to *r*TrkA-wt (Fig. 1D), matching with an increase of confined and immobile molecules. Thus, this specific lysine mutation alters receptor lateral mobility already in the absence of NGF stimulation. We then asked whether NGF binding could change the dynamics of *r*TrkA-K547N, similarly to what observed for the wt counterpart [24], and accordingly analyzed by SPT the effect of 15 minutes NGF stimulation in the two cases. From the analysis of the D distributions, we verified that NGF-stimulated *r*TrkA-wt displays a significant slowdown and reduction of the fast-diffusing population (Figs. 1E and S2B) and a 34% increase of the immobile mode of motion (Fig. 1D

and [24]). When analyzing the same for *r*TrkA-K547N, we again found a significant slowdown and reduction of fast-diffusing trajectories, but this was not as prominent as in the *r*TrkA-wt case (Figs.1E and S2B). Also, immobilization is less represented for *r*TrkA-K547N than for *r*TrkA-wt in the presence of NGF (Fig. 1D). We also calculated the distribution of confinement length for non-mobile trajectories [24] of *r*TrkA-K547N, observing no significant changes upon NGF stimulation, as instead we observed for the wt counterpart (Fig. 1F). These data indicate that NGF has an effect on *r*TrkA-K547N membrane dynamics, but with different features and weaker than on the *r*TrkA-wt one. Interestingly, we found that *r*TrkA-K547N displays a 3-fold higher surface density than *r*TrkA-wt; densitometric analysis of western blot from whole cell lysates suggests that this is not due to an increase of the total protein level (Fig.1G). We next investigated whether NGF has an effect in clearing this membrane accumulation, similarly to the internalization occurring for activated TrkA-wt [39], [40]. We set up a single-molecule internalization assay in which the density of membrane receptors of the two constructs was monitored by TIRF at eight time points within 60 minutes after NGF addition (Fig. 1H), and without NGF addition as control (Fig. S3). We found that *r*TrkA-wt and *r*TrkA-K547N decrease their membrane pool during time with different kinetics. For *r*TrkA-wt, the decrease starts at 5 min, becomes significant at 30 min and clearance of ~60% of the moving receptors from the cell membrane is accomplished after 40 minutes. On the contrary, *r*TrkA-K547N maintains a constant level of receptors exposed at the cell membrane up to 15 minutes after NGF stimulation; this slightly decreases in the following but reaches a significant decrease of ~36% only after 50 minutes. These results suggest that *r*TrkA-K547N remains more time at the plasma membrane despite NGF stimulation, indicating an impairment of internalization for this mutant. Given the high degree of conservation of this Lys residue in the ATP-binding pocket (Fig. 1A and [2]), our data hint at the existence of a general mechanism regulated by changes at this

specific residue. Accordingly, the corresponding mutation introduced in *m*VEGFR2 (K866N corresponding to K868N in *h*VEGFR2, Table S2), abolished kinase activity, reduced membrane mobility and increased membrane pool when compared to *m*VEGFR2-wt (Fig. S4).

