

Emerging roles for sodium dependent amino acid transport in mesenchymal cells

Review Article

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Summary. The functional aspects of sodium dependent amino acid transport in mesenchymal cells are the subject of this contribution. In a survey of the cross-talk existing among the various transport mechanisms, particular attention is devoted to the role played by substrates shared by several transport systems, such as L-glutamine. Intracellular levels of glutamine are determined by the activity of System A, the main transducer of ion gradients built on by Na,K-ATPase into neutral amino acid gradients. Changes in the activity of the System are employed to regulate intracellular amino acid pool and, hence, cell volume. System A activity has been found increased in hypertonically shrunken cells and in proliferating cells. Under both these conditions cells have to increase their volume; therefore, System A can be employed as a convenient mechanism to increase cell volume both under hypertonic and isotonic conditions. Although less well characterized, the uptake of anionic amino acids performed by System X^-_{AG} may be involved in the maintenance of intracellular amino acid pool under conditions of limited availability of neutral amino acids substrates of System A.

Keywords: Cell volume – Cell cycle – Glutamine – Glutamate

Introduction

This contribution is specifically aimed to depict some functional aspects of sodium dependent amino acid transport in cultured mammalian cells of mesenchymal origin. It describes predominantly the experimental work performed by our group on cultured human fibroblasts and NIH3T3 cells, the model cells from which most of the results presented here have been obtained. The situation depicted is quite similar to many other less well characterized mesenchymal cell models. For more complete and systematic reviews on sodium dependent amino acid transport the reader is referred to

Christensen (1990), Guidotti and Gazzola (1992), McGivan and Pastor-Anglada (1994).

In the first part of the review an overall description of the systems involved in amino acid transport is given; attention is then focused on one of these systems, the sodium-dependent, highly concentrative system A for neutral amino acids. The involvement of this system in cell volume regulation and in the progression of cell cycle is discussed on the basis of recent findings and literature data. Finally we briefly discuss possible roles played by system X_{AG}^- for anionic amino acids in the physiology of mesenchymal cells.

Amino acid traffic across the cell membrane of mesenchymal cells

The progressive characterization of amino acid transport systems has led to an increasingly complex picture of amino acid transport in mammalian cells.

In Fig. 1 the coordinated operation of some selected amino acid transport systems is shown. We shall maintain the traditional Christensen's nomenclature system (Bannai et al., 1984), since molecular characterization of several of the transport agencies described below is still lacking. It should be pointed out that each of the transport agencies indicated are likely to correspond to a family of closely related transporters. Moreover, for the sake of clarity, cationic amino acid transport through carriers of the CAT family has not been considered in Fig. 1, although this activity is probably the best characterized from a molecular point of view (see the reviews by MacLeod and by Closs in this same issue).

The description of Fig. 1 begins with system A, a secondary active transport system that operates a 1:1 symport of sodium and members of a selected

