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Altered Expression of Autoimmune Regulator in Infant Down Syndrome Thymus, a Possible Contributor to an Autoimmune Phenotype

Gabriel Skogberg,* Vanja Lundberg,* Susanne Lindgren,* Judith Gudmundsdottir, †‡ Kerstin Sandström, † Olle Kämpe, † Göran Annerén, † Jan Gustafsson, † Jan Sunnegårdh, † Sjoerd van der Post,** Eshjörn Telemo,* Martin Berglund,* and Olov Ekwall,* †‡

Down syndrome (DS), caused by trisomy of chromosome 21, is associated with immunological dysfunctions such as increased frequency of infections and autoimmune diseases. Patients with DS share clinical features, such as autoimmune manifestations and specific autoantibodies, with patients affected by autoimmune polyendocrine syndrome type 1. Autoimmune polyendocrine syndrome type 1 is caused by mutations in the autoimmune regulator (AIRE) gene, located on chromosome 21, which regulates the expression of tissue-restricted Ags (TRAs) in thymic epithelial cells. We investigated the expression of AIRE and TRAs in DS and control thymic tissue using quantitative PCR. AIRE mRNA levels were elevated in thymic tissue from DS patients, and trends toward increased expression of the AIRE-controlled genes INSULIN and CHRNA1 were found. Immunohistochemical stainings showed altered cell composition and architecture of the thymic medulla in DS individuals with increased frequencies of AIRE-positive medullary epithelial cells and CD11c-positive dendritic cells as well as enlarged Hassall’s corpuscles. In addition, we evaluated the proteomic profile of thymic exosomes in DS individuals and controls. DS exosomes carried a broader protein pool and also a larger pool of unique TRAs compared with control exosomes. In conclusion, the increased AIRE gene dose in DS could contribute to an autoimmune phenotype through multiple AIRE-mediated effects on homeostasis and function of thymic epithelial cells that affect thymic selection processes. The Journal of Immunology, 2014, 193: 2187–2195.

Down syndrome (DS), or trisomy 21, is associated with an increased frequency of autoimmune disorders such as autoimmune hypothyroidism (1), hyperthyroidism (2), insulin-dependent diabetes mellitus (IDDM) (3), alopecia, and celiac disease (4). The mechanism underlying the high frequency of autoimmune manifestations in DS is not known. The human AIRE gene is located on chromosome 21 position q22.3 and codes for a transcription factor that in mice has been shown to control the expression of numerous TRAs in medullary thymic epithelial cells (mTEC) (5). The tissue-restricted Ag (TRA) expression is crucial for the negative selection of developing thymocytes with a high affinity for TRAs are eliminated within the thymus before they reach the periphery. Aire also has been shown to have other functions in mTECs such as controlling Ag presentation (6), chemokine production (7), and maturation (8–10). Thus, an altered expression of AIRE could have a complex influence on thymic selection including changes in the expression of TRAs, the presentation of TRAs, the movement of thymocytes, and the maturation of mTECs, possibly resulting in higher rates of autoimmune manifestations in DS patients. An additional link between DS and AIRE is that DS patients and patients with autoimmune polyendocrine syndrome type 1 (APS1), which is an autosomal recessive disease caused by mutations in AIRE, share specific autoantibodies. Autoantibodies against aromatic l-amin acid decarboxylase and cytochrome P450A2 have not been found in other patient groups and are so far unique for DS and APS1 (11), except for aromatic l-amin acid decarboxylase autoantibodies found in a small subgroup of patients with isolated Addison’s disease (12). Previous investigations of DS thymic tissue have described a decrease in thymic size (13), altered thymocyte subpopulations (14), increased thymocyte depletion, markedly enlarged Hassall’s corpuscles (HCs) (15), decreased thymic output (16), and a decrease in the number of AIRE+ cells in the medullary region (17).

The thymic tissue also produce exosomes (18, 19), which are small membrane-bound vesicles that are released by various types of cells. Exosomes are important for intercellular communication.