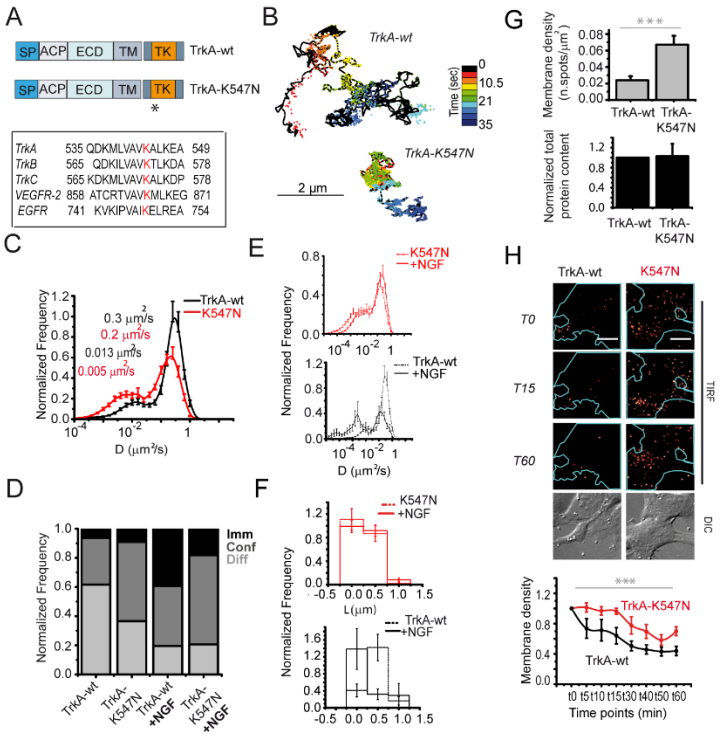

Fig. 1 Membrane immobilization and accumulation of *r*TrkA-K547N mutant. A) Scheme of *r*TrkA-wt and *r*TrkA-K547N (SP: signal peptide, ACP: acyl carrier protein tag, ECD: extracellular domain, TM: transmembrane domain, TK: Tyrosine Kinase domain); the asterisk highlights where the mutation is located. Below: sequence alignment of a portion of TKD for human sequences of TrkA, TrkB, TrkC, VEGFR2 and EGFR; the conserved Lys residue positioned in β3 sheet is shown in red. **B)** Typical trajectories obtained for moving *r*TrkA-wt (top) and -K547N (bottom) particles. **C)** Distribution of diffusion coefficient (D) with estimated uncertainty obtained from mobile *r*TrkA-wt (black curve, n=1989) and -K547N (red curve, n=1558) trajectories. **D)** Stack-column histogram plot of diffusive (light-grey), confined (grey) or immobile (black) receptors for *r*TrkA-wt without (n=2279 trajectories) and with NGF (n=513 trajectories), *r*TrkA-K547N without (n=2085 trajectories) and with NGF (n=2909 trajectories). The total number of trajectories was normalized to 1. **E)** Distribution of D coefficient with estimated uncertainty of mobile trajectories for *r*TrkA-K547N after NGF administration (top, red solid curve, n=2909 trajectories) and *r*TrkA-

wt (bottom, black solid curve, n=529 trajectories); the D distribution of resting *r*TrkA-K547N (red) and *r*TrkA-wt (black) are reported as dotted curve as a reference. **F)** Distributions of confinement length (L) with estimated error for non-mobile *r*TrkA-K547N (red) and *r*TrkA-wt (black) trajectories in the presence (solid; $n_{TrkA\text{-}K547N}$=616 and $n_{TrkA\text{-}wt}$=101 trajectories) or absence (dotted; $n_{TrkA\text{-}K547N}$=572 and $n_{TrkA\text{-}wt}$=290 trajectories) of NGF. p=0.38 (*r*TrkA-K547N) and $p=4.9\times10^{-4}$ (*r*TrkA-wt), according to χ^2 test. **G)** Density of labelled receptors per cell area (n=22 cells for *r*TrkA-wt, n=34 cells for *r*TrkA-K547N). ***p<0.0001 according to Mann-Whitney test. Below: densitometric analysis of total *r*TrkA-wt and *r*TrkA-K547N bands obtained averaging four independent blots; *r*TrkA-K547N signal was normalized to that of *r*TrkA-wt; error bars are standard errors. **H)** TIRF images of single receptor spots during a time-course after NGF stimulation. Cell borders are highlighted by a guide for the eye line. Every image corresponds to a time point for the same cell: t0 (time of NGF administration), t5, t15, t60 minutes. On the bottom, corresponding DIC image; scale bar=10 µm. The membrane density quantification for *r*TrkA-wt and *r*TrkA-K547N is reported as mean±sem from cells acquired at each time point normalized for the respective density at time 0. *** $p_{construct}$<0.001 and p_{time}<0.001, according to two-way ANOVA. All data are pools from up to 20 different cells collected in three independent replicas.

3.2 A structural rearrangement of the TKD correlates with *r*TrkA-K547N membrane immobilization

Mutation of Lys544 in *h*TrkA sequence (Lys547 in *r*TrkA) impairs kinase activity, recruitment of intracellular effectors and receptor ubiquitination [22], [23]. As impairment of any of these functions may potentially lead to the observed altered membrane dynamics (Fig. 1), we produced three additional *r*TrkA mutants to dissect the individual contributions to TrkA mobility. As reported in Fig. 2A, we generated: i) the Y499F/Y760F/Y794F mutant (recruitment mutant of *r*TrkA, RM); ii) the Y679F/Y683F/Y684F mutant (kinase mutant of *r*TrkA, KM); and iii) *r*TrkA-P791S mutant (ubiquitination mutant). The last one is modified in the binding site for the E3 Ubiquitin-ligase Nedd 4-2 [22]. This presumably accounts for the most abundant TrkA ubiquitination: indeed, differently from others, ubiquitination by Nedd 4-2 does not require

overexpression of ubiquitin constructs to be detected [22], [23]. We transfected RM, KM and *r*TrkA-P791S in SHSY5Y cells, and receptors were labelled to monitor their membrane dynamics by TIRF. Quantification of the obtained trajectories revealed that none of the compromised functions is responsible for *r*TrkA-K547N altered dynamics. Indeed, the modes of motion displayed by RM, KM, *r*TrkA-P791S were almost superimposable to those of *r*TrkA-wt (Fig. 2B).

