A Canonical Correlation Analysis of AIDS Restriction Genes and Metabolic Pathways Identifies Purine Metabolism as a Key Cooperator

1. Introduction

Human immunodeficiency virus (HIV) is the basis for acquired immune deficiency syndrome (AIDS) pathogenesis and destroys the lymphoid system with prodigious replicates, which reduces a patient’s ability to survive. Since HIV was identified in the 1980s, this pathogen has taken more than 10 million people’s lives throughout the world. Researchers have developed considerable information on HIV involving immunology, virology, host genetics, and treatment over the past few decades.

Human genetics research involving the infectious disease HIV has progressed considerably after initiation of the human genome project (HGP), which is sequencing the entire human genome, both physically and functionally [1]. Many host genetic factors that influence AIDS epidemiological heterogeneity have been characterized [2–4]. From the HIV entry receptor on lymphoid cells to oncogenes in human glioblastomas, AIDS restriction genes (ARGs) are widely involved in biological pathways, and nearly 40 ARGs have been studied in depth through functional analyses [5–12]. Host genomic analysis is a key approach to studying AIDS epidemiology [13].

Further, genome, transcriptome, proteome, and metabolome biodatasets related to HIV have grown exponentially due to advanced sequencing technology. However, an integrative study on these datasets is limited in terms of understanding the complicated biological network.

Recent studies have revealed that metabolic pathways exert certain effects on the control of AIDS disease progression [14]. For example, the oxygen concentration can modulate T-cell differentiation through controlling metabolic status [15]. Metabolizing ATP to adenosine inhibits HIV-specific effector cells. Further, HIV infection is affected by dNTP hydrolysis. Efficient HIV-1 infection of CD4(+) lymphocytes requires sufficient glucose uptake via the Glut1...
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Tryptophan and phenylalanine metabolism also play an important role in HIV because HIV pathophysiology is associated with inflammatory stress due to dysregulated amino acid metabolism [17]. The HIV protein NEF impacts lipid-related metabolism through impairing cholesterol metabolism in both infected and bystander cells [18, 19]. This evidence suggests that cross talk between AIDS and the host metabolism is an important research topic that is necessary to resolve the disease mechanism and aid in therapy. Integrating biodatasets with an in-depth analysis of host AIDS restriction genes and metabolic pathways is imperative.

In the transcriptome, gene coexpression is a model for understanding how individual genes are correlated in certain conditions [20, 21]. Based on advances in this field, researchers hypothesize that the coexpression of genes in certain pathways indicates an integrative correlation between the two molecular pathways. Full genes in metabolic pathway are available for the human genome. Identifying correlations between a group of metabolic pathway genes and ARGs is a more comprehensive means for understanding integrative biodatasets. However, traditional methods using a Pearson or partial correlation are only suitable for a single gene. A canonical correlation analysis (CCA) is an efficient and powerful approach for measuring coexpression between two sets of genes. A Childhood Asthma Management Program (CAMP) study using a CCA successfully detected genetic regulatory variants [22]. Using the CCA, the glioblastoma transcriptomes of 45 patients were thoroughly analyzed to identify the glioma pathway genes [23].

In this paper, we used a CCA to analyze coexpression between ARGs and metabolic pathways from KEGG. We discuss the most important metabolic pathways coexpressed with the ARGs, which may imply strategies for AIDS diagnosis and therapy.

2. Methods

2.1. Datasets. Human genome expression datasets were downloaded from the website COPRESDB (http://coppresdb.jp/), which contains approximately 4000 experiments and expression data on 20,000 human genes. Metabolic pathway genes were downloaded from KEGG (http://www.kegg.jp/); this dataset includes 129 typical metabolic pathways with predicted genes. The ARGs were collected from published literature. Two expression datasets were generated to include metabolic pathway gene and ARG expression data, respectively (Tables 1 and 2).

2.2. Canonical Correlation Analysis. To analyze the correlations between ARG and metabolic pathway gene expression, we used a CCA, which integrates multiple correlations into a few significant correlations. This statistical method calculates the correlation between two sets of variables and generates statistically independent pairs of new variables, which are referred to as canonical variables. The linear combination of the variables creates a component of the canonical variable pair in each group of the original variables.

