

REVIEW ARTICLE

## The three Rs along the TRAIL: Resistance, re-sensitization and reactive oxygen species (ROS)

Gregory Mellier<sup>3</sup> & Shazib Pervaiz<sup>1,2,3,4</sup>

<sup>1</sup>Department of Physiology, Yong Loo Lin School of Medicine, Singapore, <sup>2</sup>NUS Graduate School for Integrative Sciences and Engineering, National University of Singapore, <sup>3</sup>Duke-NUS Graduate Medical School, Singapore, and <sup>4</sup>Singapore-MIT Alliance, Singapore

### Abstract

Ligation of the Tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) death receptors has been associated with cancer specific apoptotic execution in a number of model systems. This has generated tremendous interest in the use of TRAIL as a potential therapeutic modality. However, recent evidence indicates that resistance to TRAIL might present with a therapeutic challenge. In this short report, we review the basic biology of TRAIL signalling in cancer cells, highlight the mechanisms underlying resistance to TRAIL and the ability of small molecule compounds to re-sensitize cells to TRAIL-mediated apoptosis. In particular, we provide evidence that intracellular reactive oxygen species could be critical in regulating the response of cancer cells to TRAIL.

**Keywords:** apoptosis, death receptors, oxidative stress, redox, TNF family

### TRAIL and TRAIL-mediated apoptosis

Tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) belongs to a large family of proteins grouped under the TNF superfamily [1,2]. Since its discovery, TRAIL has generated a lot of interest due, notably, to its ability to specifically target tumour cells both *in vitro* and *in vivo* with minimal toxicity towards normal cells [1–4]. However, numerous studies have since then showed that many human tumours are resistant or could easily acquire resistance to TRAIL-induced apoptosis [5–7]. Hence, the focus was switched towards the identification and development of novel small molecule compounds that could restore cancer cells sensitivity to TRAIL.

TRAIL is expressed as a type II transmembrane protein or as a cleaved soluble form (extracellular domain). TRAIL interacts with the death receptors (DRs) DR4/TRAIL-R1/TNFRSF10A [8] and DR5/TRAIL-R2/KILLER/TNFRSF10B [9,10], the decoy receptors DcR1/TRAIL-R3/TNFRSF10C [9,10] and DcR2/TRAIL-R4/TNFRSF10D [11] and with a soluble receptor called osteoprotegerin although with low affinity [12]. The first step of the death receptor apoptotic pathway, also known as the extrinsic pathway, is the binding of a trimerized form of TRAIL to the DRs, which induces a conformational change in the death domain of the receptors. In association with the DRs' clustering and oligomerization, the TRAIL/DR ligation constitutes the functional activation of the receptors. Once activated, the receptors, via their death domains, recruit the adaptor protein Fas-associated protein with

death domain (FADD). In turn, FADD recruits caspases-8/10 through interaction of their death effector domains [13]. This complex is termed as the death-inducing signalling complex (DISC) [14] and promotes the activation of initiator caspases [15]. Caspases-8/10 then triggers the activation of the downstream effector caspase-3 leading to the subsequent cleavage of caspase substrates, which are important regulatory and structural proteins [16,17], and ultimately, apoptosis as evidenced by the appearance of its associated hallmarks (e.g. nuclear shrinkage, DNA fragmentation and membrane blebbing [18]). As an alternative, the initiator caspases can engage the intrinsic or mitochondrial apoptotic pathway by cleaving the protein Bid (a pro-apoptotic member of the Bcl-2 family). Bid, in its truncated form, then binds to BAX and BAK leading to their oligomerization and translocation to the mitochondrial outer membrane as well as the subsequent decrease in the mitochondrial membrane potential and the formation of pores responsible for the permeabilization of the mitochondrial outer membrane [19]. Disruption of mitochondria structural integrity permits the release into the cytosol of cytochrome *c* and Smac/DIABLO, among other pro-apoptotic proteins. Once in the cytosolic compartment, cytochrome *c* interacts with ATP and APAF-1 to form the apoptosome, thus enabling the activation of caspase-9. Caspase-9 can in turn activate caspase-3, -6 and -7 [20] and commit the cells to apoptosis as described earlier. Interestingly, according to the two cell types defined by Ozeren and El-Deiry [21], the cleavage of Bid can either serve as an amplification loop for the apoptotic

signal in cells that do not depend on the intrinsic pathway for apoptosis induction (type I cells, e.g. thymocytes, colorectal adenocarcinoma cell line SW480, B lymphoblastoid cell line SKW6.4) or as the primary mechanism of TRAIL-mediated cell death, by engaging the intrinsic pathway, in cells where the extrinsic pathway is impaired or insufficient to induce cell death alone (type II cells, e.g. hepatocytes, colorectal carcinoma cell line HCT116, T lymphocyte cell line Jurkat).