It is well known that this mutated Lys (Fig. 1A) has a key structural role in the definition of a salt bridge linking strand β3, containing the Lys, to a Glu (563 in *r*TrkA and 560 in *h*TrkA) in the αC helix in the N lobe of TKD [43]. This salt bridge is highly conserved across different RTKs [2]. We thus hypothesized that the K→N mutation leads to a structural rearrangement of TrkA TKD that, independently of the functional impairment, may account for the observed entrapment in the membrane. This prompted us to perform molecular dynamics (MD) simulations of the *h*TrkA TKD in the wt configuration or after insertion of K544N mutation; we also simulated the behavior of a *h*TrkA-K544R mutant, in which the Arg possibly maintains the aforementioned salt bridge, while still compromising phosphorylation (Table S1). We focused on possible structural alterations induced by the K→N mutation. Surprisingly the MD simulations, while predicting a limited impact on strand β3, highlight a higher destabilization in the αC helix (Fig. 2C and Fig. S5C). This leads to distinct sub-populations characterized by different positioning of the αC helix with respect to strand β3 and C lobe, including one triggered by the formation of a new salt bridge between Glu560 in the αC helix and Arg673, located between β8 and β9 (Fig.2D and Fig. S5A). This effect is strictly dependent on the lack of Lys544-Glu560 salt bridge: indeed, substitution of Lys544 with salt-bridge preserving Arg (Fig. 2C-D) maintains the stability of the αC helix in the MD simulations (Fig. 2C and Fig. S4B). Conversely, two different but both salt-

bridge abolishing amino acids like Ala or Pro are predicted to destabilize the αC helix (Fig. S4B-C). These results prompted us to express and Qdot-label an ACP-tagged *r*TrkA-K547R in SHSY5Y cells; we found that, although this mutant is not phosphorylated, its membrane dynamics is more similar to that of *r*TrkA-wt than of *r*TrkA-K547N (Fig. 3A-B and Fig. S6). Thus, the K→N mutation in β3-sheet is predicted to yield specific structural rearrangements; a possible consequence of these could be an aggregation of the TKDs that may favor the formation of receptor homo-clusters with the consequent decrease in the measured diffusion. Indeed, TrkA crystal structure already showed the possibility to form dimers and probably oligomers in the crystal unit [29]. To test this hypothesis, we analyzed the intensity step-photobleaching profile of *h*TrkA-wt, *h*TrkA-K544N and *h*TrkA-K544R single molecules in the membrane of fixed cells (red boxes of Fig. 3C). For each spot, we quantified the number of photobleaching steps as a direct measure of the number of molecules in an isolated spot [28]. The results highlight no significant changes in the monomer, dimer and oligomer populations in the three cases (M, D, O in Fig. 3D, respectively), thus ruling out the possibility of increased homo-aggregation as the molecular cause for the observed *h*TrkA-K544N membrane dynamics.