Abbreviations used in this article: AIRE, autoimmune regulator; APS1, autoimmune polyendocrine syndrome type 1; DC, dendritic cell; DS, Down syndrome; HC, Hassall’s corpuscle; HPA: human protein atlas; IDDM, insulin-dependent diabetes mellitus; IHC, immunohistochemistry; IVL, INVOLUCRIN; K5, keratin 5; MS, mass spectrometry, qPCR, quantitative PCR; TEC, medullary thymic epithelial cell; Treg, regulatory T cell; TG, thyroglobulin; TPO, thyroid peroxidase; TRA, tissue-restricted Ag.

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and and show proteins, nucleic acids, and lipids (20). We have previously shown that exosomes containing TRAs are abundant in human thymic tissue (18), but exosomes from DS thymuses have previously not been studied.

On the basis of these observations, we analyzed thymic tissue from individuals with DS and controls without DS regarding the expression of AIRE/AIRE and selected TRAs, thymic cell sub-populations, and proteomic profile of thymic exosomes.

**Materials and Methods**

**Collection of human thymic tissue**

Human thymus removed during cardiac surgery of children 0–6 mo of age with DS and without DS at the Sahlgrenska University Hospital (Gothenburg, Sweden) were collected. The tissue was immediately put in 4% paraformaldehyde or RPMI 1640 medium (In Vitrogen, Paisley, Scotland) on ice. Parents gave informed consent, and the study was approved by the local ethics committee (number 477-05, 2006-12-18). Thymic tissue for RNA extraction was frozen in 50-ml tubes with 50% RPMI 1640 medium (In Vitrogen), 40% FBS, and 10% DMSO (both Sigma-Aldrich, St. Louis, MO) stepwise frozen from −20 to −85°C.

**Thymic thawing RNA isolation and cDNA preparation**

Thymic tissue was thawed in a 37°C water bath and RNA from each thymus was isolated from six different 20-mg pieces. The thymic tissue was pressed against a 100-μm mesh, followed by extensive washing with PBS to flush away thymocytes. To assess the enrichment of stromal cells in the preparation, expression analysis of TE markers FONXI and K5 (5) as well as the thymocyte marker CD3γ was performed using RT-quantitative PCR (qPCR) (see below). Remaining tissue was placed in RLT lysis buffer (1% 2-ME), followed by lysis in QiaGen TissueLyser (Qiagen), according to the manufacturer’s instructions.

**RT-qPCR**

AIRE (Hs00230829_m1), INSULIN (Hs02741908_m1), GAPDH (Hs99999905_m1), THYROGLOBULIN (TG) (Hs00968962_m1), THYROID Peroxidase (TPO) (Hs00892519_m1), GADI (Hs01656893_m1), CHRNA1 (Hs00175578_m1), ABAT (Hs01026288_m1), FONXI (Hs00880965_m1), K5 (Hs00031851_m1), CD3γ (Hs00926186_m1), and XCL1 (Hs00751481_s1) TaqMan assays 1 μl/reaction (Life Technologies, Foster City, CA), RNAse-free water 7 μl/reaction, using a calibrator sample. The samples were run in triplicates, and single samples were set to taxonomy Human, MS mass tolerance 5 ppm, 0.5 Da MS/MS mass tolerance, 1% false discovery rate for both taxonomy and ion type. The most intense double or triple protonated ions were selected for fragmentation in the linear ion trap using collision-induced dissociation fragmentation and afterwards excluded for selection for 60 s. Spectral data were searched using Mascot (version 2.3; Matrix Science) against the SwissProt database (release 2011_04, 20075 entries). Search parameters were set to taxonomy Human, MS mass tolerance 5 ppm, 0.5 Da MS/MS mass tolerance, trypsin allowing one missed cleavage, fixed modification of propionamidate on cysteine and as variable modifications oxidized methionine and acetylation at protein N-terminal. The threshold for protein identification was set to <1% false discovery rate both for peptide and protein identification based on a minimum of one unique peptide. Overlap in protein identifications between the samples was determined by Venn diagrams generated using the gplots package in R (www.R-project.org). Expression of the identified proteins for 80 different tissue types was extracted from the human protein atlas (HPA) version 13 (22) when available, converted to numerical values (0–3 for negative, weak, moderate and strong expression respectively and missing observations as blanks), and evaluated by hierarchical cluster analysis, using “Euclidean distance” as similarity metric combined with complete linkage clustering. A TRA was defined when expressed in five tissue cell types or less according to the HPA. Known thymocyte proteins and proteins with an immune expression profile (bone marrow, lymph node, tonsil, or spleen expression) in the HPA were not considered TRAs.