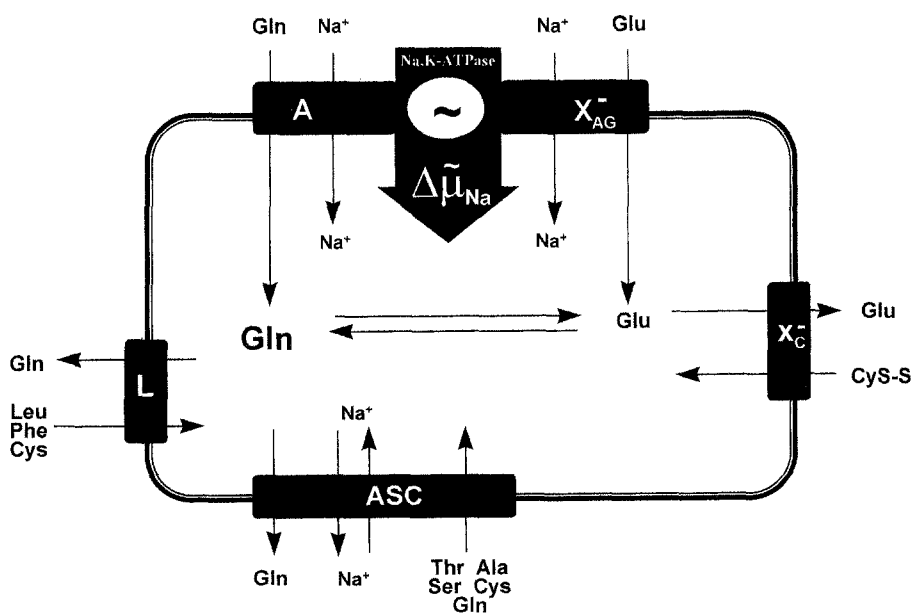


Fig. 1. A model of neutral and anionic amino acid transport in mesenchymal cells

group of neutral amino acids (such as L-proline, L-glutamine, L-alanine, L-serine) strictly dependent upon the transmembrane gradient of electrochemical potential for sodium (Gazzola et al., 1980; Dall'Asta et al., 1991); the operation of the system is therefore functionally linked to the activity of Na,K-ATPase. Thus, the accumulation of the substrates of system A can be described as the conversion of the transmembrane gradient of electrochemical potential for sodium into a transmembrane gradient of chemical potential for amino acids. Several examples of a coordinated regulation between the activities (and, presumably, the expression) of Na,K-ATPase and of system A have been described in the literature (reviewed in McGivan and Pastor-Anglada, 1994).

The operation of system A can be easily linked to that of the exchange routes characterized in several models and also in the human fibroblast (Gazzola et al., 1980; Franchi-Gazzola et al., 1982; Dall'Asta et al., 1990; Bussolati et al., 1991). These routes can be sodium-independent, as the so-called system L, or sodium-dependent, in the case of system ASC. It should be added that, while a general agreement exists about the impossibility of system L to build a significant net gradient of substrates across the membrane (Christensen, 1990; Guidotti and Gazzola, 1992), contrasting evidence exists with respect to system ASC. Indeed, data obtained in our laboratory with cultured human fibroblasts indicate that the system works predominantly by exchange (Bussolati et al., 1992). In contrast, the expression of ASC-related clones (Shafqat et al., 1993; Arriza et al., 1993) provokes a current in heterologous models (Arriza et al., 1993), implying a net flux of charges and, hence, an active nature of the transport operation performed by the system. It is not clear if these diverging results stem from the cell models employed or, rather, from the existence of closely related ASC-type carriers. We can conclude that for both systems L and ASC the demonstration of "bona fide" active nature has not yet been obtained. However, since both systems L and ASC are endowed with substrate specificities partially overlapping that of system A, the transmembrane gradient built up by the operation of system A can be somewhat redistributed among the whole large group of neutral amino acids. This means that even quasi-specific substrates of system L (i.e., leucine) or of system ASC (i.e., threonine) can reach high transmembrane distribution ratios, provided that their entry is strictly coupled to the efflux of another amino acid pre-accumulated via system A. This particular form of energizing amino acid accumulation has been defined a "tertiary active" transport process.

For tertiary active transport processes the important amino acids are those that can attain high intracellular concentrations via system A and then exchange via systems ASC and L with other amino acids. One such compound is L-glutamine that, in mesenchymal cells, exhibits a good affinity for all the three systems for neutral amino acids (Dall'Asta et al., 1990). It might be noted that we have not considered the so called system N, a transport pathway specific for glutamine, asparagine, and histidine (Kilberg et al., 1980) since no data are yet available about its bioenergetics; moreover, system N activity has been described in some (Hundal et al., 1989) but not in all mesenchymal cells

(Dall'Asta et al., 1990; Bussolati et al., 1993a). Thus, it is likely that L-glutamine is somehow at the center of the intracellular amino acid network. Interestingly, glutamine is one of the most abundant amino acids in various compartments of human body (Armstrong and Stave, 1973; Souba, 1993) as well as in most culture media. Furthermore, its intracellular concentration can reach very high values in several mammalian cells, such as in cultured human fibroblasts (Dall'Asta et al., 1994b).