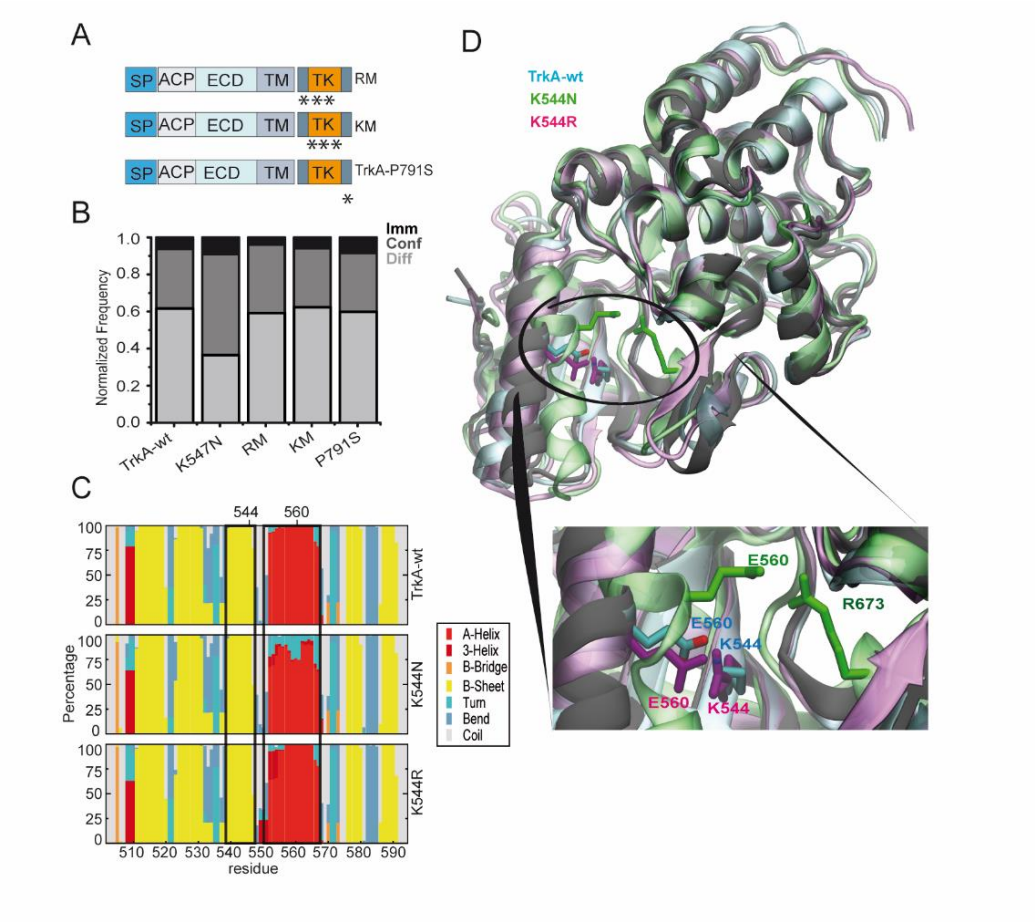

Fig. 2 A structural change of the TKD correlates with *r*TrkA-K547N membrane immobilization. A) Scheme of recruitment mutant (RM), kinase mutant (KM) and ubiquitination mutant (*r*TrkA-P791S). SP: signal peptide, ACP: acyl carrier protein tag, ECD: extracellular domain, TM: transmembrane domain, TK: Tyrosine Kinase domain; asterisks highlight the positions of the single mutations in the intracellular region (Y to F in RM and KM). **B)** Stack-column histogram plot for diffusive (light-grey), confined (grey), immobile (black) receptors obtained for *r*TrkA mutants. The total number of trajectories (RM: n=6638, KM: n=7777 and *r*TrkA-P791S: n=1841 trajectories; *r*TrkA-wt and *r*TrkA-K547N of Fig. 1D are here reported as a reference) was normalized to 1. All data are pools from up to 20 different cells collected in three independent replicas. **C)** MD analysis of secondary structure elements encompassing residues 501 to 593 in *h*TrkA-wt (top), *h*TrkA-K544N (middle) and *h*TrkA-K544R (bottom). The regions corresponding to the αC helix and the β3 sheet are highlighted by a black rectangle. **D)** Selected snapshots from MD simulations of *h*TrkA-wt TKD (cyan), and its K544N (green) and K544R (magenta) mutants superimposed on the *h*TrkA-wt TKD crystal structure (PDB: 4f0i, gray).