### TRAIL resistance and re-sensitization

As alluded to earlier, the promising debut of TRAIL as a potential therapeutic agent was hampered by a growing number of studies showing that numerous cancer cell lines exhibit or acquire resistance to TRAIL. No consensus regarding the development of TRAIL resistance has yet been reached, however, several mechanisms by which cancer cells evade TRAIL-mediated apoptosis at several levels of the apoptotic pathway have been described. Fortunately, the growing understanding of such mechanisms has helped to put in place novel approaches permitting the identification of sensitizing drugs. Indeed, several studies have shown that in many cases, TRAIL-resistant cancer cells could reacquire sensitivity to TRAIL when treated with such compounds in combination with TRAIL, often with a synergistic drug interaction [22]. In the following section, we discuss the most common apoptotic blockades involved in TRAIL resistance as well as the mechanisms of re-sensitization offered by small compounds used in combination with TRAIL.

#### *Defects in death receptors and DISC*

As the ligation of TRAIL to DR4 and DR5 and formation of the DISC are the first steps of TRAIL-induced apoptosis, changes in the protein structure of the DRs and/or their expression at the cell surface can dramatically decrease the efficiency of the apoptotic signal conveyed by TRAIL. Interestingly, many of the studies on TRAIL re-sensitization have focused on this first critical step of TRAIL-induced apoptosis transduction.

In this regard, it was shown that the epigenetic silencing of DR4 [23,24], loss-of-function mutations in DR4 and DR5 [25,26], deficient transport of the DRs to the cell surface [27], an increased TRAIL-decoy to death receptors ratio [28,29] and overall low or no expression of the DRs were all correlated to resistance to TRAIL. Our own group has demonstrated that LY303511, an inactive analogue of the PI3K inhibitor LY294002, has the ability to amplify the sensitivity of neuroblastoma cells to TRAIL via a MAPK-dependent upregulation of both DR4 and DR5 [30]. In the similar manner, drugs such as curcumin, sulphoraphane and trichostatin A sensitize tumour cells of different origins by increasing DR5 surface expression [31–33]. Additionally, modulation of the DRs mRNA levels has been shown to contribute to DRs upregulation. The proteasomal inhibitor Bortezomid

increases DR5 half-life by stabilizing its mRNA [34], while MG132 – another proteasomal inhibitor, silibinin and withaferin A enhance TRAIL sensitivity by upregulating DR5 in a C/EBP Homologous Protein (CHOP)-dependent manner [35–37]. Taken together, these findings support the critical importance of DRs upregulation in the re-sensitization process.

Similarly, deficiency of DRs clustering and oligomerization that can, for example, occur via post-translational modifications of the DRs such as O-glycosylation and S-palmitoylation, can promote resistance to TRAIL [38,39]. Indeed, aggregation of the receptors in lipid rafts – sphingolipid – and cholesterol-enriched microdomains in the plasma membrane facilitates the transduction of the apoptotic signal [40]. Martin *et al.* have presented evidence of enhanced apoptosis following redistribution of DR5, FADD and caspase-8 to lipid rafts upon co-treatment of TRAIL with cyclooxygenase-2 (Cox-2) inhibitors [41]. Likewise, compounds, such as quercetin, its derivative LY303511 or aplidin, were shown to facilitate the clustering and oligomerization of the DRs and hereby sensitize cells to TRAIL-induced apoptosis [42–44]. Interestingly, the disruption of lipid rafts using methyl- $\beta$ -cyclodextrin or nystatin abrogated the DRs redistribution and TRAIL sensitization in another research study [45], hence substantiating the critical role played by raft-associated receptors in TRAIL sensitization.

