L-Arginine transport and metabolism in *Giardia intestinalis* support its position as a transition between the prokaryotic and eukaryotic kingdoms

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Arginine is metabolized by the arginine dihydrolase pathway in *Giardia intestinalis* trophozoites and is an important metabolic fuel for this parasite. Radiolabelled arginine was used to characterize the transport of arginine into *Giardia intestinalis* trophozoites. The transporter had a high affinity for arginine ($K_m$, 15 μM) and a high activity [$V_{max}$ 76 nmol min$^{-1}$ (mg protein)$^{-1}$ at 25 °C]. Substrate specificity studies indicated an absolute requirement for the α-amino and carboxyl groups, but a tolerance for some substitutions in the guanidino group. The use of non-metabolized arginine analogues in combination with HPLC amino acid analysis of intra- and extracellular pools demonstrated that the arginine transporter is an arginine-ornithine antiport. Investigations of the first step of arginine metabolism, involving arginine deiminase, revealed a relatively high affinity for arginine ($K_m$, 0.16 mM) and a large maximal velocity [$V_{max}$ 550 nmol min$^{-1}$ (mg protein)$^{-1}$ at 37 °C]. Substrate specificity studies showed that the arginine deiminase had a characteristically different substrate recognition profile to that of the arginine transporter. Overall, the combination of the transporter and the deiminase result in very low intracellular arginine concentrations and their properties are consistent with the rapid transport of arginine for metabolism via the arginine dihydrolase pathway.

**Keywords**: arginine transport, arginine deiminase, *Giardia intestinalis*

**INTRODUCTION**

Arginine is a major nutrient for many organisms and cells. However, in order for it to be utilized, there must be an appropriate mechanism for transporting the arginine from the external medium to the intracellular milieu, where it can be metabolized. The mechanism of transmembrane transport of arginine varies from prokaryotes to eukaryotes. For some prokaryotes, such as *Pseudomonas* and *Streptococcus* spp., arginine can be metabolized via the arginine dihydrolase pathway (Cunin et al., 1986). In these cases, the transport of arginine is via an arginine-ornithine antiporter which accumulates arginine in exchange for intracellular ornithine, an end product of the arginine dihydrolase pathway (Driessen et al., 1987; Bourdineaud et al., 1993). For most eukaryotes, arginine transport involves the $y^+$ system, which is a high-affinity, sodium-independent system, specific for cationic amino acids (White, 1985). There is no evidence to date of this being an obligatory arginine-ornithine antiporter.

The metabolism of arginine by the eukaryotic protozoan parasite *Giardia intestinalis* is unusual. The arginine dihydrolase pathway, which is normally confined to the prokaryotic kingdom, is operational in *G. intestinalis* and is a major route for energy production (Schofield et al., 1992). However, recent evidence places *Giardia* on one of the earliest diverging branches of the evolutionary tree (Sogin et al., 1989), and as such it may show metabolic and physiological properties characteristic of a transition between the eukaryotic and prokaryotic kingdoms.

We report in this paper the characterization of the arginine transporter in *G. intestinalis* and, on the basis of substrate specificity and kinetic studies, distinguish its properties from those of arginine deiminase, which is the first step of arginine metabolism. We propose that the transport
system is an arginine-ornithine antport, which is pro-

caryotic in nature and may be related to the bacterial

transporters previously described for Streptococcus lactis
(Driessen et al., 1987) and Pseudomonas aeruginosa
(Bourdineaud et al., 1993).

