Step 1: Import Required Libraries

In this step, we import all the necessary Python libraries for data handling, clustering, visualization, and evaluation. These include:

- `pandas` and `numpy` for data operations
- `seaborn` and `matplotlib` for visualizations
- `scikit-learn` for clustering, PCA, and evaluation
- `scipy` for hierarchical dendrograms

In [70]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
from sklearn.cluster import KMeans, AgglomerativeClustering
from sklearn.decomposition import PCA
from sklearn.metrics import silhouette_score
from scipy.cluster.hierarchy import dendrogram, linkage
```

Step 2: Load the Dataset

We load the simulated healthcare wellness dataset, which includes features like:

- Daily exercise time
- Healthy meals per day
- Sleep hours per night
- Stress level score
- BMI

This dataset will be the foundation for our clustering and PCA analysis.

In [73]:
```
df = pd.read_csv("simulated_health_wellness_data.csv")
df.head()
```

Out[73]:

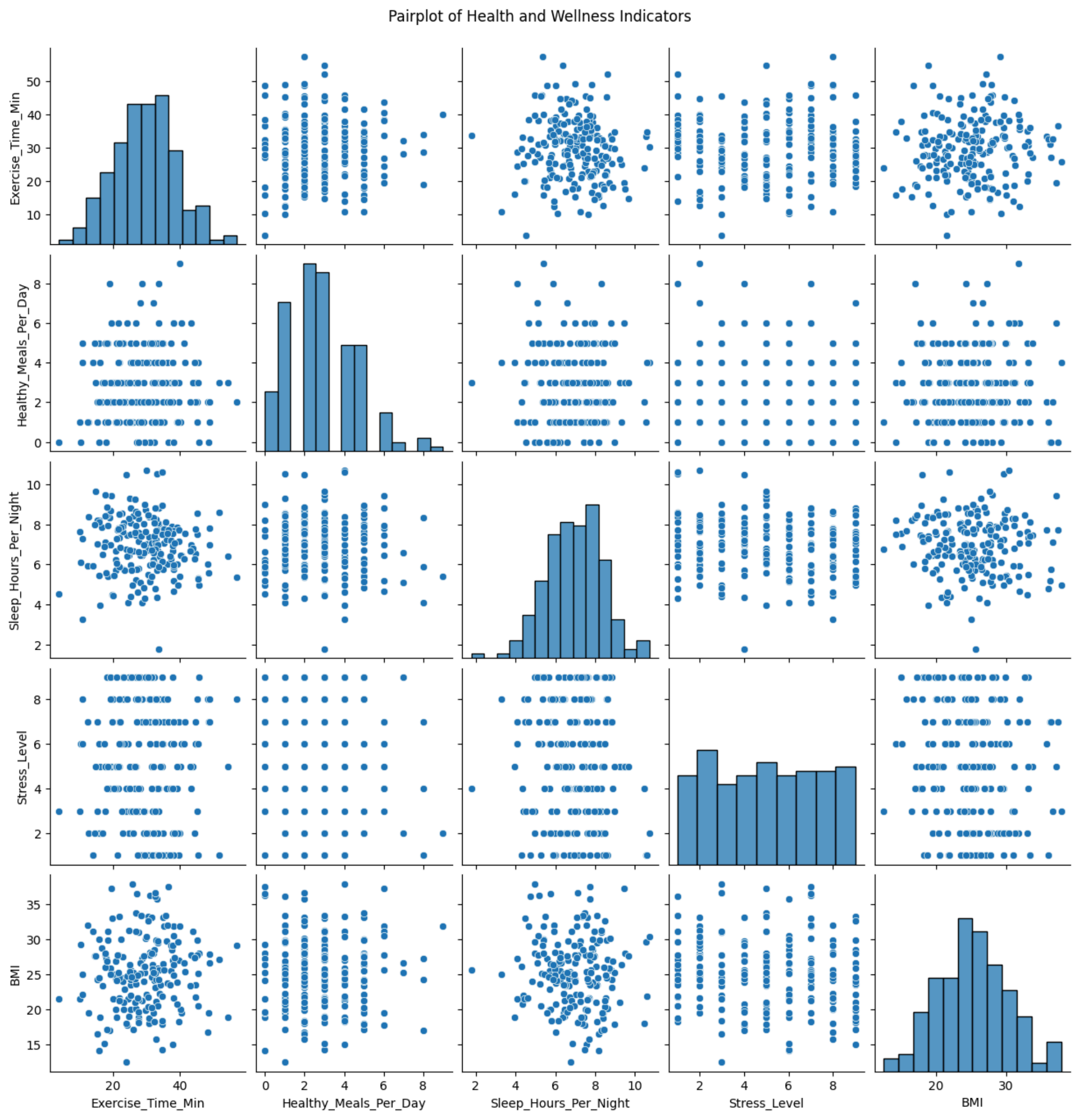
	Exercise_Time_Min	Healthy_Meals_Per_Day	Sleep_Hours_Per_Night	Stress_Level	
