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Plant Uncoupling Mitochondrial Protein and Alternative Oxidase: Energy Metabolism and Stress

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Energy-dissipation in plant mitochondria can be mediated by inner membrane proteins via two processes: redox potential-dissipation or proton electrochemical potential-dissipation. Alternative oxidases (AOx) and the plant uncoupling mitochondrial proteins (PUMP) perform a type of intrinsic and extrinsic regulation of the coupling between respiration and phosphorylation, respectively. Expression analyses and functional studies on AOx and PUMP under normal and stress conditions suggest that the physiological role of both systems lies most likely in tuning up the mitochondrial energy metabolism in response of cells to stress situations. Indeed, the expression and function of these proteins in non-thermogenic tissues suggest that their primary functions are not related to heat production.

KEY WORDS: PUMP; AOx; mitochondria; energy metabolism; stress.

MITOCHONDRIAL ENERGY METABOLISM

In eukaryotic cells, mitochondria generate most of the cellular ATP. Redox freeenergy is stepwisely utilized by complex I (NADH dehydrogenase), complex III (cytochrome bc_l), and complex IV (cytochrome c oxidase) of the electron transport chain, to pump protons from the matrix out to the intermembrane space, producing an electrochemical proton potential ($\Delta\mu_H+$) across the inner mitochondrial membrane. This proton potential is the driving force used by the ATP synthase (Complex V) to phosphorylate ADP (Mitchell, 1961). It can also be directly used to drive other processes, such as ion transport and ATP^{4-}/ADP^{3-} exchange across the inner mitochondrial membrane. The brown adipose tissue possesses a specialized mechanism to convert $\Delta\mu_H+$ into heat by a process called nom-shivering thermogenesis (Nicholls and Locke, 1984). Finally, changes in $\Delta\mu_H+$ may also be involved in defense mechanisms under situations of oxidative stress (Kadenbach, 2003).

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It is known that the rates of both respiration and ATP synthesis can be regulated by substrate availability (reducing equivalents, ADP, and O_2) and by the degree of coupling between respiration and phosphorylation. The regulation by substrates is complex, since their concentrations are rarely optimal because the energy metabolism of eukaryotes has to cope with variable energy demands. These include, coupling between the rate of respiration and the rate of ATP utilization, increasing thermogenesis at low temperatures, efficient utilization of nutrients under starvation, degradation of excess food intake, and stimulation of ATP synthesis under stress conditions.

Two distinct processes can regulate the coupling between respiration and phosphorylation: redox potential-dissipating systems (intrinsic regulation) represented by alternative oxidases (AOx) or proton electrochemical potential-dissipating systems (extrinsic regulation) represented by uncoupling proteins (UCP). The mechanism of intrinsic regulation prevents $\Delta\mu_{\rm H}+$ formation during respiration, whereas extrinsic regulation is mediated by electrochemical proton dissipation without ATP synthesis (Vercesi *et al.*, 1995; Ježek *et al.*, 2001; Vercesi, 2001; Kadenbach, 2003), This mini-review focuses on the possible roles of plant alternative oxidase, and plant uncoupling mitochondrial protein (PUMP) on plant mitochondrial energy metabolism.

ALTERNATIVE OXIDASE

AOx are mitochondrial enzymes widespread within the eukaryotic world with exception of animals; AOx proteins were identified in various plants (Elthon et al., 1989; Siedow and Umbach, 1995; Day and Wiskich, 1995), fungi (Lambowitz et al., 1989, Sakajo et al., 1991), and other organisms (Clarkson et al., 1989; Jarmuszkiewicz et al., 1997). Gene searches lead to the discovery of AOx gene superfamily that consists of at least two families of genes encoding AOxs (Considine et al., 2002). Members encoding AOxs of type 1 (AOx1 family) were identified in both monocotyledonous and dicotyledonous plants, while AOxs of type 2 (AOx2 family members) were identified only in dicotyledonous plants (Considine et al., 2002). Very recently, the existence of the third AOx family (AOx3 family) was inferred in Arabidopsis (Borecký J., Nogueira, F.T.S, Maia, I.G., Vercesi, A.E., and Arruda, P., unpublished results). Expression of AOx1 genes seems to be closely related to stresses, while AOx2 family members are expressed in a constitutive manner. Expression of the Arabidopsis member of AOx3 family was downregulated after exposure of Arabidopsis plantlets to low temperature (4°C), indicating that AOx3 plays possibly a distinct physiological role in energy metabolism.