METHODS

Parasites and materials. Giardia intestinalis trophozoites
(Portland 1 strain) were grown in TYI-S-33 medium supple-
mented with ox bile as described previously (Knodler et al.,
1994). Whole-cell suspensions were prepared in phosphate-
buffered saline (PBS) [1.8 mM KH₂PO₄/5 mM KH₂PO₄/0.9 %
(w/v) NaCl pH 7-4] and left on ice until required. Protein
concentrations of whole-cell suspensions were determined by
the Lowry method. ~-[2,3,4,5-3H]Arginine and
concentrations of whole-cell suspensions were determined by
system is an arginine-ornithine antiport, which is pro-

"-

~-[2,3,4,5-3H]arginine (10 mCi mmol⁻¹) at a temperature of 25
°C and in a

After 5 min preincubation at 25 °C, cells were added to the
permeant to initiate the reaction conditions. Concurrent experiments were conducted to de-
termined by the method of Bradford (1976). Arginine
dehydrogenase was routinely assayed by the colorimetric deter-
mination of citrulline as described previously (Schofield et al.,
1992), except that 40 mM HEPES buffer pH 7.0 replaced 40 mM
MES buffer pH 7.0. In inhibition studies, the production of
citrulline was measured over a 10 min time period at 37 °C with
1 mM arginine and 0.1 mg protein, in the presence or absence of
potential competitors (10 mM). For Kₐ determinations the more sensitive colorimetric assay of Prescott & Jones (1969)
was used, since the method of Boyd & Rahmatullah (1980)
proved unsuitable due to poor sensitivity at the low arginine
concentrations required for kinetic studies. The initial rate of
arginine deiminase activity was measured over a 2.5 min time
period at 37 °C using a range of arginine concentrations from
0.07 to 1 mM and 0.04 mg protein.

RESULTS

Arginine transport and metabolism

The centrifugation through oil method proved very
reliable for assaying the uptake of arginine over short time
periods. Uptake was monitored using L-[2,3,4,5-
3H]arginine. The uptake of 100 μM arginine was very
rapid, with linearity at 25 °C extending to 8 s only (Fig. 1).
Over a 30 s time period, radioactivity was reproducibly
accumulated to levels of approximately 20 nmol arginine
(mg protein)⁻¹. The uptake of arginine was much slower at
4 °C (Fig. 1).

The extent of arginine metabolism at a number of points
over a 30 s time course was investigated via the ac-
cumulation of [U-14C]arginine (100 μM), instead of
[3H]arginine, and determining the products by TLC
analysis. The results are presented in Table 1. The zero
timepoint was representative of the time required for the
Arginine transport and metabolism in *G. intestinalis*

![Figure 1](image)

**Fig. 1.** Time course of uptake of 100 µM arginine uptake by *G. intestinalis* trophozoites at 25 °C (○) and 4 °C (■). Cells were incubated with l-[2,3,4,5-3H]arginine and at specific time points centrifuged to the bottom of an oil layer. The amount of radioactivity accumulated in the cell pellet was determined. Results are the mean of triplicate timepoints from a single representative experiment; further repeats showed less than 20% variation in the 4 s timepoint.

**Table 1.** Profile of 14C-labelled metabolites following uptake of [U-14C]arginine by *G. intestinalis* trophozoites at 25 °C

<table>
<thead>
<tr>
<th>Time point (s)</th>
<th>Metabolite (% of accumulated radioactivity)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Arginine</td>
</tr>
<tr>
<td>0</td>
<td>24±5.5</td>
</tr>
<tr>
<td>4</td>
<td>16±2.2</td>
</tr>
<tr>
<td>10</td>
<td>43±2.5</td>
</tr>
<tr>
<td>30</td>
<td>1.2±0.7</td>
</tr>
</tbody>
</table>

Intact cells were incubated with l-[U-14C]arginine at a final concentration of 100 µM. At specific time points the cells were centrifuged through an oil layer into 40 µl 5% (v/v) perchloric acid. The oil layer was washed and removed by aspiration, and then 40 µl 1 M KOH/1 M KHCO₃ was added with an amino acid tracer mix. This was vortexed, left on ice for 15 min, and then centrifuged at 16000 g for 3 min. A 65 µl sample of clear supernatant was vacuum-dried and then resuspended in 25 µl 0.1 M HCl. After a quick centrifugation, a 5 µl sample was spotted onto a 10 cm x 10 cm silica gel TLC plate. The amino acids were separated in two dimensions and after drying the plate the radioactivity was located by PhosphorImager analysis. Values are means of results ± SD from at least four separate experiments.