In this study, these variables were defined at each flag as follows: ARG expression described by \( M \) genes in the vector \( c = (c_1, c_2, \ldots, c_M) \) and metabolic pathway gene expression described by \( N \) genes in the vector \( k = (k_1, k_2, \ldots, k_M) \). The respective sets of canonical variables \( s = (s_1, s_2, \ldots, s_M) \) and \( p = (p_1, p_2, \ldots, p_M) \) are results from the linear combination of ARG and metabolic pathway gene expression. The ARG expression canonical variables are included in the vector \( s \), which is the result of the linear combination comprising the \( c \) vector (original ARGs expression) and the canonical coefficients vector as \( s = A^t c \). The vector contains the canonical variables for metabolic pathway gene expression, which result from the linear combination of the vector (original metabolic

| Table 1: HIV host genetic factor genes. |
|----------------------------------------|
| Gene symbol | Gene ID | Effect               |
|-------------|---------|----------------------|
| APOBEC3B    | 9582    | Increase infection   |
| APOBEC3G    | 60489   | Accelerates AIDS     |
| CCL11       | 6356    |                      |
| CCL17       | 6361    |                      |
| CCL18       | 6362    |                      |
| CCL2        | 6347    |                      |
| CCL4        | 6351    |                      |
| CCL5        | 6352    |                      |
| CUL5        | 8065    | Accelerates CD4 loss |
| CXCR1       | 3577    |                      |
| CXCR6       | 10663   | Accelerates AIDS     |
| DC-SIGN     | 30835   | Decreases infection  |
| DEFB1       | 1672    |                      |
| GML         | 2765    |                      |
| HCP5        | 10866   | HIV set point        |
| HLA-A       | 3105    | Delays AIDS          |
| HLA-B       | 3106    | Delays AIDS          |
| HLA-C       | 3107    | Delays AIDS          |
| IDH1        | 3417    | Prevents infection   |
| IFNG        | 3458    | Accelerates AIDS     |
| IL10        | 3586    | Accelerates AIDS     |
| IL4         | 3565    |                      |
| IRF1        | 3659    |                      |
| KIR         | 2669    | Delays AIDS          |
| LY6D        | 8581    |                      |
| MYH9        | 4627    | End stage renal disease |
| NCOR2       | 9612    | Increase infection   |
| PECI/ECI2   | 10455   | Accelerates AIDS     |
| PPIA/CypA   | 5478    | Accelerates AIDS     |
| PROXI       | 5629    | Delays AIDS progression |
| SDF1/CXCL12 | 6387    | Delays AIDS          |
| Slurp1      | 57192   |                      |
| Slurp2/Ly6  | 6004    |                      |
| TLR4        | 7099    |                      |
| TLR8        | 5131    |                      |
| TLR9        | 5406    |                      |
| TRIM5a      | 85363   | Increase infection   |
| TSG101      | 7251    | Accelerates AIDS     |
| ZNRD1       | 30834   |                      |
### Table 2: Human metabolism pathway for KEGG.

| Pathway name                                         | KEGG ID | Class of metabolism pathway                  | Gene number |
|------------------------------------------------------|---------|-----------------------------------------------|-------------|
| Glycolysis/gluconeogenesis                           | 10      | Carbohydrate metabolism                       | 67          |
| Citrate cycle (TCA cycle)                            | 20      | Carbohydrate metabolism                       | 31          |
| Pentose phosphate pathway                            | 30      | Carbohydrate metabolism                       | 29          |
| Pentose and glucuronate interconversions             | 40      | Carbohydrate metabolism                       | 34          |
| Fructose and mannose metabolism                      | 51      | Carbohydrate metabolism                       | 36          |
| Galactose metabolism                                 | 52      | Carbohydrate metabolism                       | 30          |
| Ascorbate and aldarate metabolism                    | 53      | Carbohydrate metabolism                       | 27          |
| Starch and sucrose metabolism                        | 500     | Carbohydrate metabolism                       | 56          |
| Amino sugar and nucleotide sugar                     | 520     | Carbohydrate metabolism                       | 49          |
| Pyruvate metabolism                                 | 620     | Carbohydrate metabolism                       | 42          |
| Glyoxylate and dicarboxylate metabolism              | 630     | Carbohydrate metabolism                       | 24          |
| Propanoate metabolism                               | 640     | Carbohydrate metabolism                       | 32          |
| Butanoate metabolism                                | 650     | Carbohydrate metabolism                       | 29          |
| Inositol phosphate metabolism                        | 562     | Carbohydrate metabolism                       | 61          |
| Oxidative phosphorylation                            | 190     | Energy metabolism                             | 133         |
| Nitrogen metabolism                                 | 910     | Energy metabolism                             | 27          |
| Sulfur metabolism                                   | 920     | Energy metabolism                             | 18          |
| Fatty acid biosynthesis                              | 61      | Lipid metabolism                              | 6           |
| Fatty acid elongation                                | 62      | Lipid metabolism                              | 23          |
| Fatty acid metabolism                                | 71      | Lipid metabolism                              | 44          |
| Ketone bodies                                        | 72      | Lipid metabolism                              | 9           |
| Steroid biosynthesis                                 | 100     | Lipid metabolism                              | 18          |
| Primary bile acid biosynthesis                       | 120     | Lipid metabolism                              | 17          |
| Steroid hormone biosynthesis                         | 140     | Lipid metabolism                              | 56          |
| Glycerolipid metabolism                              | 561     | Lipid metabolism                              | 55          |
| Glycerophospholipid metabolism                       | 564     | Lipid metabolism                              | 91          |
| Ether lipid metabolism                               | 565     | Lipid metabolism                              | 42          |
| Sphingolipid metabolism                              | 600     | Lipid metabolism                              | 47          |
| Arachidonic acid metabolism                          | 590     | Lipid metabolism                              | 68          |
| Linoleic acid metabolism                             | 591     | Lipid metabolism                              | 33          |
| Alpha-linolenic acid metabolism                      | 592     | Lipid metabolism                              | 25          |
| Biosynthesis of unsaturated fatty acids              | 1040    | Lipid metabolism                              | 21          |
| Purine metabolism                                    | 230     | Nucleotide metabolism                          | 173         |
| Pyrimidine metabolism                                | 240     | Nucleotide metabolism                          | 107         |
| Alanine, aspartate, and glutamate metabolism         | 250     | Amino acid metabolism                          | 32          |
| Glycine, serine, and threonine metabolism            | 260     | Amino acid metabolism                          | 37          |
| Cysteine and methionine metabolism                   | 270     | Amino acid metabolism                          | 34          |
| Valine, leucine, and isoleucine degradation          | 280     | Amino acid metabolism                          | 44          |
| Valine, leucine, and isoleucine biosynthesis         | 290     | Amino acid metabolism                          | 2           |
| Lysine biosynthesis                                  | 300     | Amino acid metabolism                          | 2           |
| Lysine degradation                                   | 310     | Amino acid metabolism                          | 49          |
| Arginine and proline metabolism                     | 330     | Amino acid metabolism                          | 57          |
| Histidine metabolism                                 | 340     | Amino acid metabolism                          | 28          |
| Tyrosine metabolism                                  | 350     | Amino acid metabolism                          | 39          |
| Phenylalanine metabolism                             | 360     | Amino acid metabolism                          | 18          |
| Tryptophan metabolism                                | 380     | Amino acid metabolism                          | 40          |
| Phenylalanine, tyrosine, and tryptophan biosynthesis | 400     | Amino acid metabolism                          | 5           |
Table 2: Continued.