0	34.967142	5	7.618856	2	33.06
1	28.617357	8	4.105473	7	27.26
2	36.476885	4	6.024123	1	23.77
3	45.230299	1	8.565319	8	29.82
4	27.658466	3	8.301648	3	30.94

Step 3: Exploratory Data Analysis (EDA)

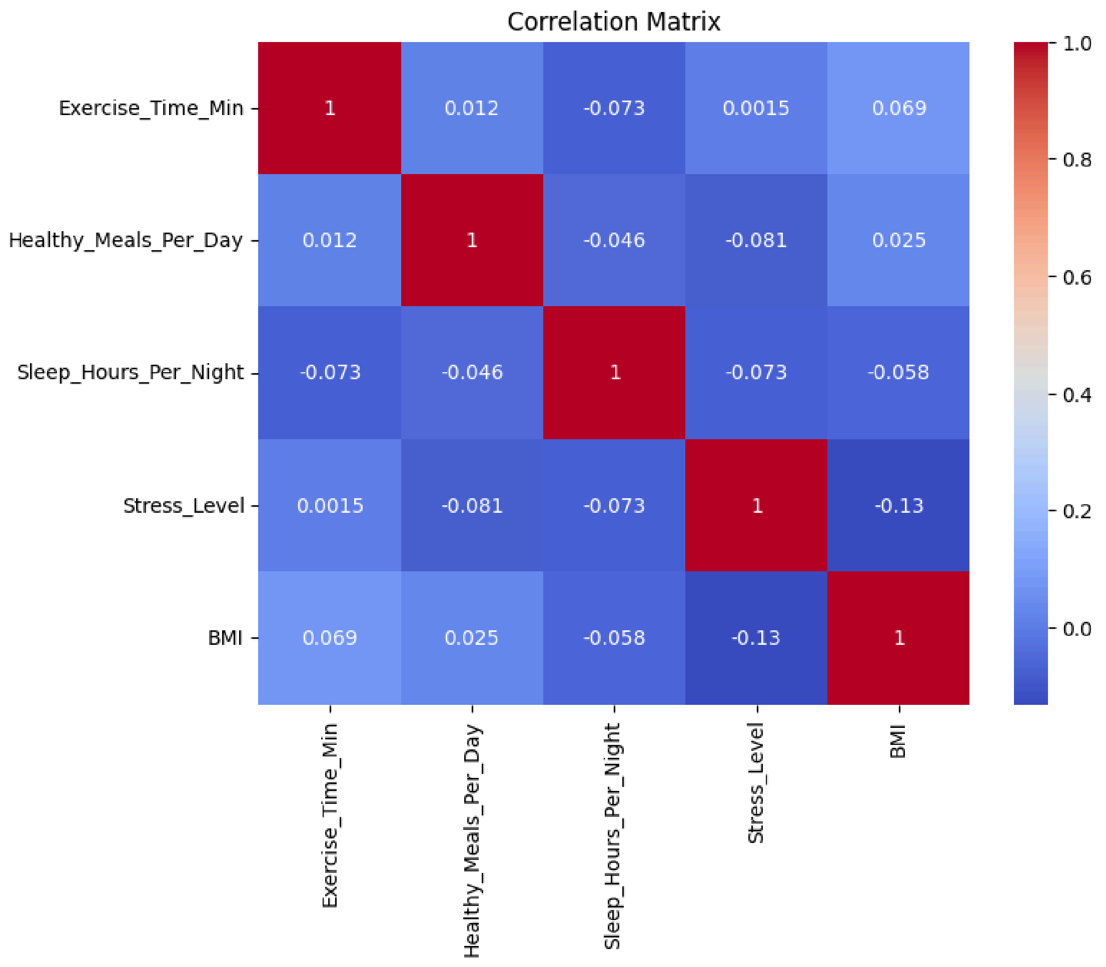
We perform EDA to understand relationships and correlations among variables:

- `Pairplot` to visualize distributions and feature pairings
- `Heatmap` to identify strong or weak correlations
- `describe()` to get summary statistics

In [76]:
```
# Visualize relationships
sns.pairplot(df, diag_kind='hist')
plt.suptitle("Pairplot of Health and Wellness Indicators", y=1.02)
plt.show()
```



In [47]:
```
# Correlation heatmap
plt.figure(figsize=(8, 6))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
plt.title("Correlation Matrix")
plt.show()
```



In [49]:
```
# Summary statistics
df.describe()
```

Out[49]:

	Exercise_Time_Min	Healthy_Meals_Per_Day	Sleep_Hours_Per_Night	Stress_Level
count	200.000000	200.000000	200.000000	200.000000
mean	29.592290	2.875000	6.933582	4.995000
std	9.310039	1.815449	1.422471	2.605556
min	3.802549	0.000000	1.778787	1.000000
