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Megacomplex organization of the oxidative phosphorylation system by structural analysis of respiratory supercomplexes from potato

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The individual protein complexes of the oxidative phosphorylation system (OXPHOS complexes I to V) specifically interact and form defined supramolecular structures, the so-called “respiratory supercomplexes”. Some supercomplexes appear to associate into larger structures, or megacomplexes, such as a string of dimeric ATP synthase (complex V2). A row-like organization of OXPHOS complexes I, III and IV into respiratory strings has also been proposed. These transient strings cannot be purified after detergent solubilization. Hence the shape and composition of the respiratory string was approached by an extensive structural characterization of all its possible building blocks, which are the supercomplexes. About 400,000 molecular projections of supercomplexes from potato mitochondria were processed by single particle electron microscopy. We obtained two-dimensional projection maps of at least five different supercomplexes, including the supercomplex I+III2, III2 +IV1,V2, I+III2 +IV1 and I2 +III2 in different types of position. From these maps the relative position of the individual complexes in the largest unit, the I+III2 +IV1 supercomplex, could be determined in a coherent way. The maps also show that the I+III2 +IV1 supercomplex, or respirasome, differs from its counterpart in bovine mitochondria. The new structural features allow us to propose a consistent model of the respiratory string, composed of repeating I+III2 +IV1 units, which is in agreement with dimensions observed in former freeze-fracture electron microscopy data.

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1. Introduction

Many processes in the cell require energy which can be stored in a chemical way. Adenosine triphosphate (ATP) is such a storage molecule. Hydrolysis of ATP produces besides inorganic phosphate and adenosine diphosphate (ADP) “free energy” which can be used to drive energy-requiring processes. The main eukaryotic cell compartment for ATP production is the mitochondrion, where energy of oxidation is coupled with the formation of ATP. This is performed by ATP synthase which utilizes an electrochemical gradient of protons created by three respiratory protein complexes (NADH dehydrogenase — complex I, dimeric cytochrome c reductase — complex III2, cytochrome c oxidase — complex IV) across the inner mitochondrial membrane. Proton translocation depends on the transfer of electrons from NADH or FADH2 through complex I, III, IV and succinate dehydrogenase (complex II) to oxygen which is reduced into water. Electron flow between the complexes is mediated by two mobile electron carriers, ubiquinone and cytochrome c, which are located in the inner membrane and the intermembrane space, respectively [1]. Nowadays, availability of high-resolution structures of complex II, III, and IV (reviewed in [2]), the hydrophilic arm of complex I [3] and most of the complex V (or ATP synthase) subunits [4–7] gives more detailed insight into the function of individual complexes in mitochondrial respiration.

A pioneering electron microscopy (EM) study of the freeze-fractured and deep-etched inner mitochondrial membranes from Paramecium multimicronucleatum revealed at least two types of repeating structures in the membrane and thereby gave the first indication of an ordered organization of respiratory complexes in the membrane [5]. The first periodic structure, a double row of particles following the full length of the outer curve of helically shaped tubular cristae, was identified as ribbons of dimeric ATP synthase. In another study, rows of ATP synthase particles were visualized by cryo-electron tomography of Neurospora mitochondria [8]. Recently, a tomographic analysis of the inner mitochondrial membrane from bovine mitochondria showed the structure of these ribbons of dimeric ATP synthase in greater detail [9]. The second type of non-random arranged complexes, consisting of large 13 × 22 nm particles with a spacing of 26–30 nm, was interpreted as rows of dimeric complex I [10], but has not been confirmed by other structural investigations.