AOx functions as a dimer and catalyzes ubiquinol-oxygen oxidation/reduction that is not linked to proton pumping and thus does not contribute to $\Delta\mu_{\rm H}+$ formation (Vanlerberghe and McIntosh, 1997; Sluse and Jarmuszkiewicz, 1998; Affourtit *et al.*, 2001a; Milani *et al.*, 2001). The activity of AOx has a very intricate nature. Firstly, it depends on substrate availability, i.e. total ubiquinol (UQ) concentration in the membrane as well as on actual O₂ concentration in the cell. AOx becomes active only when the UQ pool is 40–50% reduced, and then its activity increases sharply and non-linearly with higher reduction level of UQ (Moore *et al.*, 1988; Dry *et al.*, 1989). Furthermore, the apparent affinity of AOx for O₂ depends on

species, tissues, and age of the plants investigated ($K_{\rm m} \sim 1-20~\mu{\rm M}$; Ikuma et al., 1964; Bendall and Bonner, 1971; Millar et al., 1994; Ribas-Carbo et al., 1994) and is much lower than the cytochrome c oxidase affinity ($K_{\rm m} \sim 0.1-0.15~\mu{\rm M}$; Barzu and Satre, 1970; Bendall and Bonner, 1971; Rawsthorne and LaRue, 1986). Moreover, the apparent $K_{\rm m}$ of AOx for O_2 seems to vary with ubiquinol reduction level: the more reduced the ubiquinol pool the lower is the AOx affinity for O₂ (Ribas-Carbo et al., 1994). AOx dimer can be linked with a disulfide bridge and thus is also sensitive to its proper redox state, with the reduced AOx dimer being four- to fivefold more active than the oxidized form (Umbach and Siedow, 1993; Umbach et al., 1994; Moore et al., 1995). Reduction of the AOx dimer can occur during oxidation of Krebs cycle substrates (isocitrate and malate) that reduce NADP⁺ in plant mitochondria (Vanlerberghe et al., 1995). Thus, it has been proposed that the AOx reduction state depends on NADPH generation and involves NADPH-reduced glutathione or the thioredoxin coupling system (Umbach and Siedow, 1993; Day and Wiskich, 1995; Siedow and Umbach, 1995; Vanlerberghe et al., 1995). AOx is not sensitive to inhibitors of cytochrome pathway such as cyanide, antimycin A, or miyxothiazol, but is inhibited by primary hydroxamic acids (Schonbaum et al., 1971) such as benzohydroxamate (BHAM) and by fatty acids (Minagawa et al. 1992b, Sluse and Jarmuszkiewicz, 2000). In some tissues, AOx can be stimulated by α -keto acids, such as pyruvate (Millar et al., 1993; Day et al., 1995).

The only confirmed function for AOx is the thermogenic respiration in *Arum* sp. and other species, where heat produced during anthesis volatilizes aromatic compounds to attract pollinators (Meeuse and Buggeln, 1969; Meeuse, 1975; Raskin *et al.*, 1987; Seymour *et al.*, 2003). Thermogenic activity of AOx was described mainly in spadices of *Arum maculatum* (Moore and Siedow, 1991), *Symplocarpus foetidus* (Berthold and Siedow, 1993), and *Sauromatum guttatum* (Rhoads and McIntosh, 1991). Energy for thermogenesis is provided by an increase in mitochondrial respiration through the AOx and is controlled by salicylic acid. However, *AOx1* expression is induced by salicylic acid both in thermogenic and in non-thermogenic plants (Raskin *et al.*, 1987, 1989; Rhoads and McIntosh, 1991; Van Der Straeten *et al.*, 1995; Maxwell *et al.*, 2002).