25%	22.948723	2.000000	5.967243	3.000000
50%	29.958081	3.000000	6.972331	5.000000
75%	35.008525	4.000000	7.886509	7.000000
max	57.201692	9.000000	10.708419	9.000000

Step 4: Feature Scaling

We scale the dataset using `StandardScaler` so that all features contribute equally to distance-based models like K-Means and Hierarchical Clustering. This is a crucial preprocessing step.

In [81]:
```
scaler = StandardScaler()
X_scaled = scaler.fit_transform(df)
```

Step 5: Clustering Model Development

K-Means Clustering

We use the **Elbow Method** to determine the optimal number of clusters (`k`) by plotting Within-Cluster Sum of Squares (WCSS).
Then, we apply **K-Means** with the chosen `k=3` .

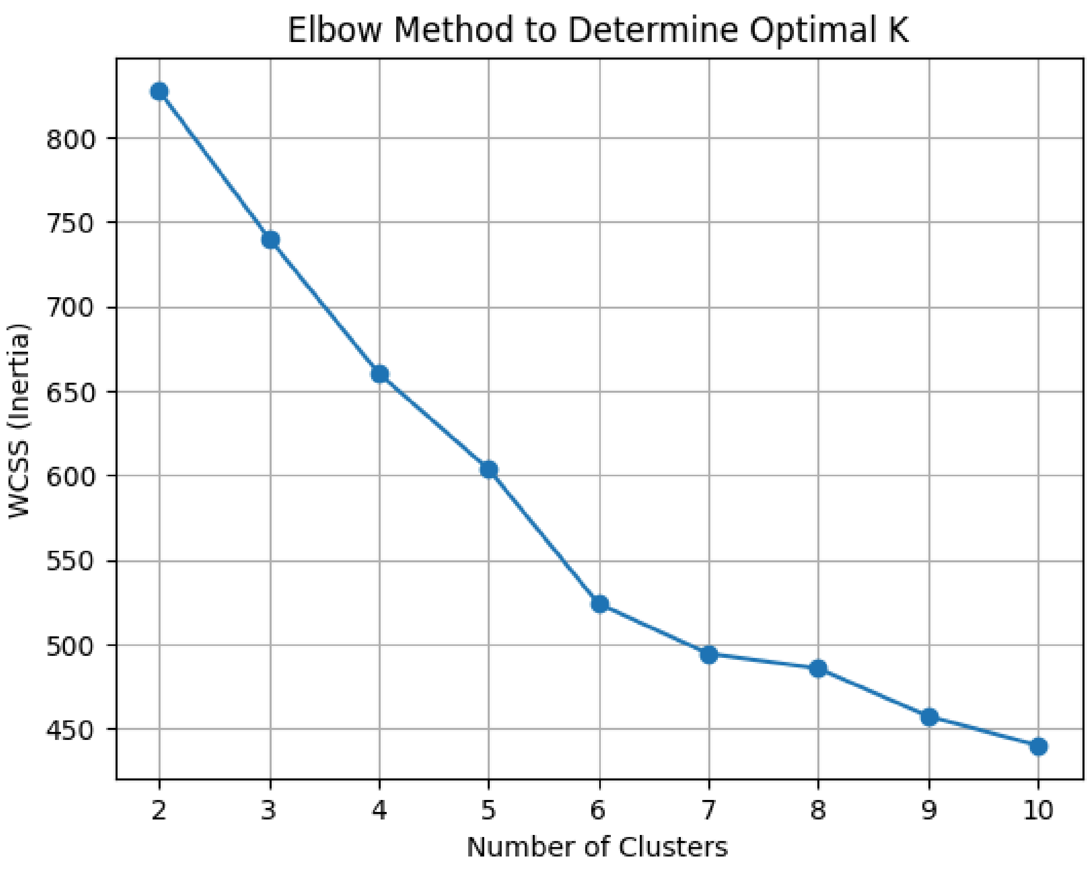
Hierarchical Clustering

We generate a **Dendrogram** to visualize hierarchical relationships and apply **Agglomerative Clustering** with 3 clusters.

Both models are evaluated using the **Silhouette Score**.

In [87]:
```python
wcss = []
for k in range(2, 11):
    kmeans = KMeans(n_clusters=k, random_state=42)
    kmeans.fit(X_scaled)
    wcss.append(kmeans.inertia_)