Presence of such periodic structures in the inner membrane presumes a specific association between single respiratory complexes. Indeed, Schägger and Pfeiffer [11] showed that a mild solubilization of

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the inner mitochondrial membrane from yeast and bovine heart mitochondria followed by Blue-native PAGE (BN-PAGE) led to a separation of high-molecular bands with a mass between 1.2 MDa and 3 MDa, which were identified as specific supercomplexes of individual respiratory complexes. Using a similar biochemical approach, different types of respiratory supercomplexes were subsequently identified in many other organisms (reviewed in [11–14]). These supercomplexes are formed by two to three different respiratory complexes with up to four copies, with the following composition: I+I12, I+I11, I+I112, I+I112+I112, I+I112+IV1, I+I112+IV1, I+I112+IV1, I+I112+IV1, and I+I112+IV1, in different types of position. From these maps the relative position of the individual complexes could be determined in a consistent way. These new structural features allow us to propose a refined model of a respiratory string, which is also in agreement with former freeze-fracture EM data [10].

2. Material and methods

2.1. Preparation of mitochondria

Freshly harvested potato tubers (Solanum tuberosum var. cilena) were purchased from a local farmer and stored at 4 °C. Mitochondria were prepared by homogenizing 200 g of plant material at 4 °C using a Waring blender for 3 × 5 s, filtrated through four layers of muslin. Subsequently, organelles were purified by differential centrifugations and Percoll density gradient centrifugation as outlined previously [24]. Isolated mitochondria were either directly analyzed by gel electrophoresis or stored at minus 80 °C.

2.2. Purification and characterization of respiratory supercomplexes

The mitochondrial inner membrane-protein complexes of potato were solubilized using a buffer with 5% digitonin, 30 mM HEPES, 150 mM K-acetate, 10% glycerine, pH 7.4. To characterize solubilized respiratory supercomplexes, protein solution was firstly separated by one-dimensional Blue-native (BN) PAGE [25]. Secondly, to establish the subunit content, gel strips including the resolved protein complexes were placed horizontally onto a second gel dimension which was carried out in the presence of SDS (two-dimensional BN/SDS PAGE). Afterwards, the gels were stained with Coomassie-Blue.

To purify respiratory supercomplexes, solubilized complexes were loaded on a 0.3–1.5 M sucrose gradient containing 15 mM Tris base, pH 7.0, 20 mM KCl, 0.2% digitonin and separated by ultracentrifugation (17 h at 150,000g × g and 4 °C). Afterwards, the gradients were fractionated and the fractions were examined for protein complexes by one-dimensional BN/SDS PAGE and Coomassie-Blue staining. In some cases, bands from a one-dimensional BN-PAGE gel were cut out and the protein complexes were electro-eluted with elution buffer (25 mM Tricine, 7.5 mM Bis-Tris and 0.01% digitonin) at 4 °C [24]. Intactness of electro-eluted protein complexes was checked using another one-dimensional BN-PAGE.

2.3. Electron microscopy and single particle analysis

Selected fractions of the sucrose gradient were dialyzed against buffer (15 mM Tris/HC1, 20 mM KCl and 0.2% digitonin) to decrease the sucrose content and to improve a quality of EM specimen. Electro eluted protein complexes were directly used for specimen preparation without any further treatment. Negatively stained specimens were prepared with 2% uranyl acetate on glow-discharged carbon-coated copper grids. Electron microscopy was performed on a Philips CM120 electron microscope equipped with aLaB6 tip operating at 120 kV. Images were recorded with a Gatan 4000 SP 4K slow-scan CCD camera at 80,000× magnification at a pixel size (after binning the images) of 0.375 nm at the specimen level with GRACE software for semi-automated specimen selection and data acquisition [26]. Single particle projections were selected from micrographs both by hand and reference-based automated particle selection procedure incorporated into GRIP (GRöningen Image Processing) software. Single particle data sets were analyzed with the GRIP software on a PC-cluster, including multi-reference and no-reference alignments, multivariate statistical analysis, and hierarchical ascendant classification [27]. Final two-dimensional projection maps were calculated
from the best resolved classes, by summing only the best 5–20% of the projections, with the correlation coefficient determined in the alignment step as a criterion.