| Pathway name                           | KEGG ID | Class of metabolism pathway            | Gene number |
|----------------------------------------|---------|----------------------------------------|-------------|
| Beta-alanine metabolism                | 410     | Metabolism of other amino acids         | 29          |
| Taurine and hypotaurine metabolism     | 430     | Metabolism of other amino acids         | 10          |
| Selenocompound metabolism              | 450     | Metabolism of other amino acids         | 17          |
| Cyanoamino acid metabolism             | 460     | Metabolism of other amino acids         | 7           |
| D-Glutamine and D-glutamate metabolism | 471     | Metabolism of other amino acids         | 4           |
| D-Arginine and D-ornithine metabolism  | 472     | Metabolism of other amino acids         | 1           |
| Glutathione metabolism                 | 480     | Metabolism of other amino acids         | 51          |
| N-Glycan biosynthesis                  | 510     | Glycan biosynthesis and metabolism      | 49          |
| Mucin type O-glycan biosynthesis      | 512     | Glycan biosynthesis and metabolism      | 31          |
| Other types of O-glycan biosynthesis  | 514     | Glycan biosynthesis and metabolism      | 30          |
| Glycosaminoglycan biosynthesis, chondroitin sulfate/dermatan sulfate | 532     | Glycan biosynthesis and metabolism      | 20          |
| Glycosaminoglycan biosynthesis, heparan sulfate/heparin | 534     | Glycan biosynthesis and metabolism      | 24          |
| Glycosaminoglycan biosynthesis, keratan sulfate | 533     | Glycan biosynthesis and metabolism      | 15          |
| Glycosaminoglycan degradation         | 531     | Glycan biosynthesis and metabolism      | 19          |
| Glycosylphosphatidylinositol-(GPI)-anchor biosynthesis | 563     | Glycan biosynthesis and metabolism      | 25          |
| Glycosphingolipid biosynthesis, lacto- and neolactoseries | 601     | Glycan biosynthesis and metabolism      | 26          |
| Glycosphingolipid biosynthesis, globoseries | 603     | Glycan biosynthesis and metabolism      | 14          |
| Glycosphingolipid biosynthesis, ganglioseries | 604     | Glycan biosynthesis and metabolism      | 15          |
| Other glycan degradation               | 511     | Glycan biosynthesis and metabolism      | 18          |
| Thiamine metabolism                   | 730     | Metabolism of cofactors and vitamins    | 4           |
| Riboflavin metabolism                 | 740     | Metabolism of cofactors and vitamins    | 13          |
| Vitamin B6 metabolism                 | 750     | Metabolism of cofactors and vitamins    | 6           |
| Nicotinate and nicotinamide metabolism| 760     | Metabolism of cofactors and vitamins    | 28          |
| Pantothenate and CoA biosynthesis     | 770     | Metabolism of cofactors and vitamins    | 17          |
| Biotin metabolism                     | 780     | Metabolism of cofactors and vitamins    | 3           |
| Lipoic acid metabolism                | 785     | Metabolism of cofactors and vitamins    | 3           |
| Folate biosynthesis                   | 790     | Metabolism of cofactors and vitamins    | 14          |
| One carbon pool by folate             | 670     | Metabolism of cofactors and vitamins    | 20          |
| Retinol metabolism                    | 830     | Metabolism of cofactors and vitamins    | 68          |
| Porphyrin and chlorophyll metabolism  | 860     | Metabolism of cofactors and vitamins    | 43          |
| Ubiquinone and other terpenoid-quinone biosynthesis | 130     | Metabolism of cofactors and vitamins    | 10          |
| Terpenoid backbone biosynthesis       | 900     | Metabolism of terpenoids and polyketides | 21          |
| Caffeine metabolism                   | 232     | Biosynthesis of other secondary metabolites | 7           |
| Butirosin and neomycin biosynthesis   | 524     | Biosynthesis of other secondary metabolites | 5           |
| Metabolism of xenobiotics by cytochrome P450 | 980     | Xenobiotics biodegradation and metabolism | 80         |
| Drug metabolism, cytochrome P450      | 982     | Xenobiotics biodegradation and metabolism | 74         |
| Drug metabolism, other enzymes        | 983     | Xenobiotics biodegradation and metabolism | 51         |