**Isolation of exosomes from thymic explants**

Exosomes were isolated as previously described (18) from 2 DS thymus and two control thymus. Briefly, 1–2 g thymic tissue from each patient was cut into small pieces and incubated in RPMI 1640 medium (Invitrogen) with 5% exosome-depleted FBS (Sigma-Aldrich), 2 mM t-glutamine (Invitrogen), and penicillin/streptomycin (Sigma-Aldrich) for 8 h. The cultures were centrifuged for 10 min at 850 × g, and the supernatants were collected and centrifuged for another 15 min at 3000 × g to remove cell debris. Furthermore, the supernatants were spun for 30 min at 10,000 × g, followed by filtration through 0.2-μm filter. Finally the supernatants were ultracentrifuged for 70 min at 100,000 × g to pellet the exosomes. The pellets were washed in PBS and repelleted with an additional 100,000 × g centrifugation. Exosome concentration was determined with the Bradford protein concentration assay (Bio-Rad, Hercules, CA).

**Proteomic analysis of isolated exosomes**

Isolated exosomes, 50 μg/condition, were analyzed by one-dimensional SDS-PAGE (4–12% Bis-Tris Novex mini-gel; Invitrogen) and visualizing using Coomassie blue staining (Novex; Invitrogen). The full gel lanes were excised and divided into equal slices and subjected to in-gel protein digestion with trypsin overnight at 37°C (21). Extracted peptides were dried under vacuum, reconstituted in 15 μl 0.2% formic acid, and 2-μl sample injections were made with an HTC-PAL autosampler (CTC Analytics, Zwingen, Switzerland) connected to an Agilent 1200 binary pump (Agilent Technologies, Palo Alto, CA). The peptides were trapped on a precolumn (4.6 × 50 mm i.d.) and separated on a 200 × 3.0 mm analytical column packed with 4-μm Reprosil-Pur C18AQ particles (Dr. Maisch, Ammerbuch, Germany). Peptides were loaded in 0.2% formic acid and separated using a 40-min gradient 5–35% toward mobile phase B (acetonitrile). Mass spectrometry (MS) analysis was performed on an LTQ-Orbitrap operated in a data-dependent mode automatically switching between MS and MS/MS mode. Full MS scans were acquired in the orbitrap (from 400 to 1400 m/z) and followed by 100-ppm mass isolation, and the most intense double or triple protonated ions were selected for fragmentation in the linear ion trap using collision-induced dissociation fragmentation and afterwards excluded for selection for 60 s. Spectral data were searched using Mascot (version 2.3; Matrix Science) against the SwissProt database (release 2011_04, 20075 entries). Search parameters were set to taxonomy Human, MS mass tolerance 5 ppm, 0.5 Da MS/MS mass tolerance, trypsin allowing one missed cleavage, fixed modification of propionamidate on cysteine and as variable modifications oxidized methionine and acetylation at protein N-terminal. The threshold for protein identification was set to <1% false discovery rate both for peptide and protein identification based on a minimum of one unique peptide. Overlap in protein identifications between the samples was determined by Venn diagrams generated using the gplots package in R (www.R-project.org). Expression of the identified proteins for 80 different tissue types was extracted from the human protein atlas (HPA) version 13 (22) when available, converted to numerical values (0–3 for negative, weak, moderate and strong expression respectively and missing observations as blanks), and evaluated by hierarchical cluster analysis, using “Euclidean distance” as similarity metric combined with complete linkage clustering. A TRA was defined when expressed in five tissue cell types or less according to the HPA. Known thymocyte proteins and proteins with an immune expression profile (bone marrow, lymph node, tonsil, or spleen expression) in the HPA were not considered TRAs.