3. Results

3.1. Purification and characterization of respiratory supercomplexes

Solubilization of isolated potato mitochondria by digitonin and analysis of the solubilized protein complexes by two-dimensional BN/SDS PAGE allowed identification of the respiratory supercomplexes present in potato mitochondria (Fig. 1). In line with previous results [23,28], significant numbers of supercomplexes comprising of complexes I, III and IV (III2+IV, I+III2; I2+III2 and I+III2+IV) along with dimeric ATP synthase and the five individual complexes were detected.

For single particle EM analysis, solubilized respiratory supercomplexes were purified by sucrose density gradient ultracentrifugation. The gradient was subsequently fractionated and small aliquots of the fractions were analyzed by BN-PAGE to monitor their protein complex composition (Fig. 2A). Fractions enriched in specific respiratory supercomplexes were used for single particle EM analysis. If necessary, either described purification approach was repeated several times to obtain a fraction with a sufficient concentration of specific supercomplex or projections of specific supercomplex found in different sucrose gradient fractions were combined to obtain a data set with a sufficient number of projections suitable for single particle image analysis. Alternatively, EM analysis was performed on electro-eluted supercomplexes from a one-dimensional PAGE strip. To confirm the intactness of the supercomplex after electro-elution, small aliquots of the electro-eluted supercomplexes were analyzed again with one-dimensional BN-PAGE (Fig. 2B).

3.2. Structural analysis of complex I

Single particle EM and image analysis of sucrose gradient fraction enriched in content of complex I revealed a top-view and several types of side-view projections of complex I (Fig. 3). Averaged projection map of the top-view of the complex I clearly indicate that the membrane part of the complex I is characteristically curved (Fig. 3A). Side-view projections of complex I were resolved for two different orientations of complex I on the support carbon film (Fig. 3B–F). More detailed comparison of side-view projections indicates that the main differences are in the structure of the hydrophilic arm (compare Fig. 3C, D vs. B, E, F), although small differences in the membrane part are present as well. As the membrane part of the complex I in Fig. 3C and D appears to be more bended compared to the other side-view projections (Fig. 3B, E, F), different structural features of the hydrophilic arms can reflect a different orientation of complex I on the carbon support film. The reason for the slightly different orientation of complex I can be either in flexibility or contrary conformation of the hydrophilic arm, which can, subsequently, lead to distinct positions of the complex on the carbon film. The carbonic anhydrase domain, which was found to be tightly associated with the membrane part of green plant complex I

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**Fig. 1.** Analyses of protein complexes of potato mitochondria by two-dimensional Blue native/SDS PAGE. Molecular masses of standard proteins are given to the right of the gel (in kDa). Designations: I, II, IV, V: monomeric complexes I, II, IV, V; III2, V2: dimeric complexes III, V; III2+IV: supercomplex formed of dimeric complex III and monomeric complex IV; I+III2: supercomplex formed of complex I and dimeric complex III; I2+III2: supercomplex formed by dimeric complex III and two copies of monomeric complex I; I+III2+IV: supercomplex formed of complex I, dimeric complex III and complex IV. The white arrow indicates the Cox II subunit of complex IV, which forms part of (i) complex IV, (ii) of the III2+IV supercomplex and (iii) of the I+III2+IV supercomplex.

**Fig. 2.** Preparation of mitochondrial OXPHOS supercomplexes from potato for EM analyses. Protein complexes of potato mitochondria were either separated by sucrose gradient ultracentrifugation or by one-dimensional Blue-native PAGE and subsequent electro-elution. (A) Aliquots of fractions of the sucrose gradient were resolved by one-dimensional Blue-native PAGE to monitor the protein complex composition of the fractions. (B) Aliquots of electro-eluted I+III2+IV supercomplex (lane 1), I+III2 supercomplex (lane 2) and complex III2 (lane 3) were reanalyzed by one-dimensional Blue-native PAGE to monitor purity of the fractions. Identities of the resolved protein complexes are indicated to the left of the gels (for designations see Fig. 1).