In non-thermogenic plants, the supposed role for AOx is to minimize the production of ROS as described below (Vanlerberghe and McIntosh, 1997; Maxwell et al., 1999; Parsons et al., 1999; Yip and Vanlerberghe, 2001). The experiments with transgenic tobacco (*Nicotiana tabacum*) lacking or overexpressing AOx also suggested that AOx is involved in the hypersensitive response to virus infection and may prevent programmed cell death induced by downregulation of the cytochrome pathway (Ordog et al., 2002; Vanlerberghe et al., 2002). AOx is effectively induced by artificial chemical inhibition of the cytochrome pathway by poisons such as cyanide and antimycin A (Vanlerberghe et al., 1994; Wagner and Wagner, 1997). Gilliland et al. (2003) suggested that induction of AOx by cyanide/antimycin A as well as by salicylic acid is indirect, via the increase of ROS production that is known to upregulate AOx1 expression (Minagawa et al., 1992a; Vanlerberghe and McIntosh, 1996).

It is well known that cold stress activates AOx in non-thermogenic plants (Vanlerberghe and McIntosh, 1997; McIntosh *et al.*, 1998; Zhou and Solomos, 1998; Calegario *et al.*, 2003). Recent results demonstrate that the rates of CO₂ output in potato tubers stored at 5°C increased steadily during the first 4 day period, reaching

a plateau level that was maintained up to 10 days, when compared to potato tubers stored at 25°C (Fig. 1). Under these conditions, AOx activity in mitochondria isolated from potato tubers stored at 5°C for 10 days was about 10-fold higher than that from tubers stored at 25°C (Fig. 2). Despite this large increase in the respiration rate, the temperature of the tubers was maintained at 5°C. Similar results were previously obtained by Zhou and Solomos (1998), when potato tubers were transferred from 10°C to 1°C. They found that the rate of CO₂ output increased, reaching a peak in respiration rate threefold higher within 12 days at 1°C. Kannerworff and van der Plas (1994) also observed a higher O₂ consumption in tulip bulbs stored at 5°C than in bulbs stored at 20°C.

Purvis and Shewfelt (1993) postulated that cold-induction of AOx occurs in plants to prevent superoxide overproduction by mitochondria. Wagner and Wagner (1997) reported that both the total coenzyme Q content and the relative amount of its oxidized form increased in mitochondria isolated from cold-treated *Petunia hybrida*. They observed the same effect after antimycin A treatment, suggesting that it is not the cold treatment *per se*, but the stress conditions that cause induction of the AOx.

PLANT UNCOUPLING MITOCHONDRIAL PROTEIN

The first uncoupling protein (originally termed UCP and currently UCP1) was identified in brown adipose tissue in 1976 (Ricquier and Kader, 1976) and its cDNA was cloned 9 years later (Bouillaud *et al.*, 1985). Vercesi *et al.* (1995) discovered a UCP plant counterpart (the plant uncoupling mitochondrial protein, PUMP) in potato tubers, the gene of which was identified by Laloi *et al.* (1997) in potato flowers and later by Maia *et al.* (1998) in *Arabidopsis thaliana*. Using antibodies raised against potato PUMP or against recombinant PUMP isolated from *E. coli*

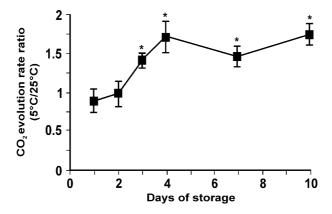


Fig. 1. Ratio between CO_2 evolution rates of intact potato tubers stored at $5\pm 1^{\circ}C$ and tubers stored at $25\pm 1^{\circ}C$. Each point represents the mean value $\pm SD$ of four determinations, each one using a group of four intact potato tubers. Significant differences (p < 0.01) between CO_2 evolution rates of cold- and warm-treated potato tubers are indicated by asterisks.