pathway genes expression) and canonical coefficient vector. The ARG and metabolic pathway gene variance-covariance matrices can be used to estimate the canonical correlation coefficients.

The magnitude of the correlation between each pair of canonical variables is described by the vector $k_i$ eigenvalues. The canonical coefficients exist in the eigenvectors and can be used to estimate the canonical variables. The variance-covariance matrices contain the variances and covariances within the groups for the ARGs and metabolic pathway genes, respectively. The covariances between variables were calculated from the variance-covariance matrices.

2.3. The Study Design and Software Tools. The canonical correlation analysis was performed using the R platform (http://www.r-project.org/). After the canonical variables were generated from the expression datasets composed of ARGs and metabolic pathway genes, we set the absolute value 0.15 as the threshold for selecting ARGs correlated with canonical variables. To select metabolic pathway genes...
correlated with canonical variables, we sorted the genes using the absolute value, and the top 50 were selected for further enrichment analyses. Functional annotations were generated and enrichment analyses were performed for the metabolic pathway genes using the web-based DAVID tool (http://david.abcc.ncifcrf.gov/). For the pathway enrichment analyses, the "KEGG_PATHWAY" was selected. The pathways with a $P$ value $< 0.01$ were considered significant.

3. Results

3.1. The ARGs and Metabolic Pathway Genes

3.1.1. The General CCA Results. Eight significant ($P < 0.01$, Wilk's Lambda, $r > 0.95$) canonical correlations were discerned between the ARG and metabolic pathway gene transcription using the CCA. 60% of the total ARG expression variance was explained by the ARGs canonical variables. Significant metabolic pathway canonical variables explained 38% of the metabolic gene transcriptome variation. Thus, ARG-metabolic pathway associations were involved in a substantial proportion of the total variance. The first pair of canonical variables had a correlation of 0.99, while the second pair of canonical variables had a correlation of 0.98.

3.2. Relationships between the Canonical Variables and Original Genes

3.2.1. Pair 1 (C1, P1). As shown in Table 3, the canonical variable C1 explains 2.4% of the variability in the original ARGs expression variables. We observed positive correlations (absolute value $> 0.15$) with all ARGs, including PPIA (0.42), ZNRD1 (0.37), MYH9 (0.36), TSG101 (0.31), IDH1 (0.28), TRIM5a (0.17), and CUL5 (0.15), but not GML ($-0.17$) and NCOR2 ($-0.31$). The greatest positive correlation was observed between C1 and PPIA. In contrast, the greatest negative correlation was observed between C1 and NCOR2. Among seven ARGs with positive correlations, the four ARGs, PPIA, TSG101, TRIM5a, and CUL5, are postentry cellular viral cofactors.

As shown in Table 4, the canonical variable P1 accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that correlated with variable P1 were enriched for purine metabolism; these genes include phosphodiesterase 4C (5143), polymerase (RNA) III (DNA directed) polypeptide K (51728), and primase (5558).