**Statistics**

Values are presented as median with interquartile range. Data were statistically evaluated using an unpaired Mann–Whitney U test and a Spearman rank correlation coefficient. Values of p < 0.05 were considered as statistically significant. All statistic tests were performed using GraphPad Prism software.
FIGURE 1. Increased expression of AIRE in DS thymuses. Isolated RNA from DS and control thymuses analyzed by RT-qPCR. GAPDH was used as endogenous control and a calibrator sample was used for comparison between plates. (A) AIRE, INSULIN, CHRNA1, TG, TPO, GAD1, and ATB4B (n = 5+5). Data are presented as median with interquartile range per group based on the median value from each individual and were analyzed using Mann–Whitney U test. A value of $p \leq 0.05$ was considered as statistically significant. (B) Data points for each piece of tissue in each individual for expression of AIRE (left panel), INS (middle panel), and CHRNA1 (right panel). (C) Individual specific expression of AIRE (*) and INSULIN (○, top left panel) and CHRNA1 (○, bottom left panel), based on median values from the six pieces of thymic tissue presented with interquartile range. Top right panel, Correlation of INSULIN expression versus AIRE expression ($r = 0.64$, $p = 0.054$, $n = 10$). Bottom right panel, correlation of CHRNA1 expression versus AIRE expression ($r = 0.77$, $p = 0.0126$, $n = 10$) in DS individuals (●) and controls (○).
Results

AIRE, INSULIN, and CHRNA1 are overexpressed in DS thymic tissue

To assess the expression of AIRE and TRAs in the thymic tissue, we pressed and washed the thymi to remove thymocytes and thus enrich the thymic stroma. AIRE expression was significantly increased in DS patients compared with controls (p = 0.0079) (Fig. 1A). Trends toward increased expression also were found for INSULIN (p = 0.056) and CHRNA1 (p = 0.056) in DS patients compared with controls (Fig. 1A). For AIRE, INSULIN, and

![Image of IHC images showing increased expression of AIRE, CD11c, and IVL in DS thymic tissue.](image-url)
in others regardless of group. In the medulla, both small and larger
of small positive cells in cortex while they were completely absent
both in cortex and medulla. Some individuals displayed a network

Increased frequency of AIRE+ mTECs, CD11c+ dendritic cells,
and enlarged IVL+ HCs characterizes thymic medulla in DS
To investigate whether the overexpression of AIRE also resulted in
more cells expressing the AIRE protein, we performed immuno-
histochemistry (IHC) on DS and control thymic tissue sections.
The investigated area was medulla, excluding HC area, and for
CASPASE3, the investigated area was cortex plus medulla ex-
cluding HC area. The number of AIRE+ cells per square millimeter
were significantly increased in DS thymic medullas compared with
controls (DS\text{median} = 174.5, \text{Control}_{\text{median}} = 127, p = 0.0084)
(Fig. 2A, 2B). Notable also was that AIRE expression adjacent to
HCs was more frequently seen in DS patients. Furthermore,
staining for the dendritic cell (DC) marker CD11c revealed higher
number of CD11c+ cells per square millimeter medulla in the DS
group (DS\text{median} = 268, \text{Control}_{\text{median}} = 178, p = 0.022) (Fig. 2C,
2D). No differences were found in the number of FOXP3+ cells
per square millimeter (DS\text{median} = 1045, \text{Control}_{\text{median}} = 1015, p =
0.84), K5+ (percent stained area: DS\text{median} = 12.3, \text{Control}_{\text{median}} =
15.5, p = 0.56), or CASPASE 3+ cells per square millimeter
(DS\text{median} = 118, \text{Control}_{\text{median}} = 140.5, p = 0.24) between DS
and controls (Fig. 2E–J). Notable, however, was that DS K5+ mTECs
were more spindly and orientated in a more distinct circular pat-
tern around the HCs than corresponding cells in control stainings
(Fig. 2G, 2H). In agreement with the previously reported striking
enlargement of HCs in DS (15), we observed a markedly increased
area stained for IVL in HCs (percent stained area: DS\text{median} = 3.6,
\text{Control}_{\text{median}} = 2.2, p = 0.0040). Also, small non-HC areas within
the medullas of DS thymus were positive for IVL while com-
pletely absent in controls (Fig. 2K, 2L). Furthermore, a positive
correlation between AIRE and HC area was observed (r = 0.85,
p = 0.0001) (Fig. 3, left panel) as well as between AIRE and IVL
(r = 0.61, p = 0.02) (Fig. 3, right panel). K8 staining was present
both in cortex and medulla. Some individuals displayed a network
of small positive cells in cortex while they were completely absent
in others regardless of group. In the medulla, both small and larger
cells were positive to varying extent. Also, HCs stained positive to
varying extent (data not shown).