This picture can be further expanded since, in the intracellular compartment, L-glutamine can be easily converted into L-glutamate and vice versa. On the other hand, the intracellular pool of L-glutamate can also be fueled by specific transport systems. One of these, system X_{AG}^- (Gazzola et al., 1981; Dall'Asta et al., 1983), is an active transport system which has the same operational features as the members of the family of Na,K-dependent glutamate carriers, cloned from nervous system and absorptive epithelia (Kanai and Hediger, 1992; Pines et al., 1992; Storck et al., 1992). The other, system x_c^- (Bannai and Kitamura, 1980; Bannai and Kitamura, 1982; Bannai, 1986; Bussolati et al., 1986; Bussolati et al., 1993a), is an exchange, membrane potential independent, ubiquitous system, through which cystine uptake is energized by a glutamate counterflux; thus this system, under normal conditions, should not take up glutamate but, rather, dissipate the existing transmembrane gradient of the anionic amino acid.

We conclude that the establishment of high intracellular concentrations of glutamine and glutamate is a necessary condition for maintaining a large intracellular amino acid pool. The attainment of concentrations higher than 100mM primarily depends upon two transport systems, system A (through glutamine uptake) and system X_{AG}^- (through glutamate uptake). In mesenchymal cells the kinetic features of these two agencies are very different; the V_{max} of system A is much higher than that of system X_{AG}^- ; conversely, the affinity of system A for its substrates is much lower than that of system X_{AG}^- . Hence, mammalian cells grown in media containing high concentrations of glutamine and little glutamate achieve glutamine entry through system A. This represents the most important device for the establishment and maintenance of the intracellular amino acid pool. Several examples can be furnished to support this point. For instance, in cultured human fibroblasts cystine entry through system x_c^- depends upon extracellular glutamine, that, of course, fuels the intracellular pool of glutamate employed for the exchange (Bannai and Ishii, 1988). The intracellular pools of glutamine and glutamate can reach very high values, with concentrations that are markedly higher than the K_m value of most of the enzymes that are involved in their metabolism. Thus, an obvious question arises: Why do mammalian cells maintain these high intracellular concentrations of amino acids?

Role of system A in volume regulation of mammalian cells

The field of cell volume regulation in higher eukaryotic models has seen an increasing number of studies during the last few years (see for review Sarkadi and Parker, 1991; Spring and Hoffmann, 1992; Hoffmann and Dunham, 1995).

The complex array of mechanisms through which cells restore their volume upon incubation under anisotonic conditions are collectively named RVI (Regulatory Volume Increase, for volume gain after hypertonic shrinkage) and RVD (Regulatory Volume Decrease, for volume loss after hypotonic swelling). Many cell types are not able to recover their volume efficiently when transferred directly from isotonic to hypertonic conditions (hypertonic RVI). Usually, a pretreatment in hypotonic medium (the so called RVI-post-RVD protocol) is required to somehow sensitize cells to anisotonic conditions (Sarkadi and Parker, 1991; Spring and Hoffmann, 1992; Hoffmann and Dunham, 1995). It has been suggested that the reduced intracellular chloride concentration after RVD plays a permissive role in the activation of Na, K, 2Cl cotransport in several cell types (Hoffmann and Dunham, 1995). The competence for an hypertonic RVI is strictly dependent from the availability of organic osmolytes in the extracellular compartment, at least in human fibroblasts (Gazzola et al., 1991). Indeed, after the cell shrinkage caused by hypertonic treatment, human fibroblasts can easily recover their volume in complete growth medium; on the contrary, no volume recovery is detected in serum supplemented, amino-acid-free saline solution. Again, if the hypertonic shock is performed in a complete growth medium deprived of glutamine (which represents the most abundant neutral amino acid in D-MEM), no volume recovery is observed; conversely, if glutamine is added to the saline solution a complete volume restitution is observed. The next step was to demonstrate that only neutral amino acids and methylamines substrates of system A can behave as volume-active compounds. In this context, it is of particular interest that α -(methylamino)isobutyric acid, MeAIB, the non metabolizable analogue that constitutes the most specific substrate of the system, can work as a volume-protecting compound as well as natural, fully metabolizable substrates, such as L-proline (Gazzola et al., 1991). The message stemming from these results is clear: in the volume recovery process neutral amino acids are not used as metabolites but simply as osmolytes, whose accumulation calls water into the cell.

