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Invited review

Post-translational dysfunctions in channelopathies of the nervous system

Benedetta Terragni ^a, Paolo Scalmani ^a, Silvana Franceschetti ^a, Sandrine Cestèle ^{b,c}, Massimo Mantegazza ^{b,c,*}^a U.O. Neurophysiology and Diagnostic Epileptology, Foundation IRCCS Neurological Institute C. Besta, 20133 Milan, Italy^b Institute of Molecular and Cellular Pharmacology (IPMC), CNRS UMR7275, 06560, Valbonne-Sophia Antipolis, France^c University Côte d'Azur (UCA), 06560, Valbonne-Sophia Antipolis, France

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ABSTRACT

Channelopathies comprise various diseases caused by defects of ion channels. Modifications of their biophysical properties are common and have been widely studied. However, ion channels are heterogeneous multi-molecular complexes that are extensively modulated and undergo a maturation process comprising numerous steps of structural modifications and intracellular trafficking. Perturbations of these processes can give rise to aberrant channels that cause pathologies. Here we review channelopathies of the nervous system associated with dysfunctions at the post-translational level (folding, trafficking, degradation, subcellular localization, interactions with associated proteins and structural post-translational modifications). We briefly outline the physiology of ion channels' maturation and discuss examples of defective mechanisms, focusing in particular on voltage-gated sodium channels, which are implicated in numerous neurological disorders. We also shortly introduce possible strategies to develop therapeutic approaches that target these processes.

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Contents

1. Maturation and functional modulation of ion channels	00
2. Neuronal channelopathies caused by folding/trafficking defects and negative dominance	00
3. Neuronal channelopathies caused by dysfunctional protein interactions	00
4. Neuronal channelopathies caused by dysfunctional structural post-translational modifications (PTMs)	00
4.1. Glycosylation	00
4.2. Phosphorylation	00
4.3. Ubiquitylation	00
4.4. SUMOylation	00
4.5. S-palmitoylation (or S-acylation)	00
4.6. Proteolysis	00
5. Possible therapeutic approaches	00
6. Conclusions	00
Acknowledgements	00
References	00

* Corresponding author. Institute of Molecular and Cellular Pharmacology (IPMC), CNRS UMR7275, University Côte d'Azur (UCA), 660 Route des Lucioles, 06560 Valbonne-Sophia Antipolis, France.

E-mail address: mantegazza@ipmc.cnrs.fr (M. Mantegazza).

Ion channels are pore-forming trans-membrane proteins that control the movement of ions across cells' membranes, according to their electro-chemical gradients. The flow of ions through channels

is regulated by specific stimuli and modulations, and generates electrical currents that in turn establish trans-membrane voltage and can modify ion concentration gradients, effects that are essential for diverse physiological functions: e.g. membrane potential generation and modulation, neurotransmitters release, signal transduction, hormone secretion, muscle contraction, etc. Channelopathies comprise heterogeneous diseases arising from defects of ion channels (Kullmann and Waxman, 2010; Curran and Mohler, 2015; Ptáček, 2015; Imbrici et al., 2016). The most common and direct cause are mutations in the encoding genes that alter channels' biophysical properties, thus producing gain or loss of function effects that compromise the function of the cell/tissue in which mutant channels are expressed. However, mutations impairing functional properties are not the only underlying mechanism for channelopathies. Indeed, decades of extensive research on the physiology of ion channels have shown that channels are not simply trans-membrane proteins with a pore that allows ions to flow, but rather heterogeneous multi-molecular complexes originating from a complex maturation process comprising numerous steps, which occur after that channels are translated. Perturbations of these processes can give rise to aberrant channels causing pathological conditions (Cobbold et al., 2003; Dib-Hajj and Waxman, 2010; Curran and Mohler, 2015).

Our review focuses on channelopathies of the nervous system

associated with dysfunctions at the post-translational level: folding, trafficking, post-translational modifications, degradation, subcellular localization and protein interactions (see Table 1 and Fig. 1 for a summary). We will briefly outline the physiology of ion channels' maturation and then discuss examples of defective mechanisms, focusing in particular on voltage gated sodium channels (Na_v), which are implicated in numerous neurological disorders (Mantegazza et al., 2010a; Catterall, 2012; Eijkelkamp et al., 2012).