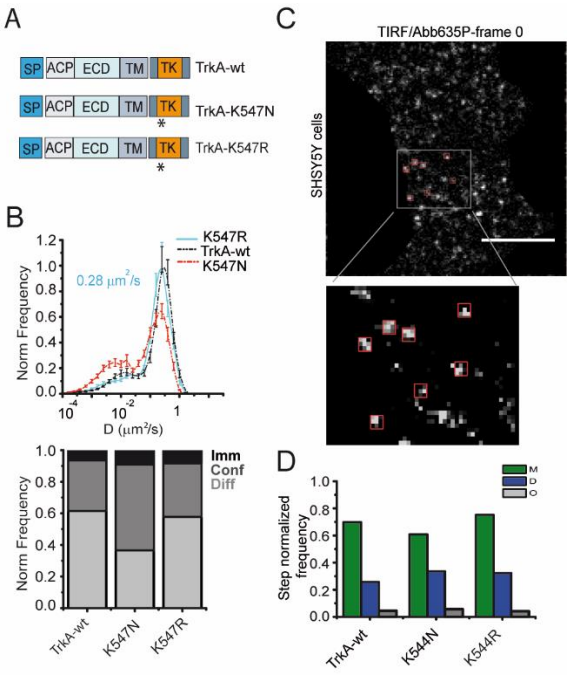

Fig. 3 *r*TrkA-K547N membrane immobilization depends on the lack of Lys-Glu salt bridge but not on increased receptor homo-aggregation. A) Scheme of *r*TrkA-wt, *r*TrkA-K547N and *r*TrkA-K547R (SP: signal peptide, ACP: acyl carrier protein tag, ECD: extracellular domain, TM: transmembrane domain, TK: Tyrosine Kinase domain); the asterisk highlights where the single point mutations are located. **B)** Top: distribution of diffusion coefficient (D) with estimated uncertainty obtained for mobile *r*TrkA-K547R trajectories (dark cyan curve, n=936). Bottom: stack-column histogram plot of diffusive (light grey), confined (grey), immobile (black) receptors obtained for *r*TrkA-K547R (1745 trajectories), *r*TrkA-wt and *r*TrkA-K547N (same data of Fig. 1D). **C)** TIRF image of Abberior635P-labelled *h*TrkA spots on the surface of fixed SHSY5Y cells: red squares in the inset are the 3×3 pixels ROI highlighting the analyzed spots in the first frame of the background-subtracted TIRF movie. **D)** Frequency of photobleaching steps (M=1 step; D=2 steps; O= at least 3 steps) counted for *h*TrkA-wt (n=245 spots), *h*TrkA-K544N (n=286 spots) and *h*TrkA-K544R (n=355 spots); differences are not significant according to χ^2 test. All data are pools from 10 to 19 different cells collected in three (B) and two (D) independent replicas.

3.4 *r*TrkA-K547N membrane mobility depends on the integrity of cortical actin

We next investigated if the altered membrane mobility of *r*TrkA-K547N could be due to new hetero-interactions maintaining the structurally rearranged receptor within different membrane domains than *r*TrkA-wt. As micro- and nano- domains in the plasma membrane are structured by fences of cortical actin, which confine in space and time the diffusivity of transmembrane

receptors [42], [43], we treated cells with drugs affecting the polymerization state of actin, either by disrupting (cytochalasin D, latrunculin B) or by stabilizing (jasplakinolide) actin fibers integrity, as evidenced by phalloidin staining of the cells after the treatment (Fig. 4A). By performing SPT measures in these conditions, we found that the *r*TrkA-K547N confined and immobile modes of motion were substantially impaired by actin depolymerization (Fig. 4C), as was the accumulation of surface *r*TrkA-K547N receptors (Fig. 4B, D); the latter turned out to slightly increase when we stabilized the polymerized form of actin fibers (Fig. 4B-D). The same treatments tested on *r*TrkA-wt showed an opposite trend in the modes of motion after actin depolymerization (Fig. 4E), and no significant effect on the density of surface receptors (Fig. 4B, F). These data suggest that *r*TrkA-K547N, but not *r*TrkA-wt, is either stably entrapped within membrane regions maintained by the actin meshwork, or directly interacts with it, justifying the specific slow membrane dynamics and the surface accumulation displayed by this mutant.