A more complete analysis of RVI response of cultured human fibroblasts has demonstrated, on quantitative grounds, that the whole volume recovery of hypertonically shrunk human fibroblasts depends on the accumulation of amino acids, while potassium does not give a significant contribution (Dall'Asta et al., 1994c). As a whole, intracellular amino acid concentration rises by more than 60% during 4h of hypertonic treatment; most of this increase is due to changes in glutamine and glutamate. It is possible to conclude that in cultured human fibroblasts hypertonic regulatory volume increase relies entirely upon the activity of system A. This conclusion gives the proper functional context to observations describing a stimulation of system A activity and an expansion of amino acid pool in hypertonically treated avian and mammalian fibroblasts (Tramacere et al., 1984; Silvotti et al., 1991). Moreover, it is fully consistent with an increasing amount of data obtained by other groups in both epithelial (Soler et al., 1993; Ruiz-Montasell et al., 1994) and non epithelial cell models (Chen et al., 1994; Ruiz-Montasell et al., 1994; Yamauchi et al., 1994). In this context it is interesting that an analysis of

changes in intracellular osmolytes in rat tissues after hypertonic stress *in vivo* (Bedford and Leader, 1993) demonstrates changes in total content of amino acids and composition of amino acid pool that are comparable to those observed in our *in vitro* model.

While these data strongly support the general significance of the volume regulatory role of system A, they do not yet explain how the activity of the system is modulated so as to achieve an expanded intracellular amino acid pool. In cultured human fibroblasts we have identified two distinct mechanisms for the increase in system A activity involved in the volume recovery process.

During the RVI process the activity of system A, measured as amino acid influx, exhibits a 3–6-fold increase that requires 3–4 hours of incubation under hypertonic conditions for a complete development. Kinetic analysis of transport reveals that the increase is substantially dependent upon a change in V_{max} of the system (Dall'Asta et al., unpublished results). This result was expected, since it has been known since several years that one of the most distinctive operative features of system A is the highly variable transport capacity in response to a number of environmental conditions, such as amino acid starvation, presence of hormones such as insulin and glucagon, cell density, proliferative status of the cell population, *in vitro* aging of the culture (discussed in the above cited reviews on amino acid transport). All these increases in the transport capacity of the system require prolonged times for their development and an active protein synthesis. Similarly, also the hypertonically induced increase in system A transport activity observed in cultured human fibroblasts requires several hours of active protein synthesis, since it is blocked by cycloheximide (Dall'Asta et al., 1994c) and by actinomycin D (Dall'Asta et al., unpublished results). The simplest explanation of this increase is an increased transcription of the gene coding for the system A carrier itself. If so, system A would resemble other organic substrates transporters whose expression is stimulated by hypertonic stress (Uchida et al., 1992; Yamauchi et al., 1992; Uchida et al., 1993; Yamauchi et al., 1993). However, evidence obtained by the group of Pastor-Anglada (presented in Ruiz-Montasell et al., 1994, and also discussed in this same issue) would indicate that the derepressed gene product is not the carrier itself but, rather, an activator of the transport process.

A careful characterization of the bioenergetics of system A in hypertonically shrunk cells has demonstrated that the enhanced accumulation of amino acids through the system is also sustained by a cell hyperpolarization that rapidly follows hypertonic shock. The characterization of the change in membrane potential has been accomplished under the same experimental conditions adopted for amino acid accumulation employing two distinct, non invasive methods for the estimation of membrane potential in adherent, intact shrunk cells. The first method employs L-arginine as a probe for membrane potential (Bussolati et al., 1987; Bussolati et al., 1989). According to this method the value of membrane potential can be obtained from the transmembrane ratio of the cationic amino acid. Some conditions have to be fulfilled in order to employ the method for reliable results: i) the

uptake of the amino acid should be due, at least for the most part, to the sodium-independent family of CAT transporters; ii) the intracellular metabolism of the amino acid should be very slow and, iii) in the particular model employed, L-arginine should not be endowed with a peculiar metabolic relevance. In human fibroblasts these requirements have been satisfied and, provided that intracellular stores of cationic amino acids have been depleted, the cationic amino acid distributes across the plasma membrane according to a typical Nernst-type relationship; thus, under these conditions, the application of Nernst relationship to the transmembrane gradient of arginine yields reliable values of the membrane potential.