Broader total protein profile and TRA profile in DS thymic
exosomes
To further examine the possible effects of the abnormal AIRE levels
on the thymic microenvironment, we analyzed the proteomic
content of thymic exosomes in DS and control thymi. The pro-
teomic data revealed a broader protein diversity in DS individuals
compared with controls (i.e., the pool of unique proteins for a partic-
ular sample was larger in the two DS samples compared with
the two control samples both in terms of absolute numbers
[156 and 91 for DS exosomes respective 46 and 68 for control
exosomes] and percentage [8.3 and 9.2% for DS exosomes re-
spective 3.5 and 4.0% for control exosomes]) (Figs. 4, 5). Ten
TRAs were restricted to DS thymic exosomes, whereas none was
exclusive for control exosomes (Table I).
Five of 283 proteins (run–related transcription factor 1,
ubiquitin–conjugating enzyme E2G 2, lanosterol synthase,
chromosome 21 open reading frame 2, and small ubiquitin–like modifier 3)
uniquely found in the DS exosomes (three dotted fields in Fig. 4)
have their corresponding coding gene on chromosome 21 (1.8%).
Among proteins unique for control exosomes (three fields to upper
left in Fig. 4), 1 of 135 (MORC Family CW-Type Zinc Finger 3,
21q22.13) has its coding gene placed on chromosome 21 (0.7%).
This can be compared with the fact that the 230 genes located at

FIGURE 4. Skewed proteomic profile in DS thymic exosomes. Venn
diagram of protein content in thymic exosomes from two DS individuals
and two controls show an increased number and percentage of proteins
exclusively found in exosomes from DS individuals. DS individuals (DS1
and DS2) display the highest numbers (156 and 91 for DS versus 46 and 68
for controls) and percentages (8.3 and 9.2% for DS exosomes re-
spective 3.5 and 4.0% for control exosomes) of proteins found exclusively in
respective exosome sample (n = 2±2).
chromosome 21 represents ~1.2% of the 20,000 genes in the genome.

The Alzheimer’s disease associated protein DREBRIN1 (DBN1) (23) was found in thymic exosomes from both controls but in neither of the DS patients (Fig. 5).

**Discussion**

In this study, we found that patients with DS who have an extra copy of the AIRE gene also have an increased expression of AIRE at both mRNA and protein level in the thymus. This may alter thymic selection processes and affect the susceptibility for autoimmune diseases in DS patients. AIRE expression in mTECs is described to have multiple effects on various thymic functions such as TRA expression (5), mTEC differentiation (8–10), Ag presentation (6), chemokine production (7), and thymus-derived T regulatory cell (Treg) selection (24). Therefore, the net effect of an increased AIRE expression on the thymus is complex and not easily predicted.

The first aim of the current study was to investigate whether the increased copy number of AIRE in DS was accompanied by in-
increased levels of AIRE mRNA in thymic tissue. Real-time PCR measurements showed that the AIRE mRNA level was increased in DS patients compared with controls (Fig. 1A). For these experiments, the study was designed to mimic the total thymic expression in DS and controls. Although thymocytes were washed away, the stromal compartment was kept intact, and information was obtained from six different parts of each thymus yielding information on a whole organ level rather than sorted cell level, which has been reported thoroughly elsewhere (25, 26). However, because many studies have shown that mTECs are the major cell type expressing AIRE in the thymus, our results still ought to reflect an increased expression of AIRE in the mTEC population.