# Plot the Elbow
plt.plot(range(2, 11), wcss, marker='o')
plt.title("Elbow Method to Determine Optimal K")
plt.xlabel("Number of Clusters")
plt.ylabel("WCSS (Inertia)")
plt.grid(True)
plt.show()
```

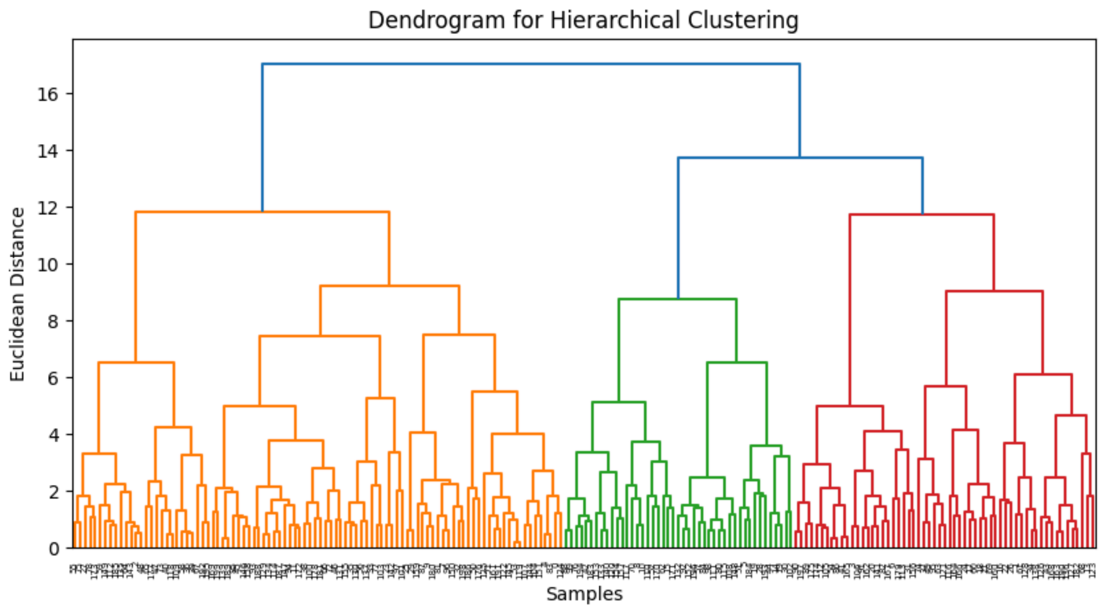


In [55]:
```python
# Apply Final KMeans Model
kmeans = KMeans(n_clusters=3, random_state=42)
kmeans_labels = kmeans.fit_predict(X_scaled)
print("Silhouette Score (KMeans on original data):", silhouette_scor
e(X_scaled, kmeans_labels))
```