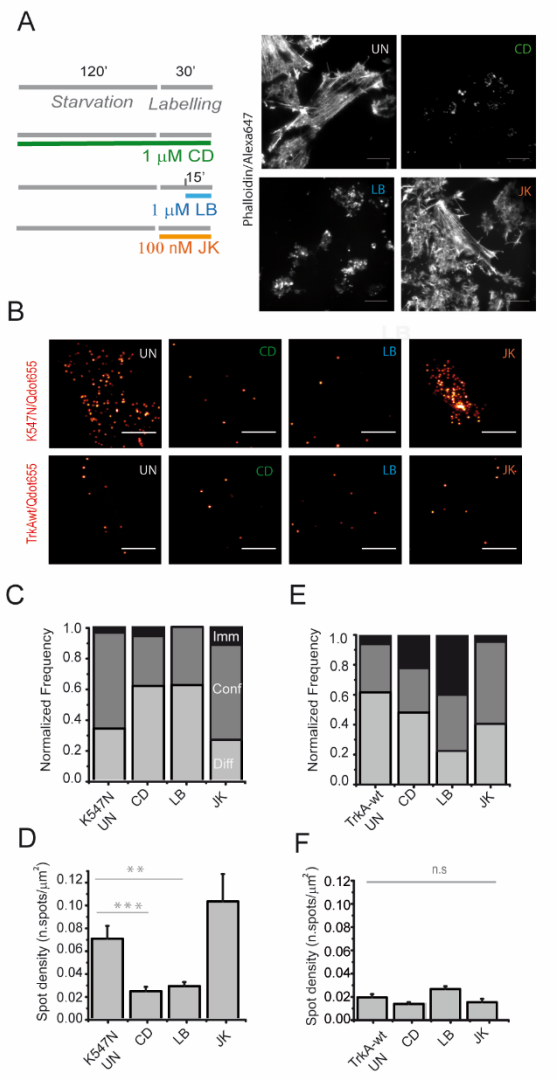

Fig. 4 Actin cytoskeleton mediates membrane immobilization and accumulation of *r*TrkA-K547N. A) Left: Timeline of the SPT experiment on *r*TrkA-K547N and *r*TrkA-wt in the presence of drugs affecting actin polymerization. CD: Cytochalasin D; LB: Latrunculin B; JK: Jasplakinolide**;** right: typical TIRF images of SHSY5Y cells labelled with Alexa647-phalloidin after the treatments (UN: untreated). Scale bar: 10 μm. **B)** TIRF images of *r*TrkA-K547N (top) and *r*TrkA-wt (bottom) transfected SHSY5Y cells after Qdot labeling, in untreated and CD-, LB- and JK- treated conditions. Scale bar=10 μm. **C)** Stack-column histogram plot for the distribution of diffusive (light grey), confined (grey) and immobile (black) *r*TrkA-K547N receptors in untreated conditions (same as Fig. 1E) and after CD, LB, JK treatments (CD, n=904; LB, n=366; JK, n=1606 trajectories). **D)** *r*TrkA-K547N surface density in untreated conditions and after CD, LB, JK treatments (untreated, n=22; CD= 15; LB=17; JK= 23 cells). ***p<0.001, **p <0.01 according to Kruskal-Wallis test followed by Dunn's Multiple Comparison test. **E)** Stack-column

histogram plot for the distribution of diffusive (light grey), confined (grey) and immobile (black) *r*TrkA-wt receptors in resting conditions (same as Fig. 1E) and in the presence of CD, LB, JK drugs (CD: n=169; LB: n= 169; JK: n=100 trajectories). **F)** *r*TrkA-wt surface density in untreated conditions and after CD, LB, JK treatments (untreated, n=10 cells; CD= 7 cells; LB=8 cells; JK= 6 cells). Differences are not significant according to Kruskal-Wallis test followed by Dunn's Multiple Comparison test. SPT data are pools from up to 23 different cells collected in three independent replicas.

3.5 Contribution of PTMs on NGF-induced TrkA membrane immobilization

From data reported in Fig. 1D-F, we concluded that *r*TrkA-wt displays a remarkably higher membrane immobilization induced by NGF stimulation, when compared to *r*TrkA-K547N. Given that ligand-induced immobilization was correlated to RTKs activation [24], [44], we aimed at understanding which functional feature is responsible for it. Biochemical analysis of *r*TrkA-K547N, RM, KM, *r*TrkA-P791S in comparison to *r*TrkA-wt revealed that NGF-induced phosphorylation and ubiquitination could be fully dissected by using these mutants. As shown in Fig. 5A, only *r*TrkA-wt showed significant phosphorylation and ubiquitination signals upon NGF stimulation; *r*TrkA-P791S was significantly phosphorylated but not ubiquitinated; TrkA-K547N was significantly ubiquitinated but not phosphorylated; RM and KM did not display significant levels of either PTM (Fig. 5A). We thus performed SPT analysis for RM, KM and *r*TrkA-P791S in the presence of NGF, as already done for *r*TrkA-wt and *r*TrkA-K547N (Fig. 1D-F), and calculated the variation of the modes of motion of all constructs after NGF stimulation. Interestingly, we found that all TrkA mutants investigated display weaker NGF-induced immobilization than *r*TrkA-wt (Fig. 5B), meaning that this effect conceivably requires both unaltered phosphorylation and ubiquitination to occur.