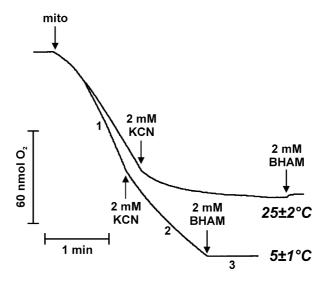


Fig. 2. Determination of AOx capacity in mitochondria isolated from potato tubers stored for 4 days at $5\pm1^{\circ}\text{C}$ or $25\pm2^{\circ}\text{C}$. Mitochondria (0.5 mg/ml) were incubated in a standard reaction medium (28°C) in the presence of 2.5 μ g/ml oligomycin, 300 μ M propranolol, 2 μ M atractyloside, 0.1 mM ATP, 0.5% BSA, 1 mM DTT, and 0.15 mM pyruvate. Additions of 2 mM KCN and 2 mM BHAM were done where indicated. Slope 1 refers to the total respiration rate, a difference between slope 1 and slope 2 refers to CN-sensitive respiration and between slope 2 and slope 3 to AOx capacity.

expression system (Borecký et al., 2001a) this protein was also detected in many plants such as tomato, spinach, carrot, cauliflower, broccoli and turnip (Ježek et al., 2000), or fruits such as banana, mango, apple, strawberry, papaya, melon, orange, pineapple, pear and peach (Ježek et al., 2001). Within 3 years after PUMP discovery, genes encoding four additional animal UCPs (UCP2, Fleury et al., 1997; UCP3, Boss et al., 1997; UCP4, Mao et al., 1999; BMCP1/UCP5, Sanchis et al., 1998) and also two Arabidopsis genes encoding PUMP (AtPUMP1, Maia et al., 1998; AtUCP2, Watanabe et al., 1999) were identified. In the last few years, one to two different PUMP sequences were identified within the plant kingdom in skunk cabbage (Ito, 1999), mango (Considine et al., 2001), tomato (Accession Number AF472619), wheat (Murayama and Handa, 2000), rice (Watanabe and Hirai, 2002), and maize (Brandalise et al., 2003). Several reviews of these UCP members were published in recent years (Borecký et al., 2001; Hourton-Cabassa et al., 2004; Ledesma et al., 2002; Ricquier and Bouillaud, 2000a; Sluse and Jarmuszkiewicz, 2002). Recently, our group (Borecký J., Nogueira F.T.S., Maia I.G., Vercesi A.E., and Arruda, P., unpublished results) identified a probably complete PUMP family consisting of five to six members present either in dicots (Arabidopsis thaliana; At-PUMP1-6, Accession numbers AJ223983, AB021706, AK117673, NM 118590, NM 127816, NM 120984) or monocots (Saccharum spp.; SsPUMP1-5, Accession numbers AY644460 to AY644464). Interestingly, distinct expression patterns among gene family members were observed between monocots and dicots and during

chilling stress (Borecký J., Nogueira F.T.S., Maia I.G., Vercesi A.E., and Arruda, P., unpublished results). These findings suggest that the members of each energy-dissipating system are subject to different cell or tissue/organ transcriptional regulation (Nogueira *et al.*, this issue).

Uncoupling proteins are supposed to be found in all eukaryotic organisms (Borecký et al., 2001b). The only exception known is Saccharomyces cerevisiae that does not possess any form of UCP (ElMoualij et al., 1997). During the last years, UCP gene sequences were also found in birds (Vianna et al., 2001; Hirabayashi et al., 2005; Talbot et al., 2004), ectothermic vertebrates, such as frog (Xenopus octopus; Klein et al., 2002), carp (Ciprinus carpio) and zebrafish (Danio rerio; Stuart et al., 1999), insects (Drosophila melanogaster; Fridell et al., 2004) and in the primitive eukaryotic organism Caenorhabditis elegans (CeUCP, Accession number AAB54239). UCP has also been identified in mitochondria from Acanthamoeba castellanii (Jarmuszkiewicz et al., 1999), Dictyostelium dis-(Jarmuszkiewicz et al., 2002), Candida parapsilosis Jarmuszkiewicz et al., 2000), Candida albicans (Cavalheiro et al., 2004), and in trophozoites of the malaria parasite Plasmodium Berghei (Uemura et al., 2000). The existence of UCPs in protozoa, fungi, plants, insects, and fishes suggests that uncoupling proteins emerged early during evolution as a distinct member of the mitochondrial anion carrier family (MACF), probably before the divergence of plant, animal, and fungi kingdoms.