centrifuge to reach a sufficient velocity in order to pellet the cells and was estimated to be approximately 3 s. Over a 30 s time period, the proportion of radiolabel in arginine decreased but was always relatively low, with only 15% of the total incorporated radioactivity unmetabolized as arginine after 4 s. The majority of the intracellular radioactivity (> 80%) was present as citrulline, which is the first breakdown product of arginine metabolism by the action of arginine deiminase. HPLC amino acid analysis confirmed that the major proportion of transported arginine was present as intracellular citrulline, with the absolute amount of accumulated citrulline corresponding to the amount of [3H]arginine transported. Only minimal quantities [less than 1 nmol (mg protein)-¹] of intracellular arginine could be detected by amino acid analysis over the 30 s time period studied. The proportion of radiolabel present as citrulline was relatively constant over the 30 s time period (between 79 and 97%). There was little incorporation of radiolabel into intracellular ornithine over the time course studied. TLC and PhosphorImager analysis of incubation medium showed that approximately 8% and 20% of the arginine taken up appeared as extracellular ornithine after 4 s and 30 s respectively.

The initial rate of arginine uptake (4 s time point) at 25 °C over an arginine concentration range of 7–50 µM showed saturaability with respect to arginine. Kinetic analysis from two separate experiments gave *Kₘ* values of 15±4 µM and 15±1 µM and *Vₘₐₓ* values of 75±9 nmol min⁻¹ (mg protein)⁻¹ and 76±2 nmol min⁻¹ (mg protein)⁻¹ for arginine uptake. Linearity over the 4 s time period was confirmed for both ends of the concentration range (results not shown). Investigation by TLC of the extent of arginine metabolism at the lowest concentration used (7 µM) revealed that 89% of the radiolabelled arginine had been converted to citrulline within 4 s, but no labelled ornithine could be detected (results not shown).

**Specificity of arginine uptake**

The uptake of 100 µM l-[2,3,4,5-3H]arginine over a 4 s time period was monitored in the presence and absence of a number of potential inhibitors and substrates of the arginine transporter, all at a final concentration of 5 mM. Inhibition of arginine uptake would suggest competition and binding to the transporter, with the possibility of transport into the cell and subsequent inhibition of the arginine deiminase. The results are presented in Table 2. Alteration or removal of the a-amino group of arginine, as in L-ornithine or N⁡-⁡acetyl-L-arginine, gave no inhibition of arginine uptake. Removal of the carboxyl group also resulted in relatively little inhibition of arginine uptake.

Removal or attenuation of the guanidino group and alteration of the number of methylene groups in the side chain of arginine had varying effects. l-Oxornithine, which has the same number of methylene groups as arginine, but has the guanidino group replaced by an amino group, strongly inhibited arginine uptake. Altering the number of methylene groups decreased the inhibition (e.g. l-2,4-diaminobutyric acid and lysine). Substituting the guanidino group of arginine with a methyl group (N⁡-⁡methyl-L-arginine) resulted in strong inhibition of arginine uptake. However, substitution by a nitro group...
Table 2. Inhibition of arginine uptake in *G. intestinalis* trophozoites and giardial arginine deiminase activity by various arginine analogues

The initial rate of uptake of 100 μM [3H]arginine over a 4 s time period was studied in the presence and absence of various arginine analogues at a concentration of 5 mM. The influence of arginine analogues at a final concentration of 10 mM on the activity of arginine deiminase from *G. intestinalis* with 1 mM arginine at 37 °C over 10 min was also studied. In both cases the results are presented as a percentage of the rate in the absence of competitor. The *K*_i values for competition of arginine uptake were determined by the method of Hunter & Downs (1945). All compounds were the L-isomer unless otherwise stated. All values are means ± SD from at least three separate determinations. ND, Not determined since these compounds interfere with the chromogenic assay system; ADI, arginine deiminase.