Previous work by Peterson et al. (27) showed that overexpression of murine Aire in vitro results in an increased expression of TRAs. To examine whether the increased expression of AIRE in DS thymus leads to an altered expression of TRAs, the expression of both AIRE-dependent and AIRE-independent TRAs was analyzed. One predicted effect of AIRE overexpression is an increased expression of INSULIN, a known AIRE-dependent TRA, and in agreement with this a trend toward an increased expression of INSULIN in DS and an overall positive correlation between AIRE expression and INSULIN expression was seen (Fig. 1). This was also the case for AIRE-dependent CHRNA1, which codes for the α-subunit of the nicotinic acetylcholine receptor (Fig. 1) (28). For other TRAs reported not to be Aire dependent in mice, such as tg (29) and gad67 (5), the overexpression of AIRE did not seem to affect the expression level of the corresponding human genes Tg and GAD1 in DS thymic tissue (Fig. 1A). For TPO, a TRA with an enigmatic relation to Aire (30) and ATB4β, which is reported to be AIRE dependent (28), AIRE dependency was not confirmed in the DS phenotype (Fig. 1A). The reason could be that the effects of trisomy 21, other than the trisomy of AIRE, affect the expression levels of TPO and ATB4β, overcoming their possible AIRE dependency.

Immunohistochemical stainings confirmed the increased expression of AIRE on the mRNA level with more cells expressing AIRE protein in the thymic medulla in the DS group (Fig. 2A, 2B). At the same time, no difference was seen in the relative staining of K5 in the medullary regions, suggesting that the elevated number of AIRE+ cells per square millimeter in DS reflects a larger proportion of AIRE+ mTECs rather than an altered total number of mTECs. This could be explained by a general increase of AIRE expression in mTECs making a higher frequency of AIRE+ mTECs detectable by the IHC technique. An alternative explanation is that the mTEC turnover is affected so that a larger proportion of mTECs are in an AIRE expressing late phase of mTEC differentiation. The latter explanation is supported by studies showing that Aire promotes terminal differentiation of mTECs (31).

In a contrasting study, Lima et al. (17) demonstrated decreased protein expression of AIRE in thymic tissue from DS patients compared with controls. This discrepancy could be because of differences in the study design. In the current study, thymic tissue was collected from children of 0–6 mo of age, whereas Lima et al. (17) included thymic tissue from patients from 4 mo to 12 y of age, with the youngest group examined being 4 mo to 1 y of age. Differences in the IHC data could also in part be explained by the fact that in the current study the HC area was excluded from the medullary area when counting AIRE+ cells, whereas Lima et al. (17) use the whole “medullary region.” This could be of importance because, as shown in this and other studies, the HCs are massively enlarged in DS thymus compared with controls. Thus, if HCs are included in the medullary area, the number of AIRE+ cells per square millimeter will decrease in the DS group compared with the control group.

The results of the current study are strengthened by a study by Sabater et al. (32) in which they investigated the effect of IDDM2 alleles and AIRE levels on thymic INSULIN expression. In their material, the individual with the highest expression of both AIRE and INSULIN was a 6-y-old patient with DS, this despite the fact that the patient had a low classIII/classII IDDM2 ratio with classIII being the protective allele associated with higher INSULIN expression (this was the only DS patient in the study) (32).

The enlarged HCs seen in DS thymus also suggest that the increased AIRE expression in DS is affecting mTEC maturation (Fig. 2K, 2L). In addition, the increased staining of IVL seen in DS thymus points to an increased degree of epithelial cell turnover, because IVL is mainly present in terminally differentiated epithelial cells. Furthermore, as a comparison, Aire knockout mice have more mTECs, smaller HCs, and less I VL (33). Because Aire has been suggested to drive mTEC maturation into a post-TRA expression state characterized by formation of HCs (8), it is interesting to note that the increased AIRE expression and the elevated number of AIRE+ cells per square millimeter in DS thymus is accompanied by enlarged HCs and increased I VL expression. Hence, the enlarged HCs seen in DS thymus could be a result of an accelerated maturation of mTECs because of the overexpression of AIRE. These results strengthen the hypothesis that an altered AIRE expression affects the differentiation program of mTECs in DS. K8 expression was notoriously varying between individual sections and was therefore excluded from the analysis (data not shown).

Unexpectedly, the number of CD11c+c+ cells per square millimeter was elevated in DS thymic medulla compared with controls. Because it has been reported in mice that the production of the DC attracting chemokine XCL1 is Aire dependent (34), the level of XCL1 in DS and control tissue was measured. However, no difference between the two groups was found (data not shown). Possibly, elevated expression of AIRE directly influences CD11c+c+ DCs because thymic DCs in humans are known to express low levels of AIRE (26). At the same time, this CD11c+c+ population

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<td>AZGP1</td>
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<td>CACNA2D1</td>
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also could be a contributor to the higher levels of detected AIRE/aire in the DS thymus.