Finally, slightly downstream of TRAIL-DRs interaction and activation, a change in the expression of caspase-8 protein, through silencing, point mutation or increased protein degradation [24,46], or its inhibitor, cellular FLICE Inhibitor Protein (c-FLIP) [47–49] has been shown to significantly decrease cancer cells sensitivity to TRAIL-mediated cell death. C-FLIP, and its two main isoforms c-FLIP<sub>S</sub> and c-FLIP<sub>L</sub>, is very efficient at inhibiting the apoptotic signal provided by TRAIL due to its structural similarity to caspase-8 and its over-expression is commonly observed in cells resistant to TRAIL. As an example, treatment of cells with the PPAR $\gamma$  agonist rosiglitazone enhances TRAIL sensitivity by selectively down-regulating c-FLIP<sub>S</sub>, and such re-sensitization is abrogated if c-FLIP is over-expressed [50]. C-FLIP down-regulation can either be transcriptional, as it is the case upon treatment with withaferin A, or post-translational via proteasomal degradation as shown with quercetin [36,50]. Alternatively, prevention of caspase-8 degradation by bortezomib was also shown to re-sensitize [51]. Taken together, these results indicate a strong reliance of TRAIL-resistant cancer cells on keeping caspase-8 inhibited and the viability of using small molecules targeting this dependence.

#### *Resistance at the mitochondrial level*

As stated earlier, TRAIL-induced cell death is also able to engage the intrinsic apoptotic pathway to serve either as an amplification mechanism for the extrinsic pathway or as the primary pathway leading to the demise of the targeted cells.

In regards to the involvement of mitochondria in TRAIL-mediated cell death, members of the Bcl-2 family, and more specifically the ratio of pro-apoptotic to anti-apoptotic members, have been shown to play a crucial role [52]. Indeed, on one hand, cancer cells lacking pro-apoptotic proteins BAX and/or BAK failed to undergo apoptosis following treatment with TRAIL [53–56]. On the other hand, an increased expression of anti-apoptotic proteins, such as Bcl-2, Bcl-X<sub>L</sub> and Mcl-1 confers resistance to TRAIL [47,57,58]. To further illustrate the role Bcl-2 can play in TRAIL resistance, Sun *et al.* over-expressed Bcl-2 in TRAIL-sensitive human non-small cell lung carcinoma cells and observed that those cells had acquired a resistant phenotype [59]. In the light of those studies, the pro-apoptotic members of the Bcl-2 are, with reason, valid therapeutic targets. In this regard, the BH3-mimetic ABT-737, which specifically inhibits Bcl-2, Bcl-X<sub>L</sub> and Bcl-w, could efficiently restore sensitivity to TRAIL, either by releasing Bim and Bak from their inhibitory interaction with anti-apoptotic members of their family, or by affecting Bax distribution [60,61]. Similar reversals of resistance were obtained with the use of daidzein or flavopiridol through down-regulation of Bcl-2 or Mcl-1, respectively [57,62].

Members of the inhibitor of apoptosis protein (IAP) family, upregulated in a variety of cancers, represent another major apoptotic block downstream of the mitochondria. IAPs are able to bind and inhibit caspases and are themselves inhibited by Smac/DIABLO when it is released from the mitochondria into the cytosol. Hence, a defective release of Smac/DIABLO would impede the transduction of the apoptotic signal through the intrinsic pathway. Indeed, over-expression of Smac/DIABLO was shown to overcome X-linked IAP (XIAP) apoptotic block [63], an effect mirrored when XIAP, c-IAP-1/2 were

knocked-down [64,65]. More interestingly, while TRAIL can induce Smac/DIABLO release when used as a single agent, it was suggested that the extent of such release can determine whether cancer cells are sensitive or resistant to TRAIL [66]. Incidentally, countering over-expression of IAPs, such as XIAP, c-IAP-1/2 or survivin has been associated with encouraging results. Smac mimetics and small molecules XIAP inhibitors have been used to significantly increase cancer cells sensitivity to TRAIL [67–69]. Likewise, a number of drugs such as roscovitine and rottlerin have been shown to down-regulate both XIAP and survivin, thereby restoring caspases' activation and sensitivity to TRAIL [70,71]. To note, the flavonoids quercetin and kaempferol target survivin through upregulation of its proteasomal degradation [72,73].