More recently, we have developed a method that employs the fluorescent dye bis-oxonol in confocal microscopy. This anionic probe is used (Rink et al., 1980) for spectrofluorimetric estimation of membrane potential. We have found that confocal microscopy can be conveniently used to yield images of membrane potential changes in real time and at single cell level (Dall'Asta et al., 1994a). The depolarization caused by an increase in extracellular potassium provides a marked signal enhancement and, conversely, cell hyperpolarization obtained by activation of Na,K-ATPase is easily seen. Measurements of cell associated bis-oxonol at several extracellular potassium concentrations allows the calibration of the fluorescence signal versus the membrane potential measured with the arginine method.

With both these methods it has been possible to demonstrate that hypertonically shrunken cells rapidly hyperpolarize. Although the mechanism for this hyperpolarization is not yet clear, it is possible to determine its magnitude, that in cells incubated at an osmolality of 400 mosm/kg is more than 10 mV, and its duration, that in cultured human fibroblasts lasts well over 3 h of incubation. The observed hyperpolarization increases the transmembrane electrochemical potential gradient for sodium, the energy source for system A (see the review by Eddy, 1992 and, for cultured human fibroblasts, Dall'Asta et al., 1991); therefore it can easily explain the increased transmembrane gradient of amino acids in RVI-exerting cells.

Given the relationship between the membrane potential and the activity of system A, one might expect a stimulation of amino acid influx. However, this is not the case; indeed, measuring the unidirectional fluxes of MeAIB 30 min after the hypertonic shock (when hyperpolarization is already clearly detectable), we have found that amino acid influx is only marginally raised; this somewhat intriguing result probably derives from the shrinkage-induced rise of the intracellular concentration of transinhibiting amino acids. On the contrary, MeAIB efflux appears significantly decreased (Dall'Asta et al., 1995). If cell hyperpolarization is hampered through an increase in extracellular potassium, MeAIB efflux rises abruptly in shrunken cells. Thus, the sustained hyperpolarization maintains the efflux of neutral amino acids at low values and contributes to the increased net uptake and, hence, to the enhanced content of amino acids that is observed during the RVI response (Dall'Asta et al., manuscript in preparation). The low efflux rate for amino acids, due to cell hyperpolarization, explains why the intracellular content of these compounds

does not decrease upon hypertonic shock although their transmembrane gradient is higher in shrunken cells.

Both devices, cell hyperpolarization and synthesis-dependent increase in transport capacity, are important for volume recovery. Indeed the synthesis of new carriers or activators can be blocked with cycloheximide and hyperpolarization can be hindered performing hypertonic treatment in the presence of high extracellular potassium. In either case RVI is delayed (Dall'Asta et al., 1994c). If both hyperpolarization and protein synthesis are blocked RVI is completely abolished (Dall'Asta et al., 1994c).

In what situations of pathophysiological relevance can system A work as a volume-active transport mechanism? It is well known that cell volume changes as a result of alterations in extracellular osmolality. Actually, most of the studies performed in cell volume regulation have employed cell models highly adapted to survive marked changes in extracellular osmolality. A well characterized example is given by cells derived from the kidney medulla, in which the osmolality of the interstitium can vary widely, even under physiological conditions. If one considers other cell types, such as mesenchymal tissues, marked changes in extracellular osmolality only occur in pathological situations, such as hypernatremic or hyponatremic states or diabetic hyperglycemia. These states are summarized in Table 1 (for a more detailed discussion, see Hoffmann and Dunham, 1995). Preliminary evidence obtained in human endothelial cells would point to an increase in system A activity upon incubation in high-glucose media (Parolari et al., 1995). It is, however, evident that, although these situations can be of great clinical relevance, they hardly justify the presence of powerful volume-regulating mechanisms in mesenchymal cells that, for most of their lifespan, should face an environment whose osmolality is kept constant by specialized organ mechanisms to maintain homeostasis.