Biochemical properties of PUMP and fungal UCPs were found to be comparable to those of UCP1 (Ježek et al., 1996, 1997, 1998; Vercesi et al., 1997, 1998; Jarmuszkiewicz et al., 1998, 2000; Kowaltowski et al., 1998; Sluse et al., 1998; Almeida et al., 1999; Borecký et al.,; Costa et al., 1999; Nantes et al., 1999). Antibodies raised either against potato PUMP, isolated from solubilized mitochondrial proteins by chromatography on hydroxyapatite column (Nantes et al., 1999), or against recombinant AtPUMP1, isolated from E. coli expression system (Borecký et al., 2001a), were both able to detect potato and tomato PUMP as well as AtPUMP1. These results indicate that potato and tomato PUMP and AtPUMP1 share a high homology. A similarly high degree of homology among proteins encoded by LePUMP, StUCP, and AtPUMP1 can be seen in phylogenetic analyses (Borecký et al., 2001b; Hourton-Cabassa et al., 2004).

Uncoupling proteins represent the foremost form of extrinsic regulation of oxidative phosphorylation efficiency. UCPs as well as PUMPs permit the return of extruded protons back to the mitochondrial matrix without ATP synthesis, dissipating the energy of $\Delta\mu_{\rm H}+$ as heat. The result is an uncoupling of respiration from ATP synthesis, a process that gave the name to this class of proteins. Two possible models of proton transport mechanisms were hypothesized: a proton-buffering model, where H⁺ is transported directly by the UCP (Klingenberg, 1990) and a protonophore model, where H⁺ transport is carried by a free fatty acid (FA) cycling. In this model, UCP mediates passage of FA anions to the outer monolayer of the inner mitochondrial membrane, where FA anions become protonated and neutral FA can readily move back across the membrane by a flip-flop mechanism, while carrying H⁺ (Garlid *et al.*, 1996).

Activity of animal as well as plant and fungal uncoupling proteins seems to be regulated by activators, such as free fatty acids (Klingenberg, 1990; Garlid et al.,

1996; Ježek et al., 1997), UQ and its redox state (Echtay et al., 2000, 2001; Jarmuszkievicz et al., 2004), and ROS (Echtay et al., 2002a; Considine et al., 2003), in addition to inhibitors such as purine nucleotides that inhibit UCPs/PUMPs in a pH-dependent manner (Borecký et al., 2001a; Rafael et al., 1994). As mentioned above, the presence of free FA is necessary to activate UCP/PUMP. Studies on UCP1 (Ježek and Garlid, 1990) and AtPUMP1 (Borecký et al., 2001a) activation by a variety of FA demonstrated a tendency that longer, more unsaturated FAs activate UCP1 and AtPUMP1 more effectively. The activating function of UQ remains unclear. Echtay et al. (2000, 2001) reported that UQ activates UCP1-3. In contrast, Jabùrek and Garlid (2003) found that the activation was not due to UO, but due to the presence of dichlormethane, a solvent used for UQ additions. However, Echtay and Brand (2001) found an activation of GDP-sensitive proton conductance of kidney mitochondria by UQ. To their surprise, the addition of superoxide dismutase strongly decreased UQ activation of mitochondrial proton conductance. For this reason, they conclude that UQ can activate UCP indirectly, via increasing superoxide production. Indeed, superoxide was found to activate UCP1-3 (Echtay et al., 2002a) and also potato PUMP (Considine et al., 2003). The proposed mechanism involves the activation of uncoupling proteins by superoxide from the matrix side of the inner mitochondrial membrane (Echtay et al., 2002b), where superoxide releases iron from proteins containing iron-sulfur centers such as aconitase. Iron (Fe²⁺) reacts with superoxide forming hydroxyl radical that promotes generation of carboncentered radicals that initiate lipid peroxidation, yielding breakdown products, such as 4-hydroxy-2-trans-nonenal, that activate UCPs (Murphy et al., 2003; Echtay et al., 2003) and PUMP (Smith et al., 2004). These results suggest conservation of basic mechanisms of UCP and PUMP activation. Recently, our group reported a different way in which UO may regulate UCP activity (Jarmuszkiewicz et al., 2004). Instead of UCP activation by UO, we found that the inhibition of FFA-induced UCP activity by GTP could be under control by the redox state of endogenous membranous UQ. The activity of muscle UCPs became GTP-sensitive when the UQ reduction level was below 64% (in state 3 respiration) and fully inhibited when it was below 57%. Thus, we propose that the UQ redox state could be a metabolic sensor that modulates the purine nucleotide inhibition of FFA-activated UCPs in muscle and probably other mitochondria.