<table>
<thead>
<tr>
<th>Analogue</th>
<th>Uptake rate (% of control)</th>
<th><em>K</em>_i (μM)</th>
<th>ADI activity (% of control)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>α</em>-Amino group blocked or absent</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4-Guanidinobutyric acid</td>
<td>97 ± 5</td>
<td>96 ± 4</td>
<td></td>
</tr>
<tr>
<td><em>N</em>²-Acetylarginine</td>
<td>104 ± 7</td>
<td>96 ± 7</td>
<td></td>
</tr>
<tr>
<td><em>N</em>³-Carbamylarginine</td>
<td>71 ± 6</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td><em>α</em>-Carboxyl group absent</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Agmatine</td>
<td>73 ± 7</td>
<td>55 ± 1</td>
<td></td>
</tr>
<tr>
<td>Putrescine</td>
<td>80 ± 4</td>
<td>54 ± 10</td>
<td></td>
</tr>
<tr>
<td>Guanidino group altered or absent</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lysine</td>
<td>37 ± 5</td>
<td>100 ± 9</td>
<td></td>
</tr>
<tr>
<td>Ornithine</td>
<td>20 ± 1</td>
<td>272 ± 26</td>
<td>24 ± 10</td>
</tr>
<tr>
<td>2,4-Diamino-n-butryic acid</td>
<td>62 ± 4</td>
<td>24 ± 7</td>
<td></td>
</tr>
<tr>
<td>DL-2,3-Diaminopropionic acid</td>
<td>97 ± 6</td>
<td>106 ± 6</td>
<td></td>
</tr>
<tr>
<td>Norvaline</td>
<td>95 ± 4</td>
<td>73 ± 9</td>
<td></td>
</tr>
<tr>
<td>Leucine</td>
<td>99 ± 3</td>
<td>95 ± 3</td>
<td></td>
</tr>
<tr>
<td>Alanine</td>
<td>103 ± 6</td>
<td>92 ± 9</td>
<td></td>
</tr>
<tr>
<td><em>N</em>²-Methyllysine</td>
<td>20 ± 4</td>
<td>170 ± 20</td>
<td>99 ± 2</td>
</tr>
<tr>
<td><em>N</em>⁶-Methylarginine</td>
<td>4 ± 3</td>
<td>18 ± 8</td>
<td>76 ± 8</td>
</tr>
<tr>
<td><em>N</em>⁶-Nitroarginine</td>
<td>74 ± 8</td>
<td>5 ± 1</td>
<td></td>
</tr>
<tr>
<td>Citrulline</td>
<td>100 ± 6</td>
<td>ND</td>
<td></td>
</tr>
<tr>
<td>Side chain altered</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Canavanine</td>
<td>13 ± 1</td>
<td>137 ± 25</td>
<td>29 ± 10</td>
</tr>
<tr>
<td>Homoarginine</td>
<td>26 ± 2</td>
<td>297 ± 45</td>
<td>16 ± 4</td>
</tr>
<tr>
<td>2-Amino-3-guanidinopropionate</td>
<td>67 ± 4</td>
<td>33 ± 4</td>
<td></td>
</tr>
<tr>
<td>Miscellaneous</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Arginine</td>
<td>31 ± 4</td>
<td>340 ± 53</td>
<td>32 ± 5</td>
</tr>
</tbody>
</table>

(*N*⁶-nitroarginine) resulted in very little inhibition. Modification of the methylene side chain of arginine, as in *L*-homoarginine and *L*-canavanine, resulted in strong inhibition of arginine uptake. Non-polar amino acids such as *L*-norvaline and *L*-alanine did not inhibit arginine uptake. Finally, the *D*-isomer of arginine appeared to interact with the arginine transporter.

Graphical determination of inhibitor constants (*K*_i) from Hunter & Downs (1945) plots showed that the six analogues chosen were all competitive inhibitors of arginine uptake. The *K*_i values for these analogues are shown in Table 2. *N*⁶-Methyl-L-arginine appeared to be an excellent ligand for the arginine transporter, with a *K*_i of 18 μM, almost identical to the *K*_m for arginine uptake. Other analogues demonstrated *K*_i values ranging from 140 μM for *L*-canavanine to 340 μM for *D*-arginine.