Results obtained in epithelial models have demonstrated that changes in cell volume may also derive from variations in the availability of solute substrates of active transport processes. In the hepatocyte, for instance, changes in the availability of these substrates can alter cell volume and, hence, trigger not only proper compensatory mechanisms (Kristensen, 1980;

Table 1. Selected examples of conditions associated with perturbations of cell volume

Changes in extracellular osmolarity	Changes in intracellular osmolytes
Cell swelling hyponatremia (water excess, Addison disease, . . .)	uptake of sugars and amino acids (liver, intestine . . .) exercising skeletal muscle ischaemic stroke (brain) presence of growth factors, insulin
Cell shrinkage hyperglycemia (diabetes) hypernatremia (dehydration) antidiuresis (kidney medulla)	secretion in all exocrine glands presence of glucagon (liver)

Kristensen and Folke, 1984) but also a number of complex cell responses (reviewed by Haussinger et al., 1993; 1994). These results led Haussinger to develop the concept of cell volume as a messenger in the regulation of cell functions. Thus, "the role of Na⁺-dependent amino acid transport systems can no longer merely be identified with amino acid translocation; these transporters rather act as a transmembrane signalling system triggering cellular function by altering cellular hydration in response to substrate delivery" (Haussinger and Schliess, 1995). It is evident that, if similar conclusions can also stand for other cell models, cell volume alterations would be endowed with general significance. These concepts prompted us to reappraise the role of system A in cell proliferation.

The role of System A in cell proliferation: a reevaluation

It has been known for several years that cell proliferation is accompanied by a stimulation of transport system A activity (Guidotti and Gazzola, 1992; McGivan and Pastor-Anglada, 1994). The strongest lines of evidence discussed in these reviews are the following:

1. The activity of the system is lowered in quiescent cultured cells and stimulated when serum and growth factors are added to the culture medium.
2. The activity of the system is lowered in confluent, highly crowded cell cultures.
3. In a well established system of proliferative stimulation *in vivo*, i.e. after partial hepatectomy, the transport activity of the system peaks in the remnant liver tissue to decrease after that the proliferative activity has slowed down.
4. In many (but not all) types of tumor cells the activity of the system is high. In particular, in Ehrlich cells system A activity is maximally stimulated (i.e., it is no further stimulated by amino acid starvation).
5. *In vitro* aging of cultured human fibroblasts is associated to a progressive decrease in system A activity.

The metabolic significance of this change has been thus far quite obscure. Indeed, it requires several hours for a full development: therefore it cannot be considered a component of the early signal events in the mitogenesis. Moreover, the fact that non essential amino acids are involved as substrates of the stimulated transport process makes it highly difficult that an increased amount of amino acids is required for metabolic reasons. Thus, in the later years, the significance of System A induction, although widely recognized, was regarded as a late metabolic event, possibly favoring an efficient protein synthesis.

On the basis of the above described role played by system A in the regulation of cell volume we suppose that an increase in the activity of the system can sustain an expansion of cell volume. This hypothesis would imply that the growth in cell size, observed during the cell cycle (Baserga, 1985; Muller et al., 1993), involves a coordinated increase of both cell dry mass and cell volume.

In support of this hypothesis we have recently demonstrated that, when a population of serum-starved NIH3T3 cells is pushed to proliferate by serum restitution, cell volume increases (Bussolati et al., in press). Actually, during the cell cycle, a cycle of volume changes occurs, with volume increasing after the entry in G_1 and returning after mitosis at values comparable to those detected in G_0 cells. The volume increase is associated with an enhanced accumulation of amino acids (Bussolati et al., in press). Among the various amino acids, glutamine and glutamate exhibit the most significant absolute and relative changes. Simultaneous measurements of transport activities of systems A and X_{AG}^- , performed in parallel, have demonstrated that, in NIH3T3 cells, neutral amino acid transport increases during the cycle while the influx of anionic compounds is markedly lowered. Thus, glutamine accumulated into the intracellular compartment (and subsequently converted partially to glutamate) probably results from an increased System A transport activity.