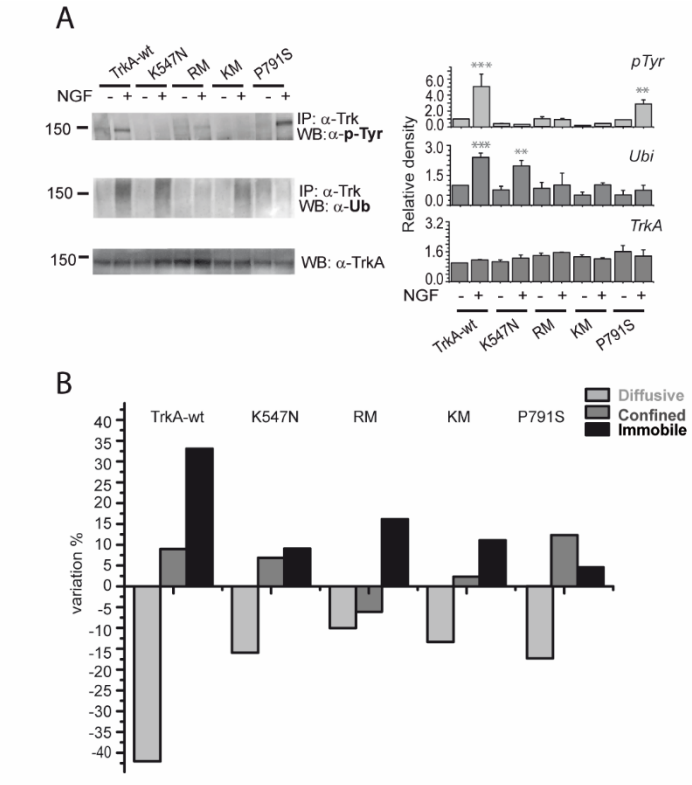

Fig.5 Impact of PTMs on NGF-induced TrkA membrane dynamics. A) WB showing Tyr phosphorylation (p-Tyr, top) and ubiquitin (Ub, middle) levels in SHSY5Y cells transfected with *r*TrkA-wt, *r*TrkA-K547N, RM, KM, *r*TrkA-P791S in the presence (+) or absence (-) of 10 minutes stimulation with 125 ng/ml NGF, after immunoprecipitation (IP) with anti-Trk antibody. The relative density of the bands is reported on the right of each blot, as mean±sem of 2-5 independent replicas; each band density was normalized to the total TrkA content obtained after membrane stripping, and divided for *r*TrkA-wt value (p-Tyr Blot: n=3 for all constructs; Ub blot: n=5, *r*TrkA-wt; n=4, *r*TrkA-K547N; n=2, RM; n=3, KM, *r*TrkA-P791S). ***p<0.001, **p<0.01, according to one-way Anova with Bonferroni's multiple comparison test. Bottom: WB showing total TrkA levels for the same samples as above. The relative density of the bands is reported on the right of the blot, as mean±sem of 3 independent replicas; the band density was normalized to the total protein content of each lane (Fig. S7), and divided for TrkA-wt value. Data are not significantly different according to one-way Anova with Bonferroni's multiple comparison test. **B)** Column plot of the variation (in percentage of the total) of diffusive (light-grey), confined (grey), immobile (black) receptor populations upon NGF stimulation for *r*TrkA-wt (n=513), *r*TrkA-K547N (n=2909), RM (n= 531), KM (n=1848) and *r*TrkA-P791S (n=1526 trajectories); the number of trajectories analyzed in resting conditions for each mutant are reported in Fig.2B. All trajectories are pools from up to 20 cells from three independent replicas.

4. Discussion

We previously demonstrated that TrkA membrane mobility measured by TIRF microscopy combined with SPT is highly predictive of its function, with immobilization and clustering being a signature of the activating ligand [24]. This ligand-dependent effect agrees with similar results reported for EGFR [44], FLS2 receptor-like kinase [45] and insulin receptor kinase [46]. Overall, these works have allowed for the definition of a direct cause-effect relationship between RTKs activation and immobilization of their membrane pool. Here, we scale-up our study by analyzing different TrkA mutants in comparison to TrkA-wt, and provide evidence that such relation may be more complicated than expected. Indeed, our results show that it is possible to distinguish at least two different TrkA membrane immobilization modes. On one hand, K544N mutation (in *h*TrkA corresponding to K547N in *r*TrkA, Table S1) in sheet β3 of TrkA TKD endows the receptor with increased confined and immobile membrane fractions with respect to TrkA-wt, independently of NGF binding (Fig. 1C-F), and with an enrichment of surface pool (Fig. 1G). The importance of these observations is strengthened by evidence that at least another RTK, VEGFR2, shares similar features upon mutation of the corresponding Lys to Asn (Figs. 1A, S4 and S5). Mutations of these Lys residues were previously adopted as kinase-dead variants of TrkA and VEGFR2 receptors (Tables S1-2), since they impair ATP allocation necessary to TKD activation and downstream phosphorylation processes [47]. Furthermore, mutation of this residue was previously linked to impaired ubiquitination [22], [23]. However, we argue that the altered membrane mobility does not singularly depend on TrkA kinase activity, on its ability to recruit intracellular effectors at phosphorylated Tyr, nor on its ubiquitination; indeed, mutants in which these functions are separately impaired do not show the same slowdown in the detected trajectories (KM, RM and *r*TrkA-P791S in Fig. 2B). Instead, our MD simulations indicate that, in