The finding of uncoupling proteins in non-thermogenic plants raised the question of their physiological role, originally considered to be solely heat production in non-shivering thermogenesis in hibernating mammals. Recent hypotheses favor a more general role—the regulation of energy metabolism in mitochondria (Ježek and Garlid, 1998; Skulachev, 1998; Ricquier and Bouillaud, 2000; Jarmuszkiewicz *et al.*, 2001) in order to avoid an extremely high $\Delta \mu_{\rm H} +$, which can lead to excessive production of reactive oxygen species (Skulachev, 1998; Brandalise *et al.*, 2003a; Considine *et al.*, 2003).

In chilling-sensitive plants, such as sugarcane (*Saccharum* sp.; Tai and Lentini, 1998), oxidative stress is a major component of chilling stress (Pinhero *et al.*, 1997). ROS, i.e., hydrogen peroxide, superoxide, and hydroxyl radicals, can react with DNA, lipids and proteins, to cause severe cellular damage (Sato *et al.*, 2001). ROS-detoxification systems are composed of multiple enzymes, whose activity varies according to the level of stress in different cell compartments (Iba, 2002). Since

mitochondria represent one of the major sources of ROS during cold stress, PUMP and AOx may act as ROS production regulators in this organelle (Kowaltowski et al., 1998; Maxwell et al., 1999). In this regard, the results found by our group (Brandalise et al., 2003b) demonstrate that overexpression of AtPUMP1 in transgenic tobacco plants led to a significant increase in tolerance to oxidative stress promoted by exogenous hydrogen peroxide as compared to nontransgenic control plants. Induction of expression of maize PUMP (ZmPUMP) by menadione, which generates superoxide, suggested that *PUMP* expression in vivo may be controlled by ROS levels (Brandalise et al., 2003a). Hence, we might consider that the purpose of the cold-stress-induced PUMP expression and activity is to balance the potentially increasing ROS production. Interestingly, analysis of the 1.0 kb promoter region upstream to transcription initiation site of Arabidopsis PUMP4, PUMP5, and AOxla using PLACE (Higo et al., 1999) and PlantCARE (Lescot et al., 2002) indicated the presence of several copies of a TCTCC core sequence. This sequence is recognized by the ADRI transcriptional factor, involved in oxidative processes and also activates peroxisomal proteins (Simon et al., 1991).

The thermogenic function is ascribed up to now only for UCP1 from mammalian brown adipose tissue (Nicholls, 1979). Recently, evidences for muscle type UCP were identified in hummingbirds (HmUCP, Vianna *et al.*, 2001) involved in thermogenesis associated with rewarming period after torpor. The existence of thermogenic activity was suggested in muscles from other birds (Hirabayashi *et al.*, 2005, Talbot *et al.*, 2004). Interestingly, endoplasmic reticulum of brown adipose tissue (de Meis, 2003) as well as white muscle cells (Barata and de Meis, 2002) possess Ca²⁺-ATPase (SERCA) able to hydrolyse ATP without transport of Ca²⁺ that also results in heat production. The authors suggest that dissipation of energy conserved in the ATP molecule by the uncoupled Ca2⁺-ATPase can increase respiration rates to restore cytosolic ATP concentration, thus increasing heat production through a pathway alternative to UCP1-mediated thermogenesis.