3.2.2. Pair 2 (C2, P2). As shown in Table 3, the canonical variable C2 explains 5.3% of the variability in the original ARG expression variables. This variable highly correlated with the ARGs PPIA (0.92), CUL5 (0.51), TSG101 (0.48), IDH1 (0.17), and PECI (0.15), but not GML ($-0.16$), APOBEC3G ($-0.17$), MYH9 ($-0.17$), IL4 ($-0.18$), TLR9 ($-0.18$), CXCR1 ($-0.25$), HLA-C ($-0.26$), NCOR2 ($-0.28$), DC-SIGN ($-0.29$), and TLR8 ($-0.36$). The greatest positive correlation was observed between C2 and PPIA. However, the greatest negative correlation was observed between C2 and DC-SIGN. Among the ARGs with large correlations, PPIA, TSG101, CUL5, and APOBEC3G are postentry cellular viral cofactors. Among the ARGs with negative correlations, CXCR1 and IL4 are related to cytokines. DC-SIGN is involved in chemokines, which play important role in HIV entry through chemokine receptors.

As shown in Table 4, the canonical variable P2 accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that highly correlate with the variable P2 are not enriched in a certain pathway.

3.2.3. Pair 3 (C3, P3). As shown in Table 3, the canonical variable C3 explains 12.7% of the variability on the original ARG expression variables. This variable positively correlated (absolute value $> 0.15$) with PPIA (1.88), NCOR2 (0.37), ZNRD1 (0.28), MYH9 (0.21), CXCR1 (0.20), and Slurp1 (0.19); in contrast, it negatively correlated with TRIM5a ($-0.15$), SDF1 ($-0.17$), IDH1 ($-0.22$), PECI ($-0.24$), TSG101 ($-0.25$), and CUL5 ($-0.87$). The greatest positive correlation was observed between C1 and PPIA. However, the greatest negative correlation was observed between C3 and CUL5. Among the ARGs that highly correlated with C3, PPIA, TSG101, TRIM5a, and CUL5 are postentry cellular viral cofactors. However, only PPIA positively correlated with C3.

As shown in Table 4, the canonical variable P3 accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that highly correlated with the variable P3 are enriched in glycolysis and pyrimidine metabolism. The glycolysis genes include phosphoglycerate mutase 1 (5223), glyceraldehyde-3-phosphate dehydrogenase (2597), and glucose-6-phosphatase (57818). The pyrimidine metabolism genes include polymerase (DNA directed), delta 2 (5425), cytidine monophosphatase (UMP-CMP) kinase 1 (51727), and uridine monophosphate synthetase (7372).

3.2.4. Pair 4 (C4, P4). As shown in Table 3, the canonical variable C4 explains 3.3% of the variability in the original ARG expression variables. This variable highly correlated (absolute value $> 0.15$) with PPIA (0.58), TLR8 (0.30), TLR4 (0.24), and PROX1 (0.16), but not DEFB1 ($-0.15$), IDH1 ($-0.17$), SDF1 ($-0.18$), CUL5 ($-0.23$), LY6D ($-0.24$), NCOR2 ($-0.27$), and Slurp1 ($-0.61$). The greatest positive correlation was observed between C4 and PPIA. However, the greatest negative correlation was observed between C4 and Slurp1. Among the ARGs that highly correlated with C3, only PPIA and CUL5 are postentry cellular viral cofactors.

As shown in Table 4, the canonical variable P4 accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that highly correlated with the variable P4 were enriched in purine metabolism. These genes include deoxyxanosine kinase (1716), polymerase (RNA) III (DNA directed) polypeptide K (51728), polymerase (RNA) III (DNA directed) polypeptide B (55703), pyruvate kinase (5313), adenylate cyclase 10 (55811), phosphodiesterase 6D (5147), polymerase (DNA directed), delta 2 (5425), polymerase (RNA) II (DNA directed) polypeptide C (5432), and phosphodiesterase 5A (8654).
Table 3: Cross-correlation of Hf genes with canonical variate.