## Reactive oxygen species and cell fate signalling

### ROS production and regulation

As the site where oxidative phosphorylation occurs, mitochondria are a major source of intracellular ROS. During this process, electrons are transferred from electron donors to electron acceptors along the electron transport chain (ETC). Due to the high flux of electrons through the ETC, electron leakage, principally from the complexes I (NADH-ubiquinone oxidoreductase) and III (ubiquinol-cytochrome c oxidoreductase) onto oxygen (O<sub>2</sub>) is not avoidable and superoxide (O<sub>2</sub><sup>-</sup>) is produced as a by-product [74]. Other significant sources of mitochondrial ROS include complexes from the Krebs cycle such as  $\alpha$ -ketoglutarate dehydrogenase ( $\alpha$ -KGDH) and pyruvate dehydrogenase [75] (Figure 1).

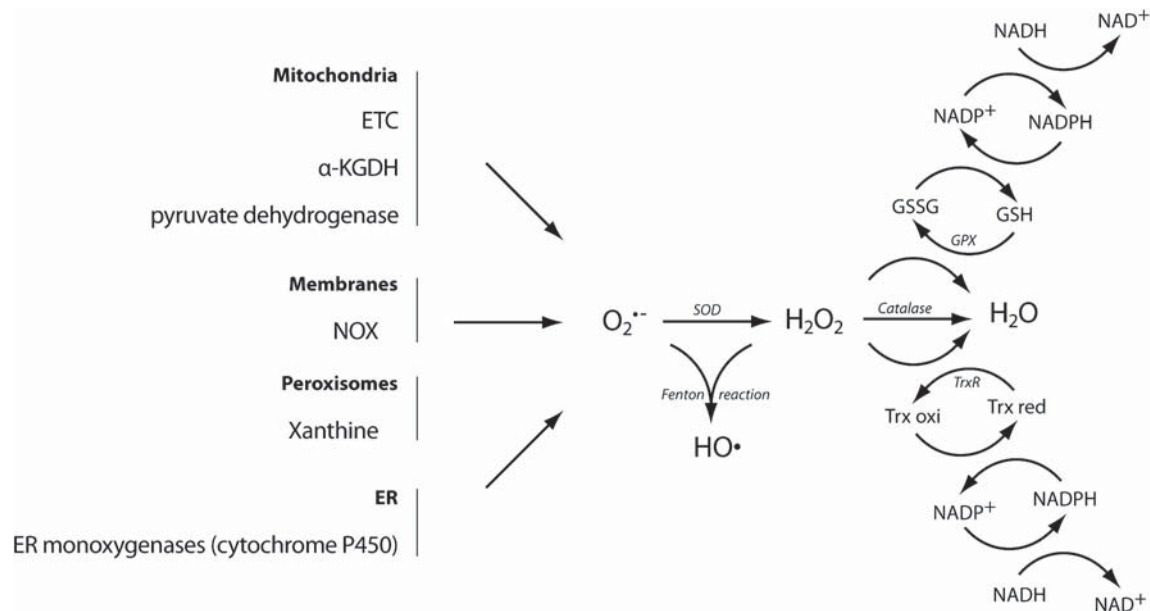


Figure 1. Redox flux. The redox flux shows the most common cellular enzymes involved in ROS production and the scavenging cellular systems in place. NAD<sup>+</sup>/NADH: nicotinamide adenine dinucleotide, NADP<sup>+</sup>/NADPH: nicotinamide adenine dinucleotide phosphate, GSH: glutathione (reduced form), GSSG: glutathione disulphide (oxidized form), GPX: glutathione peroxidase, Trx oxi/red: thioredoxin reduced/oxidized, TrxR: Trx reductase, SOD: superoxide dismutase, ETC: electron transport chain,  $\alpha$ -KGDH:  $\alpha$ -ketoglutarate dehydrogenase, NOX: NADPH oxidases, ER: endoplasmic reticulum.

Among the most prevalent sources of cytosolic ROS are NADPH oxidases (Nox). Members of the Nox family are transmembrane proteins localized in specific subcellular compartments, such as lipid rafts, membrane ruffles, caveolae, endosomes and the nucleus [76,77]. Nox produces  $O_2^-$  when using NADPH as the source of electron and molecular oxygen as the acceptor [78]. Xanthine oxidase, in peroxisomes [79], and monoxygenases, in the endoplasmic reticulum [80], are also sources of cytosolic ROS and contribute to increased cellular hydrogen peroxide ( $H_2O_2$ ) and  $O_2^-$ .

In addition,  $H_2O_2$  and  $O_2^-$  can lead to the generation of other reactive species. For example, both are involved in the Fenton reaction that allows for the generation of the highly reactive hydroxyl radical ( $\cdot OH$ ). Superoxide can also react with nitric oxide ( $\cdot NO$ ) to form peroxynitrite ( $ONOO^-$ ).