**Arginine-ornithine exchange**

HPLC amino acid analysis was used to investigate the possibility of an arginine-ornithine antiport operating in *G. intestinalis*. The accumulation of a number of arginine analogues (at 1 mM external concentration) was monitored at 25 °C over a 4 min time period. The analogues chosen were those that were most effective in inhibiting arginine uptake. In addition any concomitant efflux of intracellular ornithine was measured. A rep-
representative time course is shown in Fig. 2. The accumulation of arginine analogue over a 60 s time period and the corresponding efflux of intracellular ornithine are given in Table 3, as is the ratio of analogue accumulated:ornithine effluxed over this time period. The four chosen analogues (N\textsuperscript{\beta}-methylarginine, N\textsuperscript{\epsilon}-methyllysine, D-arginine and L-homoarginine) were all accumulated by G. intestinalis over a 4 min time period. No evidence for metabolism of the analogues was observed over this period on the basis of amino acid analysis. However, amino acid analysis revealed that L-canavanine was accumulated and subsequently metabolized by the parasite, to a compound that appeared to be the product of deamination by arginine deiminase. Therefore canavanine was not used in these exchange studies. The ratio of arginine analogue accumulated: ornithine effluxed at the 60 s time point was approximately 1:0 for all four non-metabolized analogues, suggesting the stoichiometric exchange of ornithine for arginine. The mean ratio for all experiments was 1:08 ± 0:09 (n = 8). As negative controls, 4-guanidinobutyric acid and L-norvaline uptake was examined. 4-Guanidinobutyric acid, which does not compete for arginine uptake, was not accumulated, and as such there was no concomitant efflux of ornithine. L-Norvaline, which is also not an inhibitor of arginine uptake, was taken up by the cells, but there was no concomitant release of intracellular ornithine.

**Kinetic studies of arginine deiminase**

The method of Prescott & Jones (1969) was found to be of suitable sensitivity, in combination with short assay times (2-5 min at 37 °C) and 40-60 μg protein in the enzyme assay. The activity of arginine deiminase over a concentration range of 0-07-1 mM showed typical saturation kinetics. From three separate determinations, computer analysis based on the Michaelis–Menten equation gave a K\textsubscript{m} of 0.16 ± 0.06 mM for arginine and a V\textsubscript{max} of 547 ± 124 nmol min\textsuperscript{-1} (mg protein)\textsuperscript{-1}. Assay linearity over 2.5 min was established at both the highest and lowest arginine concentrations. To determine the substrate specificity of arginine deiminase, inhibition experiments were performed in which the activity of arginine deiminase with 1 mM arginine over a 10 min period at 37 °C was monitored in the presence and absence of potential substrates (10 mM final concentration). The results are shown in Table 2. The overall pattern of inhibition of arginine deiminase was similar to that of arginine transport, but with a number of striking exceptions. L-Lysine was a poor inhibitor of arginine deiminase, but was a good inhibitor of arginine uptake.

**Table 3. Amount of amino acid accumulated and ornithine effluxed from G. intestinalis trophozoites at 25 °C over a 60 s time period**