The participation of all other isoforms in the process of thermogenesis is uncertain. Mammalian UCP2 and UCP3 seem to be involved in regulation of body weight (Arsenijevic et al., 2000) or ROS production (Li et al., 2001). Thermogenic roles of UCP2 (hypothetically in fever) or UCP3 have not yet been established (Ricquier and Bouillaud, 2000; Ježek, 2002). In plants, expression of Arabidopsis PUMP genes encoding the PUMP1, PUMP4, and PUMP5 isoforms are reported to be induced by cold (Maia et al., 1998; Borecký J., Nogueira F.T.S., Maia I.G., Vercesi A.E., and Arruda, P., unpublished results), while PUMP2 and PUMP3 expression seems to be low and insensitive to cold. Recent studies showed that the content of potato PUMP (StPUMP) also increased in potato tubers exposed to cold (5°C, Calegario et al. 2003). Simultaneously, cold storage for 4 days (Fig. 3) yielded mitochondria with well-pronounced response to recoupling by 5 mM ATP plus 1% BSA after preincubation with 10 μ M linoleic acid. On the contrary, ATP had no recoupling effect on control mitochondria from warm-stored potato tubers. The BHAM-insensitive respiration rate of mitochondria from 4 day cold-stressed potato tubers was also higher (114.5 nmol $O_2 \min^{1}$) than in controls (97.1 nmol $O_2 \min^{-1}$). After ATP and BSA additions, these respiration rates decreased to the same levels (66.2 and 63.3 nmol O₂/min/mg protein) for cold stress and controls, respectively.

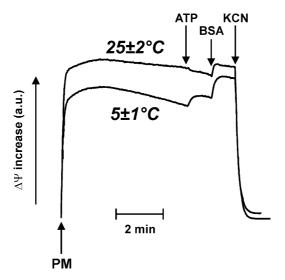


Fig. 3. Electrical transmembrane potential ($\Delta\Psi$) of mitochondria isolated from potato tubers stored for 4 days at 25 ± 2 or $5\pm1^{\circ}$ C. Potato mitochondria ("PM"; 0.5 mg/ml) were incubated in a standard medium (28°C) containing 2 μg/ml oligomycin, 7 μM atractyloside, 300 μM propranolol, 0.1 mM ATP, and 10 μM linoleic acid (LA). Additions of 5 mM ATP, 0.1% BSA, and 1 mM KCN were done where indicated. $\Delta\Psi$ was estimated as a function of changes in safranin O fluorescence (arbitrary units, here referred to as a.u.).

Thus PUMP-sustained O₂ consumption demonstrated a 44% increase in PUMP capacity induced by cold stress. However, the temperature of tubers was equal to ambient temperature, suggesting that higher functional capacity of StPUMP did not trigger thermogenesis.

CONCLUSIONS

Both intrinsic and extrinsic regulations of oxidative phosphorylation in plants are performed through energy dissipation that leads to the same final effect, i.e. increase in heat production. Nevertheless, energy-dissipating systems can manifest thermogenesis only at extremely high functional capacity. Only expression levels of UCP1 in brown adipose tissue of mammals and AOx1 in spadices of *Arum maculatum* (Moore and Siedow, 1991), *Symplcarpus foetidus* (Berthold and Siedow, 1993), and *Sauromatum guttatum* (Rhoads and McIntosh, 1991) seem to be high enough to promote thermogenesis.

A possible thermogenic role of PUMP came from observations of cold-stress-stimulated transcription of PUMP genes in roots and flowers of potato (*StUcP*; Laloi *et al.*, 1997) and *Arabidopsis thaliana* (*AtPUMP1*; Maia *et al.*, 1998). However, cold stress elevates the production of ROS that also induce transcription of PUMP genes (Brandalise *et al.*, 2003a).

Most plants, with exception of thermogenic plants, do not produce enough metabolic heat to raise the temperature of bulk tissue (Moynihan *et al.*, 1995; Breidenbach *et al.*, 1997; Calegario *et al.*, 2003). Nevertheless, a slow heat release must be concomitant to other relevant PUMP and AOx functions such as metabolic regulation (Vanlerberghe and McIntosh, 1997; Sluse *et al.*, 1998a; Affourtit *et al.*, 2001a; Ježek *et al.*, 2001) and/or prevention of excessive ROS formation (Kowaltowski *et al.*, 1998; Moller, 2001; Popov *et al.*, 1997; Wagner and Moore, 1997).

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