In agreement with previously published data that Aire does not influence the expression or function of Foxp3 (35–37), we found no difference in the frequency of FOXP3+ cells between DS and control thymus (Fig. 2E, 2F). However, a recent study of peripheral blood Tregs (CD4+CD25+FOXP3+) in DS patients reported an increased percentage of Treg, in DS compared with controls. Interestingly, at the same time, the inhibitory activity of DS CD4+CD25highCD127low was impaired in an in vitro suppression assay (38). The underlying reason for the overrepresented but less efficient Treg population is unknown.

Although the expression of CASPASE3 did not differ between DS and controls (Fig. 2I, 2J), this does not entirely rule out the possibility of altered apoptotic kinetics in negatively selected thymocytes in DS thymuses.

Because it has been speculated that exosomes may participate in the shuttling of TRAs from stromal cells to thymocytes or DCs (39, 40) and we and others have shown that thymic tissue is rich in exosomes (18, 19), we have taken interest in the characteristics and functions of thymic exosomes. When we investigated the protein profiles of thymic exosomes from DS and control patients, the proteins in exosomes from DS patients represent a greater diversity than the proteins from control exosomes (Fig. 4). This means that the group of proteins unique for each individual is larger in the DS patients compared with controls, both in terms of absolute number as well as percentage. A skewed Treg expression also is noted in the thymic exosomes because 10 TRAs are unique for DS exosomes and none for control exosomes, again indicating a broader protein expression within DS thymus (Table I). It cannot be ruled out that the increased AIRE expression in DS leads to the skewed proteomic profile, especially regarding TRA content, seen in DS thymic exosomes. The lack of DBN1 in DS exosomes in contrast to its presence in both control exosomal samples is an interesting observation because an accelerated development of Alzheimer’s disease is overrepresented among DS patients (5). A lack of DBN1 has been observed in brain tissue from Alzheimer’s patients as well as from patients with DS (41).

Given the complexity of AIRE effects on thymic function, it is not surprising that the net outcome of AIRE overexpression does not lead to the opposite effects of AIRE deficiency. As illustrated in APS1, an AIRE-deficient situation, the efficacy of the negative selection is impaired by a deficiency of AIRE-driven TRAs. In DS in contrast, the negative selection does not seem to become more efficient, even though the increased AIRE gene dose is resulting in increased levels of AIRE protein and TRAs, but rather less efficient, possibly because of AIRE functions not committed to TRA expression or other effects of the trisomy 21. An additional important factor to bear in mind is the reduced thymic organ size in DS patients (13); hence, both size and function seem impaired in this group.

As illustrated by the presence of self-reactive T cell clones in healthy individuals (42), central tolerance is a very fine tuned process, which balances at the border of autoimmunity to achieve a highly effective T cell pool against pathogens. All alterations in the prerequisites for the negative selection process and/or the production of functional Tregs may result in escape of self-reactive uncontrolled T cells into the periphery. This study has shown a number of alterations in the thymus of DS patients that could be of importance for the development of an autoimmune phenotype: 1) an increased AIRE expression; 2) a skewed thymic Ag pool with overexpression of a subgroup of Ags, such as INSULIN, as well as a lowered expression of others leading to an altered stochiometric milieu; 3) an increased frequency of AIRE expressing mTECs; 4) an accelerated mTEC maturation into apoptotic or post-AIRE stages; 5) massively enlarged, often centralized HCs, possibly affecting thymocyte movement in and into deep parts of the medulla; and 6) an accumulation of DCs, possibly altering the kinetics of Ag presentation. These alterations could all affect the selection and TCR repertoire of both conventional and regulatory T cells of importance for the development of an autoimmune phenotype in DS.

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Disclosures

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References

Isolated RNA from pieces of pressed + flushed or untreated tissue analyzed by RT-qPCR for

FOXN1, K5 and CD3γ (n=4). Enrichment of epithelial cell markers FOXN1 and K5 and

lowering of CD3γ expression is seen in pressed thymic tissues. GAPDH was used as

endogenous control. Each marker is presented as median with interquartile range.