A model can therefore be depicted (Fig. 2) that implies that the passage from G_0 to G_1 triggers an increase in the transport activity of system A; this

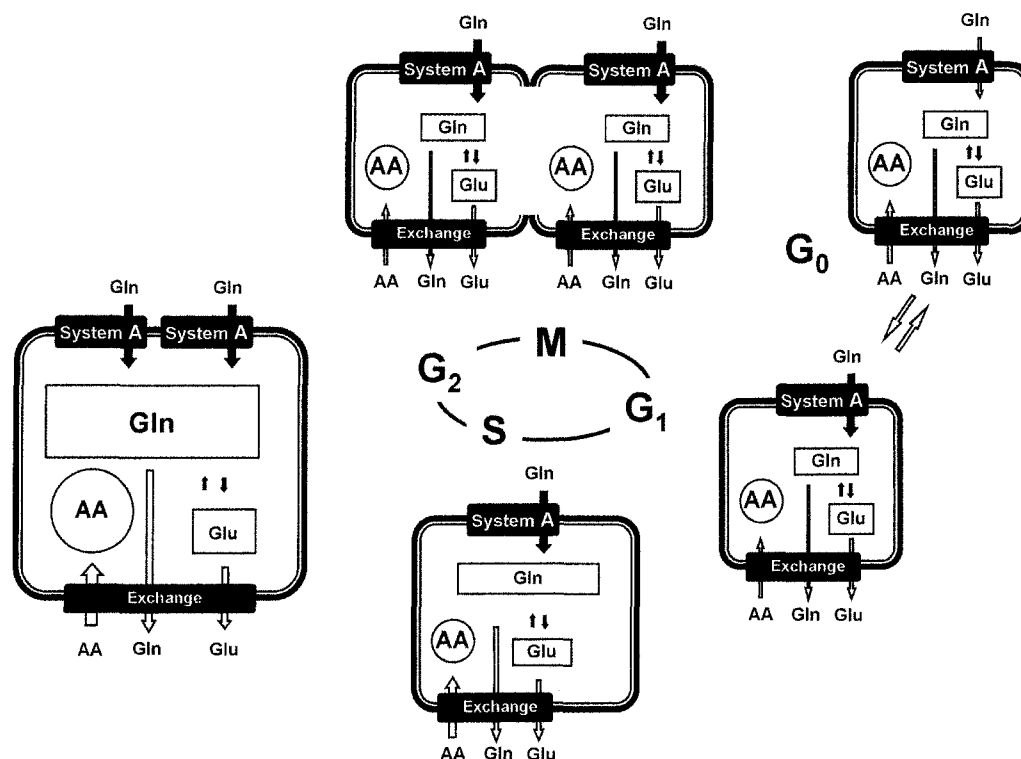


Fig. 2. Changes in amino acid transport during the cell cycle of mesenchymal cells. The increase in cell volume is explained by an increased intracellular pool of amino acids due to an enhanced transport activity for glutamine through system A. From literature data it is possible to attribute the increase of system A transport activity both to rapid mechanisms, occurring at the beginning of phase G_1 (hyperpolarization? increase in transmembrane sodium gradient?), and to a slow, protein synthesis dependent increase in the capacity of the system (synthesis of new carriers and/or activators?)

increase could be due both to rapid mechanisms such as cell hyperpolarization, and to slow responses, such as a protein synthesis dependent increase in transport capacity possibly due to an increase in the number of active carriers. As a result of the enhancement of transport activity the intracellular pools of glutamine and glutamate are raised, producing an osmotically obliged uptake of water into the cell and, therefore, an increase in cell volume; moreover, the enhanced accumulation of glutamine and glutamate lead to a generalized increase of the cell amino acid pool. This model is currently under investigation; one of its inferences would be that high concentrations of glutamine or of other system A substrates are necessary for cell proliferation not only to conduct their various metabolic roles but also to function as organic osmolytes. Actually this model works only in the presence of system A substrates in the extracellular compartment.

Halvor Christensen, discussing early attempts to define the nature of neutral amino acid transport, has stated "water movements can often be demonstrated in approximately direct relationship to solute uptake" (Christensen, 1975). These results demonstrate that, at least in the case of system A, water movements are not always a somehow untoward consequence of amino acid transport but could be, rather, the main aim of the transport process itself.