**Fig. 3.** Single particle electron microscopy of the complex I from potato mitochondria. Projection map (A) represents the top-view of the complex I. (B–F) show side-view projections of the complex I with different orientations on the support carbon film, respectively. Carbonic anhydrase domain (a white arrow), which associates to complex I in plant mitochondria, is clearly resolved in all presented projections. An unknown density attached to the membrane part of complex I was revealed in some side-view projections as indicated by a black arrow in [F]. Projection maps (A–F) are averaged class sums of 454, 276, 241, 516, 634, and 314 aligned particles, respectively. The scale bar equals to 10 nm.
3.3. Structural analysis of the I+III\textsubscript{2} supercomplex

The projection maps in Fig. 4 show the results of single particle EM and image analysis of sucrose gradient fractions enriched in the potato I+III\textsubscript{2} supercomplex. Top-view projections revealed a typical U-shaped feature of the I+III\textsubscript{2} supercomplex (including the density of the carbonic anhydrase domain) which were observed before in other plant species (Fig. 4A–C) [16,17,29]. Detailed inspection of resolved classes shows that some represent the I+III\textsubscript{2} supercomplex in a more opened conformation (Fig. 4A) compared to others (Fig. 4B and C). In addition, the carbonic anhydrase domain, attached in the center of the membrane arm of complex I, is distinguishable in some top-view projections as the most stain-excluding density (e.g. arrow, Fig. 4A). In the other two side-views, the angular position is such that the density of the carbonic anhydrase is less recognizable as it merges with densities of either the membrane-protruding part of complex III\textsubscript{2} (Fig. 4D) or the hydrophilic arm of complex I (Fig. 4F). Besides top- and side-view projections, several classes with tilted supercomplex I+III\textsubscript{2} views were found (Fig. 4C–I). Assignment of complex I in the tilted view projections was facilitated by localization of the trimeric density of the carbonic anhydrase domain, which is composed by three subunits, on the hydrophilic arm of the complex I (Fig. 4G–I). They correspond to the projection densities of singular complex I at a similar angular view (Fig. 4J). The typical feet-like features and characteristic shape of membrane-protruding part of complex III\textsubscript{2} are recognizable in the right-bottom part of the projection maps (Fig. 4G–I).

3.4. Structural analysis of I\textsubscript{2}+III\textsubscript{2} and I+III\textsubscript{2}+IV supercomplexes

Biochemical analysis indicated the presence of large supercomplexes in some sucrose gradient fractions, like the I\textsubscript{2}+III\textsubscript{2} and I+III\textsubscript{2}+IV supercomplex (Fig. 2A). Single particle EM and image analysis of these fractions revealed, indeed, the presence of large particles, although their abundance was rather low, with about 1–2 copies per EM micrograph. Fig. 5A shows a class average of one type of such a large particle, which was assigned to a side-view projection of the I\textsubscript{2}+III\textsubscript{2} supercomplex. The center of the projection map can be unambiguously assigned to the dimer of complex III, mainly due to its typical feature of the membrane-protruding part. Complex III\textsubscript{2} is symmetrically flanked by two copies of complex I, whose hydrophilic arms are recognizable. Image analysis revealed that in some cases the complex I at the right-side of complex III\textsubscript{2} is incomplete in the hydrophilic arm (Fig. 5B). Importantly, the incompleteness of the I\textsubscript{2}+III\textsubscript{2} supercomplex does not lead to a different orientation of the particle on the carbon support film and both the complete I\textsubscript{2}+III\textsubscript{2} supercomplex and the fragment reveal the same features in resolved projection maps (compare Fig. 5A and B).