| Gene symbol | C1  | C2  | C3  | C4  | C5  | C6  | C7  | C8  |
|-------------|-----|-----|-----|-----|-----|-----|-----|-----|
| TSG101      | 0.17| 0.17| −0.22| −0.17| 0.60| −0.20| 1.12| 0.63|
| IFENG       | 0.00| 0.03| 0.08| 0.07| 0.05| −0.09| −0.12| −0.07|
| IL4         | −0.12| −0.18| 0.08| 0.05| 0.01| −0.10| −0.15| 0.30|
| CXCR1       | −0.07| −0.25| 0.20| 0.00| 0.17| −0.40| −0.14| 0.08|
| IL10        | −0.02| −0.05| 0.02| 0.13| 0.05| −0.04| −0.05| −0.01|
| IFI1        | 0.07| −0.09| 0.08| 0.10| 0.23| −0.24| −0.14| −0.24|
| MYH9        | 0.36| −0.17| 0.21| −0.14| −0.49| −0.50| 0.14| 0.19|
| PPIA/CypA   | 0.42| 0.92| 1.88| 0.58| −0.54| 1.11| 0.00| 1.12|
| PROX1       | −0.14| 0.07| 0.03| 0.16| 0.23| 0.02| 0.55| −0.66|
| Slurp2/Ly6  | −0.04| −0.03| 0.00| 0.10| −0.13| 0.12| 0.09| 0.02|
| CCL2        | 0.02| −0.03| −0.04| 0.00| −0.05| 0.12| 0.08| 0.00|
| CCL4        | 0.02| −0.06| 0.02| 0.09| 0.02| 0.05| 0.04| −0.06|
| CCL5        | 0.03| −0.06| 0.01| 0.03| 0.00| 0.02| −0.14| 0.05|
| CCL11       | 0.02| −0.05| 0.01| 0.02| 0.09| −0.01| 0.25| −0.05|
| CCL17       | 0.00| −0.06| 0.05| 0.07| 0.06| −0.02| −0.19| −0.06|
| CCL18       | 0.03| −0.04| 0.00| 0.06| 0.05| 0.14| 0.09| 0.05|
| SDF1/CXCL12 | 0.09| −0.30| −0.17| −0.18| −0.26| 0.14| 0.09| 0.22|
| TLR4        | 0.06| −0.05| −0.02| 0.24| −0.15| 0.26| 0.00| 0.02|
| TSG101      | 0.31| 0.48| −0.25| −0.05| 0.17| 0.49| −0.54| −1.03|
| CUL5        | 0.15| 0.51| −0.87| −0.23| 0.19| 0.40| −0.80| −0.04|
| LY6D        | 0.01| −0.05| 0.10| −0.24| 0.10| 0.13| 0.01| −0.08|
| APOBEC3B    | 0.04| 0.03| 0.04| 0.03| 0.15| −0.12| 0.02| 0.14|
| NCOR2       | −0.31| −0.28| 0.37| −0.27| −1.10| −0.24| −0.38| 0.52|
| PECI/EC12   | 0.09| 0.15| −0.24| 0.01| −0.10| 0.06| −0.35| 0.25|
| CXCR6       | −0.06| −0.10| 0.02| −0.06| 0.03| 0.18| −0.07| 0.09|
| HCP5        | −0.04| 0.02| −0.01| −0.01| 0.32| 0.01| 0.02| −0.01|
| ZNRD1       | 0.37| 0.14| 0.28| −0.03| 0.32| −0.91| −0.04| 0.10|
| DC-SIGN     | −0.04| −0.29| 0.13| 0.00| −0.17| 0.03| 0.22| 0.33|
| TLR8        | 0.13| −0.36| −0.03| 0.30| 0.33| 0.70| −0.15| 0.17|
| TLR9        | −0.03| −0.18| 0.11| −0.06| −0.02| −0.17| −0.24| 0.36|
| Slurp1      | −0.03| −0.10| 0.19| −0.61| 0.21| 0.32| 0.04| −0.06|
| APOBEC3G    | 0.06| −0.17| −0.14| 0.11| 0.19| 0.07| −0.44| 0.39|
| TRIM5a      | 0.17| −0.13| −0.15| 0.00| 0.26| −0.30| 0.22| 0.53|

3.2.5. Pair 5 (C5, P5). As shown in Table 3, the canonical variable C5 explains 8.3% of the variability in the original ARG expression variables. This variable highly correlated (absolute value > 0.15) with IDH1 (0.60), TLR8 (0.33), ZNRD1 (0.32), TRIM5a (0.26), IRFI (0.23), PROX1 (0.23), Slurp1 (0.21), HLA-C (0.21), GML (0.21), CUL5 (0.19), CXCR1 (0.17), TSG101 (0.17), APOBEC3B (0.15), TLR4 (−0.15), DC-SIGN (−0.17), SDF1 (−0.26), HLA-B (−0.41), MYH9 (−0.49), PPIA (−0.54), and NCOR2 (−1.10). The greatest positive correlations were observed between C5 and IDH1. However, the greatest negative correlations were observed between C5 and NCOR2. Among the ARGs that highly correlated with C5, PPIA, TSG101, APOBEC3B, TRIM5a, and CUL5 are postentry cellular viral cofactors. HLA-C and HLA-B are members of the HLA system. DC-SIGN and SDF1 are related to chemokines. CXCR1 is related to the cytokine pathway.

As shown in Table 4, the canonical variable P5 accounts for the variability in the original metabolic pathway gene
expression data. The metabolic pathway genes that highly correlated with the variable \( P5 \) are enriched in inositol phosphate metabolism; these genes include synaptojanin 2 (8871), phospholipase C beta 2 (5393), and inositol-trisphosphate 3-kinase B (3707).