For a complete explanation of cell volume changes in cycling cells, however, one should also take into consideration the role of other transport systems that are stimulated in proliferating cells, such as the furosemide-sensitive Na,K,Cl-cotransport (Panet et al., 1982; Panet, 1985; Amsler et al., 1985; Panet et al., 1986; Paris and Poysssegur, 1986; Meyer et al., 1991) and the Na,H-exchanger (Moolenaar et al., 1981; Pouyssegur et al., 1982; Schuldiner et al., 1982). Interestingly, solute influx through all these transport systems depends upon the Na⁺ gradient established by Na,K-ATPase, which is also stimulated in proliferating cells (Rozengurt and Heppel, 1975; Smith and Rozengurt, 1978).

Sodium-dependent anionic amino acid transport through system X⁻_{AG}: a salvage pathway?

If neutral amino acids are not present at sufficient concentrations in the extracellular medium, the maintenance of intracellular amino acid pool cannot rely on system A activity. Functional consequences can be deleterious. We are now performing experiments in which conditions of glutamine starvation are caused by treatment of cells with the antitumor enzyme asparaginase (Uggeri et al., 1995a, 1995b; Bussolati et al., 1995). If the experiment is performed in actively growing NIH3T3 cells, the intracellular concentration of glutamine rapidly falls and a significant portion of the cell population undergoes apoptotic changes (Bussolati et al., 1995).

In cells treated with L-asparaginase also the intracellular pool of glutamate also decreases markedly (Bussolati et al., 1995); this is quite surprising since the enzyme hydrolyzes glutamine to glutamate and raises impressively the extracellular concentration of the anionic amino acid. The simplest

explanation for this effect is that these cells are not able to accumulate significant amounts of glutamate due to the limited activity of system X_{AG}^- that, in actively growing NIH3T3 cells is very low (Bussolati et al., 1993b). Thus, transport activity of system X_{AG}^- may be critical for cell survival under conditions of low availability of L-glutamine.

Several recent observations demonstrate that the activity of system X_{AG}^- is strictly regulated in mesenchymal cells. Short term stimulation of the system is caused by protein kinase C activation (Franchi-Gazzola et al. 1990, 1994). On the other hand, a long term enhancement of system X_{AG}^- activity has been characterized in rat myotubes upon glutamine starvation (Low et al., 1994). Conversely, cell proliferation is associated to a marked depression of the system (Bussolati et al., 1993b); in *ras* transfected fibroblasts the expression of the oncogene, that possibly corresponds to an extreme proliferative drive, causes the complete suppression of the system (Longo et al., 1988; Uggeri et al., 1995a).

Thus, it is possible to conclude that the activity of this system is highly regulated in non nervous tissues. System X_{AG}^- is a member of the family of Na,K-dependent high affinity glutamate transporters (Hediger et al., 1995). While the role of these transport systems is well recognized in the central nervous system, since they are responsible for the re-uptake and maintenance of low levels of excitatory amino acids in the extracellular compartment, these results would indicate that also in non-nervous tissues they play important functions. One of these functions can be probably identified in maintaining the intracellular levels of glutamate under conditions at which the uptake of glutamine through system A cannot work. Under such conditions the activity of transport system X_{AG}^- (but not that of the other two systems for glutamate transport, systems ASC and x_C^-) is directly related to the intracellular levels of the anionic amino acids (Uggeri et al., 1995a). It is then known that in several cultured cell lines the adaptation to glutamine starvation is related more to the activity of sodium dependent glutamate transport (presumably through system X_{AG}^-) than to the activity of glutamine synthase (McDermott and Butler, 1993). Moreover, recent data indicate that the membrane transport of glutamate can also influence the intracellular metabolism of the anionic amino acid; in cultured kidney cells, for instance, intracellular glutaminase activity is regulated by the influx of extracellular glutamate (Welbourne and Mu, 1995).

Conclusions

Compared with the field of glucose transport, progress in amino acid transport had lagged behind, likely because of the delay in cloning the transporters. Since this constraint is fading away, amino acid transport should be now expected to know a season of exciting developments. The appreciation of the roles that these membrane functions play in several situations of pathophysiological importance could also contribute to enhance experimental interest in this area. For instance, the elucidation of the role played by sodium

dependent amino acid transport in cell volume regulation should prompt investigators to study if changes in transport activity occur in situations associated with alterations in extracellular osmolality. Moreover, a better comprehension of the involvement of changes in amino acid transport in cell cycle progression should lead to a reappraisal of the relationships existing between cell transformation and alterations of amino acid transport systems.

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