1. Maturation and functional modulation of ion channels

When mRNA translation begins to take place in a ribosome, the nascent peptide of an ion channel exposes specific aminoacidic sequences that target the peptide/ribosome complex to the endoplasmic reticulum (ER). Here, the synthesis continues, the tertiary structure is acquired and the developing channel is inserted into the lipid bilayer. The ER is also the first quality control check-point along the synthesis pathway by means of ER-associated chaperons that mediate the retention of not properly folded nascent ion channels within the ER compartment. Unfolded or misfolded channels can be either eliminated by ER-associated degradation (ERAD), through their retrotranslocation across the ER membrane and degradation by cytosolic proteasomes, or retained for further

Table 1
Summary of post-translational dysfunctions that we have reviewed and the affected ion channels.

Post-translational dysfunction	Channel	Reference	
Folding/trafficking defects with negative dominance	Ca _v 2.1	Pietrobon, 2010; Jeng et al., 2006; Mezghrani et al., 2008; Page et al., 2010; Dahimene et al., 2016; Raïke et al., 2007	
	Ca _v 3	Mezghrani et al., 2008; Page et al., 2004	
	Ca _v 2	Mezghrani et al., 2008; Page et al., 2004	
	K _v 1.1	Chen et al., 2016	
	K _v 1.2	Syrbe et al., 2015; Helbig et al., 2016	
	K _v 2.1	Saitsu et al., 2015	
	K _v 7.2	Orhan et al., 2014; Maljevic et al., 2011	
	K _v 7.4	Gao et al., 2013	
	TRESK	Lafrenière et al., 2010; Liu et al., 2013	
	HCN1	Nava et al., 2014	
	Na _v 1.5	Sottas and Abriel, 2016; Mercier et al., 2012	
	Na _v 1.2	Kamiya et al., 2004	
	without negative dominance	Na _v 1.1	Rusconi et al., 2007; Rusconi et al., 2009; Thompson et al., 2012; Bechi et al., 2015; Cestèle et al., 2013b
		Na _v 1.2	Misra et al., 2008
		Na _v 1.6*	Blanchard et al., 2015; Sharkey et al., 2009*
		Na _v 1.7	Eijkelkamp et al., 2012
		Ca _v 1.4	Hoda et al., 2006
	Ca _v 3.2	Vitko et al., 2007; Eckle et al., 2014	
Dysfunctional protein interactions	Na _v 1.1*, Na _v 1.2*, Na _v 1.3, Na _v 1.6* and Na _v β1	Wimmer et al., 2010*; Lucas et al., 2005; Rusconi et al., 2007; Patino et al., 2011	
	Na _v 1.5 and Na _v β2, 3, 4	O'Malley and Isom, 2015	
	Ca _v 1, 2 and Ca _v β4	Escayg et al., 2000	
	Na _v 1.8 and P11*	Okuse et al., 1997*	
	Na _v 1.1, Na _v 1.6* and FGF14	van Swieten et al., 2003; Goldfarb et al., 2007*; Rusconi et al., 2009	
	K _v 7 and FGF14	Pablo and Pitt, 2017	
	Na _v and AnkG*	Lopez et al., 2016*	
	K _v and LGI1	Schulte et al., 2006	
	AMPA _r and LGI1*	Fukata et al., 2010*	
	HCN1, HCN2 and TRIP8b*	Shin et al., 2008*	
	Dysfunctional PTMs	Glycosylation	K _v 3.3, Na _v 1.6*
Phosphorylation		Na _v 1.2*, Na _v 1.7 [#] , Na _v 1.8 [#] , Na _v 1.9 [#]	
Ubiquitylation		Na _v 1.1, Na _v 1.7*	
SUMOylation		Na _v 1.2, Na _v 1.7	
Proteolysis		Na _v 1.2*, Na _v 1.6 [#] , Na _v 1.8 [§] , Na _v 1.9 [§] , Na _v β subunits	

Symbols (*, # and §) indicate experimental evidence from animal models.

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