If left unchecked, excessive accumulation of ROS could be responsible for cell and tissue injury and damage, such as lipid peroxidation, DNA damage and protein oxidation. However, under physiological conditions, intracellular levels of ROS are tightly regulated and maintained within tolerable limits. Cellular elimination of ROS is done mainly in two ways, by antioxidant enzymes that scavenge specific forms of ROS or by non-enzymatic molecules.

The glutathione system includes glutathione (GSH), glutathione reductase, glutathione peroxidase (GPX) and glutathione S-transferase (GST). GSH is the most abundant free thiol in the cell and, as such, is responsible in large part for the maintenance of an adequate intracellular redox milieu. During oxidative stress, cellular protection is achieved through two different mechanisms. One is the inactivation of electrophilic compounds by oxidation of glutathione to glutathione disulphide (GSSG) catalyzed by GSTs. The other is the GPX driven reduction of  $H_2O_2$  to  $H_2O$  where glutathione also acts as an enzymatic substrate [81]. Glutathione reductase favours a high GSH:GSSG ratio by returning glutathione to its reduced form [82].

Similarly, the thioredoxin (Trx) system is the other main family of proteins involved in cellular thiol reduction and redox regulation. It is composed of three oxidoreductases (Trx-1/3) and the Trx reductase (TrxR). Trx interacts with oxidized proteins and reduces them. TrxR activity then regenerates the reduced/active form of Trx using NADPH as an electron donor [83,84].

In addition to the GSH and Trx systems, other enzymes play a role in scavenging ROS in the cell. On the one hand, dismutation of  $O_2^-$  into  $H_2O_2$  is done by the copper/zinc superoxide dismutase (Cu/Zn SOD, SOD1) in the cytoplasm and the manganese superoxide dismutase (MnSOD/SOD2) in the mitochondrial matrix. And, on the other hand, decomposition of  $H_2O_2$  into  $H_2O + O_2$  is promoted by the activity of the enzyme, catalase [85].

### Redox balance

Tissue homeostasis depends on a tight balance between the rates of cell proliferation and cell death. This balance is itself a highly regulated process, through a multitude of intracellular signalling networks. Interestingly, it has now been well established that most, if not all, of these signalling

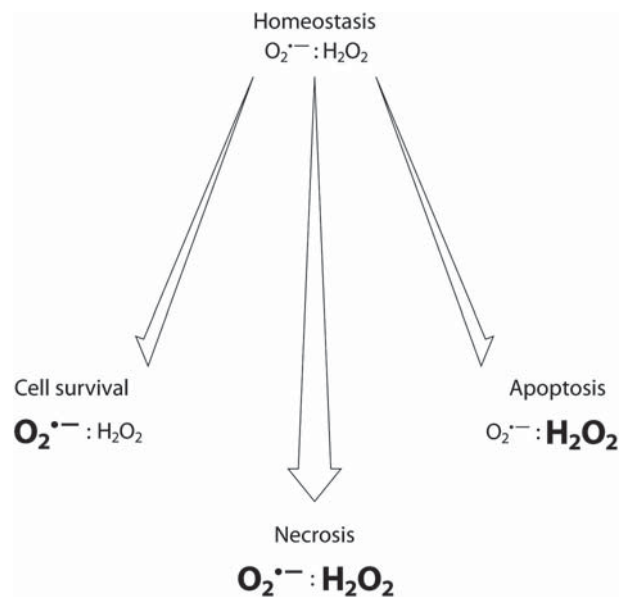


Figure 2. A ROS balance. Hypothetical schematic representation of the role on cell fate of the fine balance between two major reactive oxygen species.

pathways involved in cell fate decision are impacted in one way or another by the cellular redox status. Hence, the existence of a tight control over ROS intracellular levels is crucial in maintaining cell homeostasis. For a long time, the conventional consensus was that abnormally elevated levels of ROS and their derivatives were linked solely to cell and tissue damage and cell death [86,87]. Nevertheless, an alternate theory has been gathering increasing support in the last decade [88]. According to that theory, the effects of a moderate increase in ROS levels are much more diverse than simply cell death induction and can in fact include cell proliferation, gene transcription or DNA damage [89]. Furthermore, the effects of an increase in intracellular ROS levels seem to be dependent on the nature of the ROS species. Indeed, a slight increase in  $O_2^-$  has been shown to activate pro-survival signalling as well as, but not necessarily concomitantly, to inhibit the induction of cell death [90–92]. Conversely, a similar mild increase in  $H_2O_2$  promotes death execution by creating an intracellular milieu permissive for proteases activation [93–95], although it is important to note that, under certain circumstances, a low level of hydrogen peroxide can cause cell proliferation [96]. Additional works on oncogenic cell transformation have further strengthened the link between a pro-oxidant state and cell survival [97,98]. These studies substantiate a critical role of the intracellular redox status in processes involved in cell survival and cell death evasion (Figure 2).