*h*TrkA-K544N, the αC helix of the N lobe becomes less stable as a consequence of the loss of a salt bridge with β3 sheet (Fig. 2C-D), and can adopt different arrangements with respect to the C lobe (Fig. 2C-D and S5). *r*TrkA-K547R, a kinase-inactive mutant that maintains the salt bridge, does not display the repositioning of the αC helix (Fig. 2C-D) and does not show altered modes of motion in the analyzed trajectories with respect to *r*TrkA-wt (Fig. 3A-B). Based on results in Figs. 3-4, we hypothesize that these structural changes do not increase the propensity of the receptor to self-aggregate, but rather could account for new hetero-interactions leading to the observed confinement and immobilization at the cell surface detected by SPT. On the other hand, a different membrane immobilization is experienced by *r*TrkA-wt, at higher extent than *r*TrkA-K547N, after NGF stimulation, with D and L distributions changing considerably in the wt but not in the K547N case (Fig. 1E-F) and with less represented decrease of diffusive trajectories for TrkA-K547N (Fig. 1D). In this respect, it is noteworthy that all TrkA mutants assessed by SPT show impaired NGF-induced membrane immobilization (Fig. 5B), despite their conserved ability to bind NGF (Fig. S1). Both NGF-induced TrkA phosphorylation and ubiquitination account for it. We thus speculate that the shared tendency of all analyzed mutants to undergo only small reductions of diffusivity may simply be due to NGF binding to their ECD. This, while possibly inducing their dimerization, may not result in the robust and signaling-related immobilization typical of the wt receptor.

The lateral diffusivity of membrane proteins and lipids is modulated by the presence of specialized physical barriers [48] like actin fences [49]. These fibers, lying in close contact with the inner leaflet of the plasma membrane, can constrain transmembrane proteins within transient confinement regions called corrals [50]. The slow dynamic profile reported for *r*TrkA-K547N can be reliably ascribed to interactions with these membrane regions. Indeed, cortical-actin depolymerization (Fig. 4A) leads to an accelerated diffusion and decreased accumulation

of *r*TrkA-K547N (Fig. 4B-C-D). The same drug treatments lead to opposite changes for *r*TrkA-wt, (Fig. 4B-E-F and [24]). These data indicate different dynamic interactions of *r*TrkA-wt and *r*TrkA-K547N with the actin cytoskeleton, which might be relevant for the different signaling abilities displayed by the two receptor forms. However, whether an enhanced partitioning within the aforementioned domains or direct interactions with actin account for *r*TrkA-K547N slow membrane dynamics remains to be established.

TrkA has been reported to be ubiquitinated, in different experimental conditions, by a number of different E3-ubiquitin ligases, namely TRAF-6 E3 RING Ub-ligase [51], Nedd 4-2 E3 HECT Ub-ligase [22], [52], TRAF-4 E3 RING Ub-ligase [23], and Cbl [53]. This prompted us to investigate whether this PTM plays a role also in TrkA membrane dynamics. We found that *r*TrkA-K547N can be significantly ubiquitinated after NGF treatment (Fig. 5 A) in SHSY5Y cells, while lysine 547 mutation leads to impairment of TrkA ubiquitination in HEK293 cells in the absence of NGF [22]. However, we found that NGF addition may restore ubiquitination of different lysine 547 mutants in this cell model (Fig. S8A). Also, *r*TrkA-wt is equally ubiquitinated in resting and NGF-stimulated conditions in HEK293 cells. This may be due to a higher expression level of the construct than in SHSY5Y cells, leading to ligand-independent auto-activation (Fig. S8A). Alternatively, possible differential regulatory patterns on TrkA could be driven by different cell backgrounds. In this context, it should be noted that both *r*TrkA-wt and *r*TrkA-K547N proteins show different mobilities in HEK293 when compared to SHSY5Y cells (Fig. 1C and S8B). In any case, the observation that inhibition of *r*TrkA ubiquitination by the P791S mutation, without perturbing kinase activity (Fig. 5A), is sufficient to impair NGF-induced immobilization of *r*TrkA-wt (Fig. 5B) suggests that this PTM plays a crucial role in the regulation of its membrane dynamics.

5. Conclusions

The findings emerging from our study enrich our knowledge of RTKs, but also unavoidably call into question the interpretation of previous experiments indifferently making use of distinct mutations to achieve abolition of RTK kinase activity (Tables S1 and S2). Indeed, our data indicate that not all kinase-inactive TrkA mutants behave in the same way, at least concerning membrane mobility (Figs. 1-3) and ubiquitination (Fig. 5). Furthermore, our data also suggest that understanding the effect of a TKD mutation may benefit from analysis of its impact on the KD structure, in addition to catalytic activity. This may be useful to understand the molecular basis of pathogenicity of the several inactivating mutations disseminated along TrkA, and more in general RTKs, sequence.

Acknowledgments

The authors wish to gratefully thank A. Cattaneo and F. Beltram for helpful discussions, F. Bonsignore, F. Gobbo and L. Ceccarelli for technical help, G. Signore for making CoA-biotin reagent available, and G. Ferri for help with MATLAB codes. Grant AIRC IG17276 to SM is gratefully acknowledged. The authors declare no competing financial interests.

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