Fig. 5C shows a class average, which brings to light substantial different features of the complex III\textsubscript{2} compared to its corresponding density in the complete/incomplete I\textsubscript{2}+III\textsubscript{2} supercomplex (Fig. 5A, B). Due to the strong similarity of projection map in Fig. 5C with the side-view projection of the I+III\textsubscript{2} supercomplex (Fig. 4F), we suggest that the projection map in Fig. 5C represents the side-view of the I+III\textsubscript{2} supercomplex with an extra mass attached on the right side of the supercomplex. Furthermore, the similarity indicates that the extra mass has to represent a protein of a smaller size than e.g. the hydrophobic arm of complex I, as there is a minimal influence of the extra mass on the side-view orientation of the I+III\textsubscript{2} supercomplex on the carbon support film. Fig. 5D shows a class average, which represents a well-recognizable top-view projection of the I+III\textsubscript{2} supercomplex with an extra density attached close to the complex III along the interaction interface between complex I and complex III. Based on the biochemical analysis of sucrose gradient fractions (Fig. 2A) and the size of the extra mass, we suggest that this density represents complex IV and projection maps in Fig. 5C and D represent the side- and top-view of the I+III\textsubscript{2}+IV supercomplex, respectively. This supercomplex represents the largest individual unit in OXPHOS. It has been found previously in bovine mitochondria and was named the respirasome [11].

Fig. 4. Single particle electron microscopy of the I+III\textsubscript{2} supercomplex from potato mitochondria. Projection maps (A–C) represent top-view projections of the I+III\textsubscript{2} supercomplex in a more open (A), intermediate (B) and close conformation (C). (D–F) depict side-view projections of the I+III\textsubscript{2} supercomplex with different orientations on the support carbon film. Projections (G–I) show tilted views of the I+III\textsubscript{2} supercomplex. Projection map (J) represents complex I with a similar orientation on the support carbon film like in case of tilted views of the I+III\textsubscript{2} supercomplex shown in (G–I). Projection maps (A–J) are averaged class sums of 1422, 924, 1320, 1024, 1024, 1500, 512, 512, 512 and 1500 aligned particles, respectively. The carbonic anhydrase is indicated by white arrows in (A), (E), and (G). The scale bar equals to 10 nm.
3.5. Structural analysis of the III₂ + IV supercomplex and complex V

To prove the existence of a specific association between complex III and complex IV, we performed single particle EM analysis of the III₂ + IV supercomplex. Compared to yeast mitochondria, abundance of this supercomplex is rather low, possibly reflecting a weaker association of the two involved OXPHOS complexes. Due to its low abundance in sucrose gradient fractions, we analyzed the III₂ + IV supercomplex from an electro-eluted one-dimensional BN-PAGE band. Fig. 5E shows a side-view projection map of the III₂ + IV supercomplex, which reveals a specific association between complex III₂ and one copy of complex IV. The overall structure of the side-view projection of the potato supercomplex III₂ + IV is similar to the one found in yeast [20] (Fig. 5F), but their precise comparison is difficult due to a lower resolution of the potato projection map. In addition to the III₂ + IV supercomplex, single particle EM analysis revealed side-view projections of monomeric ATP synthase (complex V) and few copies of dimeric ATP synthase (V₂) in electro-eluted fraction (Fig. 5G and H). The structure of monomeric complex V revealed the F₀ and F₁ part as well as the stalk. Although the resolution of dimeric ATP synthase is very low, the obtained projection map indicates a small angle between associated monomers.

4. Discussion

The existence of a higher organization of respiratory complexes into rows or respiratory strings was indicated in intact mitochondria by both freeze-fracture EM studies and electron tomography experiments [8–10]. The data showing the linear association of dimeric ATP synthase (complex V) and few copies of dimeric ATP synthase (V₂) in electro-eluted fraction (Fig. 5G and H). The structure of monomeric complex V revealed the F₀ and F₁ part as well as the stalk. Although the resolution of dimeric ATP synthase is very low, the obtained projection map indicates a small angle between associated monomers.
between the membrane arm of complex I and complex III$_2$ indicates an apparent flexibility of their association (Fig. 4A–C), which can be important in vivo, where the individual complexes associate in the heavily folded mitochondrial inner membrane together with other components. As in the case of the top-view projection of singular complex I, the top-view projection of the I+III$_2$ supercomplex also represents an angular view (~10° tilt out of the membrane plane). This can be evaluated from the amount of deviation from 2-fold symmetry, expected in the projection of dimeric complex III without tilt. Unambiguous assignment of the side- and tilted views of the I+III$_2$ supercomplex could be derived from the top-view projection of the supercomplex (Fig. 6A–C, F–H). Recognition of characteristic features of complex III$_2$ in both side- and tilted view projections of the I+III$_2$ supercomplex gives us insights into the way dimeric complex III associates to complex I.