### TRAIL sensitization and ROS

#### Current studies

As detailed in the previous section, a rather large variety of compounds have shown the ability to modulate sensitivity

to TRAIL-induced apoptosis through action on different targets. Interestingly, several of those molecules are known to be efficient inducer of ROS and a number of recent studies have investigated the role of ROS in the regulation TRAIL-mediated apoptosis.

One particular area where the involvement of ROS in TRAIL-mediated apoptosis has been highlighted is the modulation of gene expression. Our group has recently demonstrated that the DRs upregulation following treatment with LY303511 was dependent on ROS as pre-incubation with catalase abrogated said upregulation as well as the subsequent sensitization [30]. Likewise, Kim *et al.* observed an inhibition of DR5 upregulation when using sulforaphane as the sensitizing agent and N-acetyl-cysteine (NAC) or catalase over-expression to scavenge ROS [32]. Additional studies have shed some light on the mechanism(s) by which ROS modulate the expression of proteins involved TRAIL-mediated apoptosis. For example, MG132-induced upregulation of DR5 was shown to involve a ROS-dependent upregulation of p53 and its binding to an intronic region of *DR5*, a phenomenon inhibited in the presence of GSH and NAC [99]. In the same way, withaferin A is reported to act in a ROS-dependent manner to increase DR5 and decrease c-FLIP levels, via CHOP and NF $\kappa$ B, respectively [36]. Other compounds have displayed a similar transcriptional multi-target facet such as dibenzylideneacetone (DBA), which was shown to down-regulate DcR2 dependently of ROS and upregulate DR4 and DR5 in a ROS-dependent CHOP-mediated manner [100]. Though DR5 regulation is more than likely to be scrutinized during such studies, it is interesting to note that most, if not all, of these studies have reported a ROS-mediated upregulation of DR5 expression, alone or among other genes, which hints that it might be a common feature of ROS-mediated sensitization to TRAIL.

### Speculations

A very recent paper by Park *et al.* highlighted a new relation between the death receptors DR4 and DR5 and ROS [101]. In this study, they showed that activation of DR4 and/or DR5 with an agonistic protein (KD548-Fc) promotes the production of superoxide and the accumulation of intracellular ROS through direct activation of NOX1, which then leads to a ROS-mediated apoptotic cell death. In the case of the sensitizing drugs reviewed in the previous paragraph, it is then possible to hypothesize that the ROS-mediated upregulation of the death receptors, due to the sensitizing compounds, could lead to a further increase in ROS production through activation of NADPH oxidases, thereby fully committing the tumour cells to apoptosis. Depending on the sensitization mechanisms and the sensitizing drug itself, the production of ROS displays a constant increase over time or, possibly, a two-wave pattern. A slight change of focus to discover where and when ROS are produced during sensitization to TRAIL, as well as which ROS are produced, would indeed greatly improve our current understanding of the cellular mechanisms involved.

### Concluding remarks

Over the last two decades, the ever-growing interest in TRAIL has allowed to characterize its signalling components as well as the resistance mechanisms developed by cancer cells. These mechanisms have been shown to spread along the entirety of TRAIL signalling pathway, from the apical signal mediated by TRAIL interaction with its cognate receptors, through the extrinsic apoptotic pathway and the mitochondrial amplification loop to the activation of executioner caspases. In parallel to the characterization of those apoptotic blockades, there has been a thorough search for small molecules able to enhance cancer cells sensitivity to TRAIL-mediated apoptosis that has led to numerous compounds. Among them, several have been shown to achieve TRAIL re-sensitization through a ROS-dependent mechanism. However, most of the current studies have only scratched at the surface and more thorough ones are needed to elucidate the intricate cellular processes leading to and originating at the ROS production during re-sensitization to TRAIL.

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### Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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