<table>
<thead>
<tr>
<th>Amino acid</th>
<th>Amino acid influx [nmol (mg protein)\textsuperscript{-1}]</th>
<th>Ornithine efflux [nmol (mg protein)\textsuperscript{-1}]</th>
<th>Ratio influx:efflux</th>
</tr>
</thead>
<tbody>
<tr>
<td>D-Arginine</td>
<td>174, 217</td>
<td>188, 186</td>
<td>0.93, 1.17</td>
</tr>
<tr>
<td>N\textsuperscript{\beta}-Methylarginine</td>
<td>100, 108</td>
<td>90, 91</td>
<td>1.11, 1.19</td>
</tr>
<tr>
<td>N\textsuperscript{\epsilon}-Methyllysine</td>
<td>148, 190</td>
<td>152, 177</td>
<td>0.97, 1.07</td>
</tr>
<tr>
<td>Homoarginine</td>
<td>165, 212</td>
<td>153, 187</td>
<td>1.08, 1.13</td>
</tr>
<tr>
<td>4-Guanidinobutyric acid</td>
<td>0, 0</td>
<td>0, 1</td>
<td></td>
</tr>
<tr>
<td>Norvaline</td>
<td>5, 2, 24</td>
<td>0, 4</td>
<td></td>
</tr>
</tbody>
</table>
N\textsuperscript{G}-Nitroarginine, which gave little inhibition of arginine uptake, appeared to be a potent inhibitor of arginine deiminase. Finally, two of the best inhibitors of arginine uptake, N\textsuperscript{G}-methyl-L-arginine and N\textsuperscript{e}-methyl-L-lysine, did not inhibit arginine deiminase.

**DISCUSSION**

L-Arginine is an important fuel in the overall energy metabolism of *G. intestinalis* (Edwards et al., 1992) and rapid flux through the arginine dihydrolase pathway requires a highly efficient transport system for the accumulation of arginine. Since L-arginine can be metabolized in *G. intestinalis* by the arginine dihydrolase pathway (Schofield et al., 1992), to distinguish between arginine transport and uptake, it was initially necessary to quantify the extent of metabolism over a representative time course. The observed rate of arginine metabolism was most unexpected, with 85% of the accumulated arginine being metabolized to citrulline within 4 s, and 97% within 30 s. However, further conversion of citrulline to ornithine was minimal. For uptake of radiolabel to be representative of transport of a radiolabelled molecule it is necessary either to have minimal metabolism of the transported molecule or to have complete metabolism to a compound (or compounds) that retain the label and are accumulated within the cell. Most investigations of transport try to adhere to the minimal metabolism criterion. However, the latter situation, which is equivalent to a coupled enzyme assay system, is equally valid. In this case, the activity of the second step, arginine deiminase, is far greater than that of the first step, the arginine transporter. Since less than 2% of the transported arginine had been metabolized to intracellular ornithine at the 4 s timepoint, with the remainder primarily as intracellular citrulline, the uptake of radiolabel from external \(^3\)H was representative of arginine transport. Over longer time periods, some of the radiolabel was detectable as extracellular: radiolabelled ornithine that had exchanged with the transported arginine, but nonetheless only in small quantities (less than 20% of the accumulated radiolabel after 30 s).

Our observations have demonstrated the presence of an arginine transporter with a high affinity for arginine \(K_m\) 15 \(\mu\)M and large capacity \([V_{max} 76 \text{nmol min}^{-1} (\text{mg protein})^{-1}]\) in *G. intestinalis*. Although some kinetic data are available for arginine transport in prokaryotes, the availability of comparative values for arginine transport in other parasitic protozoa is limited. The Trypanosomatidae family transport arginine via carrier-mediated mechanisms but all demonstrate affinities much lower than that reported here for *Giardia*, e.g. \(K_m\) values of 0-8 mM for *Trypanosoma lewisi* (Manjra & Dusanic, 1972) and 0-71 mM for *Trypanosoma gambiens* (Hansen, 1979). Whereas these trypanosomatid arginine transport systems have a non-saturable component of influx, such a system does not appear to be present in *G. intestinalis*. With respect to other amino acid transport systems described from parasitic protozoa, the *G. intestinalis* arginine transporter displays the highest affinity and maximal velocity for its substrate (Fricker et al., 1984; Bonay & Cohen, 1983; Law & Mukkada, 1979). This may reflect the relative importance of arginine metabolism to the overall energy economy of *G. intestinalis*, compared to amino acid metabolism in these other parasites.