Fig. 5C and D represent a side- and top-view projection map, which are, except of the presence of a small extra mass, similar to the maps of corresponding views of the I+III$_2$ supercomplex (Fig. 4F, A, respectively). Based on a biochemical characterization of sucrose gradient fractions and dimensions of the extra density, this extra mass was assigned to complex IV and the whole projection map to supercomplex I+III$_2$+IV, the respirasome (Fig. 6D, I). The top-view projection of the respirasome indicates that the complex IV associates to both complex I and III (Fig. 6I). The resolved projection map of the III$_2$+IV supercomplex clearly indicates a stable association between these two complexes (Fig. 5E). However, due to the low resolution of the III$_2$+IV supercomplex it is not possible to determine which site of complex IV is involved in the interaction with complex III$_2$. Since the overall shape of the supercomplex III$_2$+IV projection map from potato is rather similar to that of the yeast III$_2$+IV$_2$ supercomplex, we assume that potato complex III$_2$ and complex IV associate in a similar way like in the yeast supercomplex III$_2$+IV$_2$ [20].

Our data indicate that the structure of the potato respirasome differs from the 3D model of the bovine respirasome [22]. The proposed model for the bovine respirasome suggests that (i) complex III$_2$ associates to complex I from the site, which is opposite to the binding site we found in potato, (ii) complex IV is attached at the end to both complex I and III (Fig. 6I). The resolved projection map of the III$_2$+IV supercomplex clearly indicates a stable association between these two complexes (Fig. 5E). However, due to the low resolution of the III$_2$+IV supercomplex it is not possible to determine which site of complex IV is involved in the interaction with complex III$_2$. Since the overall shape of the supercomplex III$_2$+IV projection map from potato is rather similar to that of the yeast III$_2$+IV$_2$ supercomplex, we assume that potato complex III$_2$ and complex IV associate in a similar way like in the yeast supercomplex III$_2$+IV$_2$ [20].

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Potato mitochondria are special for I$_2$+III$_2$ supercomplexes, although these particles are not very abundant in detergent solubilized membrane fractions. Sucrose gradient fractions where at least trace amounts of the I$_2$+III$_2$ supercomplexes were detected by one-dimensional BN-PAGE (Fig. 2A), were subjected to an extensive single particle EM analysis. Fig. 5A shows, for the first time, a side-view projection map of this supercomplex. The middle part of the projection map clearly shows symmetric features, which could be unambiguously assigned to the dimeric complex III. The densities which represent both hydrophilic arms of the two complex I moieties are faint, or even absent on the right position in Fig. 5B. This can be explained by the dissection of the upper part of the hydrophilic arm, which was also observed in complex I from other species [16]. Moreover, the faint appearance is also a matter of stain embedding. Fig. 6 shows a schematic top-view of the I$_2$+III$_2$+IV$_2$ supercomplex. This indicates that in the side-view position one of the membrane arms is over 20 nm away from the carbon support film.

The side-view map of the I$_2$+III$_2$ supercomplex likely also includes two copies of complex IV but because of potentially overlapping positions their presence cannot be ascertained. Together with the top- and side-view maps of the I+III$_2$+IV supercomplex we can now deduce the relative positions in the full I$_2$+III$_2$+IV$_2$ supercomplex, of which we did not observe substantial numbers of top-view projections (Fig. 6J) and complete the assignment of the largest possible supercomplex, as deduced from 400,000 potential fragments.