3.2.6. Pair 6 \((C6, P6)\). As shown in Table 3, the canonical variable \( C6 \) explains 10.8% of the variability in the original ARG expression variables. This variable highly correlated (absolute value > 0.15) with PPIA (1.11), TLR8 (0.70), TSG101 (0.49), CUL5 (0.40), Slurp1 (0.32), TLR4 (0.26), CXCR6 (0.18), TLR9 (−0.17), IDH1 (−0.20), HLA-A (−0.22), IRF1 (−0.24), NCOR2 (−0.24), TRIM5a (−0.30), HLA-C (−0.33), CXCR1 (−0.40), MYH9 (−0.50), and ZNRD1 (−0.91). The greatest positive correlation was observed between \( C6 \) and PPIA. However, the greatest negative correlation was observed between \( C6 \) and ZNRD1. Among the ARGs that highly correlated with \( C6 \), PPIA, TSG101, TRIM5a, and CUL5 are postentry cellular viral cofactors. HLA-A, HLA-C, and HLA-B are members of the HLA system. CXCR6 is related to chemokine receptors. IRF1 and CXCR1 are related to cytokines.

As shown in Table 4, the canonical variable \( P6 \) accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that highly correlated with variable \( P6 \) are enriched in pyrimidine metabolism and methylene metabolism. These genes include uridine-cytidine kinase 1-like 1 (54963), polymerase (RNA) II (DNA directed) polypeptide F (5435), polymerase (RNA) II (DNA directed) polypeptide A (5430), alcohol dehydrogenase 5 (class III) (128), and methylenetetrahydrofolate reductase (4524).

3.2.8. Pair 8 \((C8, P8)\). As shown in Table 3, the canonical variable \( C8 \) explains 12% of the variability in the original ARG expression variables. This variable highly correlated (absolute value > 0.15) with PPIA (1.12), IDH1 (0.63), TRIM5a (0.53), NCO2 (0.52), APOBEC3G (0.39), TLR9 (0.36), DC-SIGN (0.33), IL4 (0.30), PECI (0.25), SDF1 (0.22), TLR8 (0.17), MYH9 (−0.19), HLA-C (−0.21), IRF1 (−0.24), HLA-B (−0.31), PROX1 (−0.66), and TSG101 (−1.03). The greatest positive correlation was observed between \( C8 \) and PPIA. However, the greatest negative correlation was observed between \( C8 \) and TSG101. Among the ARGs that highly correlated with \( C8 \), TSG101, APOBEC3G, TRIM5a, and PPIA are postentry cellular viral cofactors. KIR and HLA-C are in the HLA system. DC-SIGN and SDF1 are related to chemokine receptors. IL4 and IRF1 are related to cytokines. HLA-C and HLA-B are in the HLA system.

As shown in Table 4, the canonical variable \( P8 \) accounts for the variability in the original metabolic pathway gene expression data. The metabolic pathway genes that highly correlated with variable \( P8 \) are not enriched in a metabolic pathway.

### Table 4: Cross-correlation of genes enriched in metabolic pathways with canonical variate.

| Component | Term                          | Count | Pop hits | \( P \) value  | Genes                  |
|-----------|-------------------------------|-------|----------|----------------|------------------------|
| \( P1+ \) | Purine metabolism             | 3     | 153      | 4.87E − 02    | 5143, 51728, 5558      |
| \( P3+ \) | Glycolysis/gluconeogenesis     | 3     | 60       | 1.14E − 02    | 5223, 2597, 57818      |
| \( P3+ \) | Pyrimidine metabolism         | 3     | 95       | 2.72E − 02    | 5425, 51727, 7372      |
| \( P4− \) | Purine metabolism             | 4     | 153      | 7.62E − 03    | 1716, 51728, 55703, 5313|
| \( P4+ \) | Purine metabolism             | 5     | 153      | 6.23E − 04    | 55811, 5147, 5425, 5432, 8654 |
| \( P5− \) | Inositol phosphate metabolism | 3     | 54       | 6.82E − 03    | 8871, 5330, 3707       |
| \( P6− \) | Pyrimidine metabolism         | 3     | 95       | 2.72E − 02    | 5435, 51727, 84172     |
| \( P6+ \) | Pyruvate metabolism           | 3     | 40       | 3.17E − 03    | 5162, 4191, 38         |
| \( P6+ \) | Terpenoid backbone biosynthesis| 2     | 15       | 3.20E − 02    | 2224, 38              |
| \( P7− \) | Pyrimidine metabolism         | 3     | 95       | 2.72E − 02    | 54963, 5435, 5430      |
| \( P7+ \) | Methane metabolism            | 2     | 6        | 1.52E − 02    | 128, 4524             |
4. Discussion

Researchers have used numerous approaches to identify host genes related to AIDS [5–13]. Most studies use genomic information but not integration of the genome and transcriptome. However, most SNPs at ARGs impact AIDS through changing host gene transcription [7–10]. This study features novel experiments that focus on ARG cooperation at the transcription level and extends the correlation between ARGs and metabolic pathway genes to discover novel host genes related to AIDS.