Substrate specificity studies indicated that there are three major structural parameters governing recognition of the transporter with the ligand. These factors are: (a) the presence of the \(\alpha\)-amino and \(\alpha\)-carboxyl moiety; (b) the distal basic group, and (c) the methylene chain length between this distal basic group and the \(\alpha\)-amino \(\alpha\)-carboxyl moiety. Blocking the \(\alpha\)-amino group, as in N\textsuperscript{G} acetylarginine and N\textsuperscript{e}-carbamylarginine, prevents substrate recognition. Likewise, removal of the \(\alpha\)-carboxyl group, as in the diamines putrescine and agmatine, substantially reduces ligand recognition. The second parameter is the side chain length. For the naturally occurring amino acids, the two most effective as inhibitors are lysine (5 carbons between the groups) and ornithine (4 carbon chain). Further reduction of this chain length, to 2,4-diaminobutyric acid and 2,3-diaminopropionic acid, successively eliminates ligand recognition. The optimum chain length appears to be a span of 4 to 5 carbon atoms. The strong inhibition by homoarginine (5 carbon span) and canavanine (a 3 carbon span incorporating an ether linkage) are consistent with these binding requirements. Such a chain length criterion has also been described for mammalian arginine transport systems (White et al., 1982; White & Christensen, 1982). The third principal parameter dictating recognition is the presence of a distal basic group. There appears to be some flexibility in this site since substitution of the guanidino group with an amino group does not prevent recognition (as in the case of ornithine and lysine). Substitution on the guanidino group itself results in diverse effects. Methylation, as in N\textsuperscript{G}-methylarginine, did not prevent ligand binding, which is also true for mammalian arginine transport (Bogle et al., 1992; Westergaard et al., 1993). However, substitution of the much bulkier and more polar nitro group, as in N\textsuperscript{G}-nitroarginine, prevents recognition, as is also the case for mammalian cells (Bogle et al., 1992; Westergaard et al., 1993). As to stereochemical requirements for substrate recognition, the \(\beta\)-isomer of arginine competitively inhibited the transport of L-arginine, albeit with a lower affinity for the binding site than the L-isomer, suggesting that spatial arrangement of the \(\alpha\)-carbon groups is not of crucial importance in ligand binding. Enzymic assay with octopine dehydrogenase ruled out the possibility that the activity exhibited by \(\beta\)-arginine was due to contamination by L-arginine, and a non-metabolized intracellular arginine pool appeared when trophozoites were incubated with \(\beta\)-arginine. Overall, the ligand binding characteristics of the arginine transporter in *G. intestinalis* are very similar to those of mammalian cells. However, for protozoan parasites there have been very few inhibition studies to date, which prevents meaningful comparison with the giardial transporter.

From amino acid analysis, it appears that the arginine transporter is an arginine-ornithine antiporter. Exchange between intracellular ornithine and a number of extra-
Arginine transport and metabolism in G. intestinalis

cellular arginine analogues, including N\textsuperscript{G}-methylarginine and homoarginine, was observed. In such studies, it was important to use non-metabolizable analogues and this was concurrently monitored by amino acid analysis. Over a 60 s time period, the amount of accumulated arginine analogue was equimolar with the amount of ornithine released from the cell. The stoichiometric arginine:ornithine exchange reported here is consistent with in vivo growth experiment results, showing that for each mole of arginine consumed from the medium, one mole of ornithine is released into the growth medium (Edwards et al., 1992). It is metabolically sensible for such a transport system to be operational in G. intestinalis, since the arginine dihydrolase pathway only produces one mole of ATP per mole of arginine consumed. Thus, a non-energy dependent transport system for arginine is not wasteful of the metabolic energy generated from the degradation of translocated arginine. Such an arginine-ornithine antiporter has previously been demonstrated in the bacterium Streptococcus lactis, which also has a functional arginine dihydrolase pathway (Driessen et al., 1987).