Based on our 2D projection maps of potato supercomplexes we suggest a megacomplex organization in the inner mitochondrial membrane, which was previously named the respiratory string (Fig. 7). We propose that a central role is given to dimeric complex III which is able to bind up to two copies of complex I. Complex IV is supposed to play a role in connection of the I$_2$+III$_2$ supercomplexes, and probably also in clasping the flexible interaction between I$_2$+III$_2$ supercomplexes. Although EM analysis only revealed a stable association between complex III$_2$ and one copy of complex IV, binding of two complex IV molecules can be expected, due to the dimeric structure of the complex III. Moreover, biochemical data indicate that the I+III$_2$ supercomplex can associate with up to 4 copies of complex IV giving the I+III$_2$+IV$_{1-4}$ supercomplexes [28]. The fact that these complexes have not been found in this extensive search may indicate that they easily disassociate upon negative staining procedure used in the EM analysis. The C1 complex IV is supposed to play a role in connection of the I$_2$+III$_2$ supercomplexes, and probably also in clasping the flexible interaction between I$_2$+III$_2$ supercomplexes. Although EM analysis only revealed a stable association between complex III$_2$ and one copy of complex IV, binding of two complex IV molecules can be expected, due to the dimeric structure of the complex III. Moreover, biochemical data indicate that the I+III$_2$ supercomplex can associate with up to 4 copies of complex IV giving the I+III$_2$+IV$_{1-4}$ supercomplexes [28]. The fact that these complexes have not been found in this extensive search may indicate that they easily disassociate upon negative staining procedure used in the EM analysis. In the proposed model, the I$_2$+III$_2$+IV$_2$ supercomplex represents the basic building block (Fig. 7). These supercomplexes form a string by the interaction of two copies of complex IV, whereby each supercomplex contributes one molecule. This organization is based on (i), the first structure of supercomplex I$_2$+III$_2$, which shows that dimeric complex III can bind two copies of complex I, (ii), the structure of supercomplex I+III$_2$, and (ii), the structure of the I$_2$+III$_2$+IV supercomplex. Although we were not able to visualize the III$_2$+IV$_2$ supercomplex, this supercomplex was present in one-dimensional BN-PAGE gels, making it likely that the potato structure is similar to that found in yeast [20].

Previous model of string architecture of respiratory chain supercomplexes in bovine mitochondria differs from our model, because
the former is based on binding of only one copy of complex I to dimeric complex III [14]. Indeed, supercomplexes including more than one copy of complex I were not observed in beef. Further, the ratio of complexes I, III and IV in our model is 1:1:1 and differs from the previous reported ratio of 1:3:6. [32]. However, one has to realize that the 1:3:6 ratio reflects the total concentration of each complex in the inner mitochondrial membrane including the free complexes. The II+III2+IV2 repeating motif in the model proposed for potato measures about 26 nm (going from one centre of complex III2 to the next) which is comparable to the earlier observed spacing of 26–30 nm by freeze-fractured EM [10]. Wittig et al. pointed out that this distance ensures about 26 nm (going from one centre of complex III2 to the next) (see Fig. 3 in [14]). This, however, cannot be the case for potato since the length of one III2+IV2 supercomplex measured in the configuration IV+III2+IV2 equals already 26 nm [20]. Therefore, it is unlikely that two neighboring complex III2 are separated by two dimers of complex IV because addition of two copies of complex IV to the III2+IV2 complex would increase the width by about 10 nm to a final 36 nm. Presently it cannot be decided whether the string architecture is conserved in eukaryotes or rather differs in different organisms.

In conclusion, the data presented here give the first structural insight in a respiratory string from mitochondria, although in an indirect way, based on the structural characterization of supercomplexes obtained after detergent disruption of the mitochondrial inner membrane. A final proof is in theory possible by electron tomography on ice embedded mitochondria, in a way as performed to visualize the ATP synthase strings [9]. Tomography, however, has a much lower resolution than single particle analysis. The resolution is around 6–8 nm in the case of large objects such a mitochondrion. In contrast, single particle analysis typically provides information at 2 nm. Hence, present electron tomography can visualize the protruding headpieces of ATP synthase which have a diameter of 10 nm, but it cannot reveal the presence of many smaller membrane-embedded components such as complex IV, whose crucial role in the connection of the much larger dimeric complex III and complex I was suggested in our model of respiratory string.

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