For each variable in the canonical correlation analysis, HIV-1 postentry cellular viral cofactors highly cooperated at the transcription level. PPIA, TSG101, TRIM5a, APOBEC3G, and CUL5 frequently appeared together to correlate with the canonical variables. PPIA functions in cyclosporin A-mediated immunosuppression by encoding a member of the peptidyl-prolyl cis-trans isomerase (PPIase) family [24]. Formation of HIV virions requires an interaction between PPIA and HIV viral proteins. TSG101 negatively regulates cell growth and differentiation by producing a protein that interacts with stathmin [25]. TRIM5a is an E3 ubiquitin-ligase, and its ubiquitination function is involved in retroviral restriction [26]. These genes encode HIV-1 postentry cellular viral cofactors involved in different biological processes. Thus, the high correlation between these genes and canonical variables demonstrates that these genes are coordinated at the transcriptional level. These data suggest that a potential transcriptional regulator for these genes may be a key host factor related to AIDS.

The high-frequency ARGs that correlated with canonical variables include PPIA, TSG101, CUL5, NCOR2, IDH1, and MYH9. PPIA, TSG101, and CUL5 are discussed above. NCOR2 with histone deacetylases is a nuclear receptor corepressor [27]. IDH1 encodes isocitrate dehydrogenases involved in cytoplasmic NADPH production and pyruvate metabolism [28]. MYH9 aids in maintaining cell shape, cell motility, and cytokinesis as a conventional nonmuscle myosin [29]. These ARGs are not enriched in a certain biological process. However, many host genetic factors have not been studied.

The low-frequency ARGs that correlated with canonical variables include DEFB1 with C4, KIR with C7, HLA-A with C5, CCL11 with C7, LY6D with C4, APOBEC3B with C5, and CXCR6 with C6. DEFB1 is a defensin and is implicated in cystic fibrosis pathogenesis [30]. HLA-A is a major histocompatibility complex class I heavy chain paralogue; these paralogues are expressed in nearly all cells [31]. CCL11 is chemokine (C-C motif) ligand 11 and is implicated in immunoregulatory and inflammatory processes [32]. CXCR6 is chemokine (C-X-C motif) receptor [33]. LY6D is a member of the lymphocyte antigen 6 complex [34]. APOBEC3B is a member of the cytidine deaminase gene family. Recent studies have revealed that these ARGs may be RNA-editing enzymes that control the cell cycle [35]. Further, these genes only correlated with one canonical variable, which suggests that the specificity of the correlation may determine the canonical variable correlated with a certain metabolic pathway.

The most significant metabolic pathway in our analysis is purine metabolism, which featured correlations with two canonical variables and the lowest $P$ values. Recent studies analyzed purine codon patterns in variable and constant regions of HIV-1 and showed that HIV-1 RNA exhibits extreme enrichment in the purine A compared with most organisms [36]. These data suggest that a potential therapeutic agent against HIV-1 may involve novel purine derivatives [37]. Studies have elucidated twenty-four purine derivatives that act as HIV-1 Tat TAR interaction inhibitors [38]. More recently, research revealed that host cells with a modified purine biosynthesis pathway exhibit increased activity by tenofovir against sensitive and drug resistant HIV-1 [39]. In this study, we show a high correlation between ARG and purine metabolism gene expression. These data imply that purine metabolism genes are significant candidates for studying the host genomic or transcriptome influence on AIDS.

5. Conclusions

In this study, we used a CCA to analyze the correlations between ARG and metabolic pathway gene expression. The results show that HIV-1 postentry cellular viral cofactors are highly coexpressed, which suggests that regulating this group of host genes may be a key factor in studies to understand the AIDS-host interaction mechanism. Furthermore, we show that purine metabolism pathway genes coordinate with ARGs; this novel discovery supports future studies on AIDS therapy using purine derivatives. Both coexpressed ARGs and metabolic pathway genes also provide a new marker for AIDS diagnosis.

Competing Interests

The authors declare no financial interest related to this work.

Authors’ Contributions

Hanhui Ye and Jinjin Yuan contributed equally to this work.

Acknowledgments

The study was supported by the Medical Innovation Project of Fujian Health Department (Grant no. 2015-CXB-28), the Scientific Foundation of Fuzhou City (Grant no. 2015-S-143-6), and the Key Clinical Specialty Discipline Construction Program of Fuzhou, Fujian, China (Grant no. 2015l0301).

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