Since the transported arginine was so rapidly metabolized by arginine deiminase, it was necessary to define the kinetic properties of this enzyme. Preliminary investigations using the chromogenic assay system of Boyde & Rahmatullah (1980) for citrulline determination were unsatisfactory due to the insensitivity of this method at the low arginine concentrations required for the kinetic studies. The colorimetric assay of Prescott & Jones (1969) was found to be more sensitive and reproducible, especially at the lower arginine concentrations used. Using this method, the \( K_m \) of arginine deiminase for arginine was 0.16 mM. This is very similar to values published for this enzyme from other organisms, including Mycoplasma arginini (0.2 mM; Takaku et al., 1992), Pseudomonas putida (0.2 mM; Shibatani et al., 1975) and Tetrahymena thermophila (0.41 mM; Eichler, 1989). The \( V_{\text{max}} \) of arginine deiminase found in this study was greater than values we have previously reported (Schofield et al., 1992); this observed increase is due to optimization of the assay conditions cited above. The individual \( V_{\text{max}} \) values for the three enzymes of the arginine dihydrolase pathway expressed as nmol min\(^{-1}\) (mg protein\(^{-1}\)) are: arginine deiminase, 550 (at 37 °C); ornithine transcarbamoylase, 170 (at 37 °C); and carbamate kinase, 2100 (at 30 °C). These activities are consistent with ornithine transcarbamoylase, and not arginine deiminase, being rate limiting and with the observed accumulation of citrulline in arginine uptake experiments.

The substrate specificity for arginine deiminase suggests that the same three structural constraints operating for the arginine transporter ligand binding also apply to substrate recognition for arginine deiminase from G. intestinalis. However, although there are some similarities in the binding requirements, there are also some marked differences. For the arginine deiminase, blocking or removal of the \( \alpha \)-amino group prevents recognition, but absence of the \( \alpha \)-carboxyl is tolerated in that agmatine and putrescine compete with arginine for the active site. Secondly, the carbon chain length between the guanidino group and the \( \alpha \)-amino \( \alpha \)-carboxyl moiety is not critical for enzyme activity. Shortening the chain length to two (2-amino-3-guanidinopropionic acid) and lengthening the carbon chain length to five (homoarginine) does not destroy recognition. Such binding requirements have been reported for arginine deiminase from Euglena gracilis (Park et al., 1984) and Pseudomonas putida (Shibatani et al., 1975), but they differ from those of the arginine deiminase of Mycoplasma arbofleidis (Smith et al., 1978). However, when the distal basic group is an amino group, the chain length of the analogue is more critical. Recognition is optimal with a 3 to 4 carbon chain substrate, in that ornithine and 2,4-diaminobutyric acid inhibit arginine binding, whereas lysine and 2,3-diaminopropionic acid do not. Modification to the guanidino (or side chain amino) group seems to be the critical factor differentiating between arginine transport and arginine metabolism by arginine deiminase. \( N^G \)-Nitroarginine potently inhibits arginine deiminase, whereas \( N^G \)-methylarginine (and \( N^G \)-methyllysine) have no effect; for the transporter the opposite occurs. Clearly, these differential effects can be used to advantage in distinguishing between arginine transport and metabolism and their individual characteristics. Surprisingly, \( \delta \)-arginine is a ligand for arginine deiminase, implying that for the enzyme, like the transporter, stereochemical conformation is not crucial. However, \( \delta \)-arginine was not a substrate for arginine deiminase. A similar effect has been observed for arginine deiminase from E. gracilis (Park et al., 1984), but \( \delta \)-arginine had no effect on the deiminase from P. putida (Shibatani et al., 1975) or M. arbofleidis (Smith et al., 1978). Overall, the inhibition pattern of arginine deiminase from G. intestinalis closely resembles that reported for deiminases from prokaryotic organisms, suggesting that they have common structural requirements for catalytic activity.

In summary, the combination of the high-activity arginine transporter and the high affinity for arginine coupled to its operation as an arginine-ornithine antiport ensures substantial uptake of arginine for the rapid proliferative growth of G. intestinalis. These observations support the view that this protozoan parasite displays prokaryotic features, and occupies a transition between the prokaryotic and eukaryotic kingdoms.

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