```
Silhouette Score (KMeans on original data): 0.1516159911787657
```

In [57]:
```python
# Hierarchical Clustering
# Dendrogram to visualize hierarchy
linked = linkage(X_scaled, method='ward')
plt.figure(figsize=(10, 5))
dendrogram(linked)
plt.title("Dendrogram for Hierarchical Clustering")
plt.xlabel("Samples")
plt.ylabel("Euclidean Distance")
plt.show()

# Apply Agglomerative Clustering
agg_cluster = AgglomerativeClustering(n_clusters=3)
agg_labels = agg_cluster.fit_predict(X_scaled)
print("Silhouette Score (Hierarchical):", silhouette_score(X_scaled,
agg_labels))
```



```
Silhouette Score (Hierarchical): 0.13628495765267165
```

Step 6: PCA for Dimensionality Reduction

We apply **Principal Component Analysis (PCA)** to reduce the dataset from multiple dimensions down to 2. This:

- Simplifies visualization
- Helps us assess how well clusters can be separated in a lower-dimensional space

We also print the **explained variance ratio** to understand how much information is retained.

In [89]:
```python
pca = PCA(n_components=2)
X_pca = pca.fit_transform(X_scaled)

# Explained Variance
print("Explained Variance by PCA:", pca.explained_variance_ratio_)
```

```
Explained Variance by PCA: [0.23691549 0.22082517]
```

Step 7: Visualizations of Cluster Results

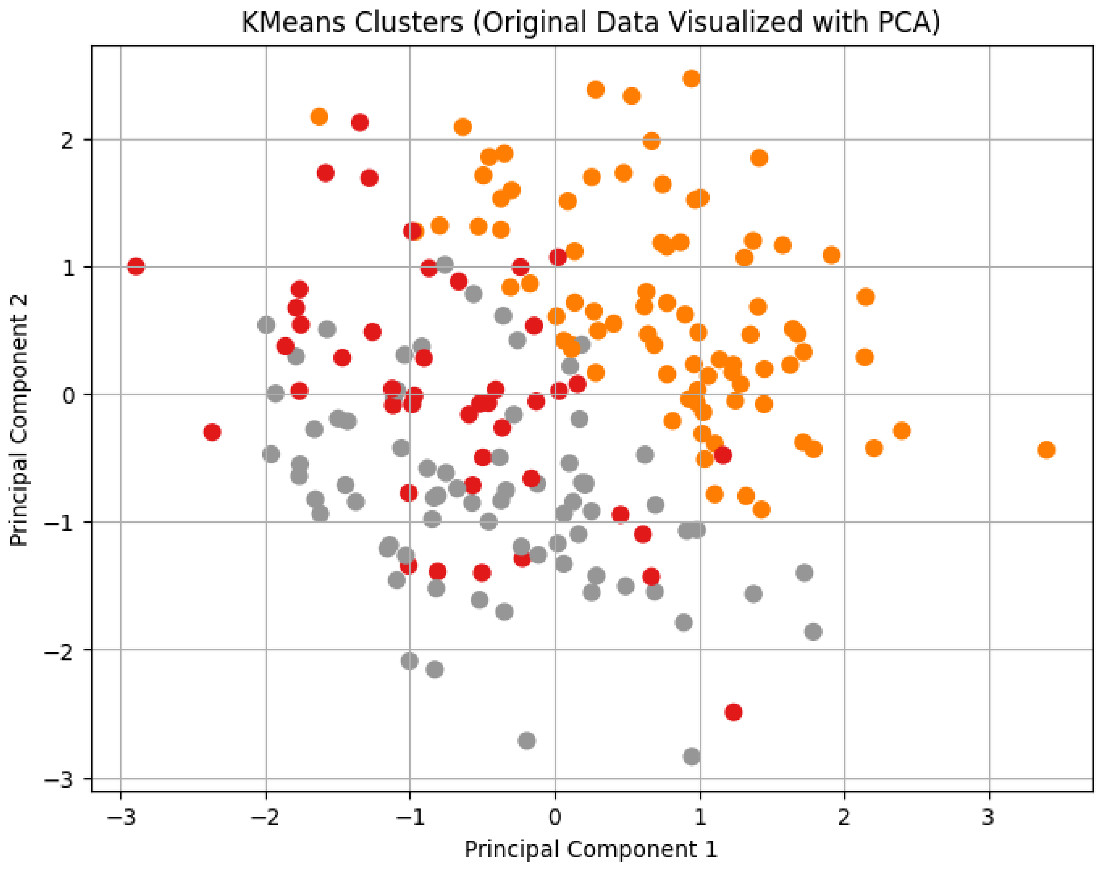
KMeans clusters (Original Data) visualized with PCA

We plot the 2D PCA components and color points by the KMeans labels from the original (scaled) dataset.

KMeans clusters on PCA-reduced data

We also run KMeans directly on the PCA-reduced dataset and visualize those results to compare clustering effectiveness visually.

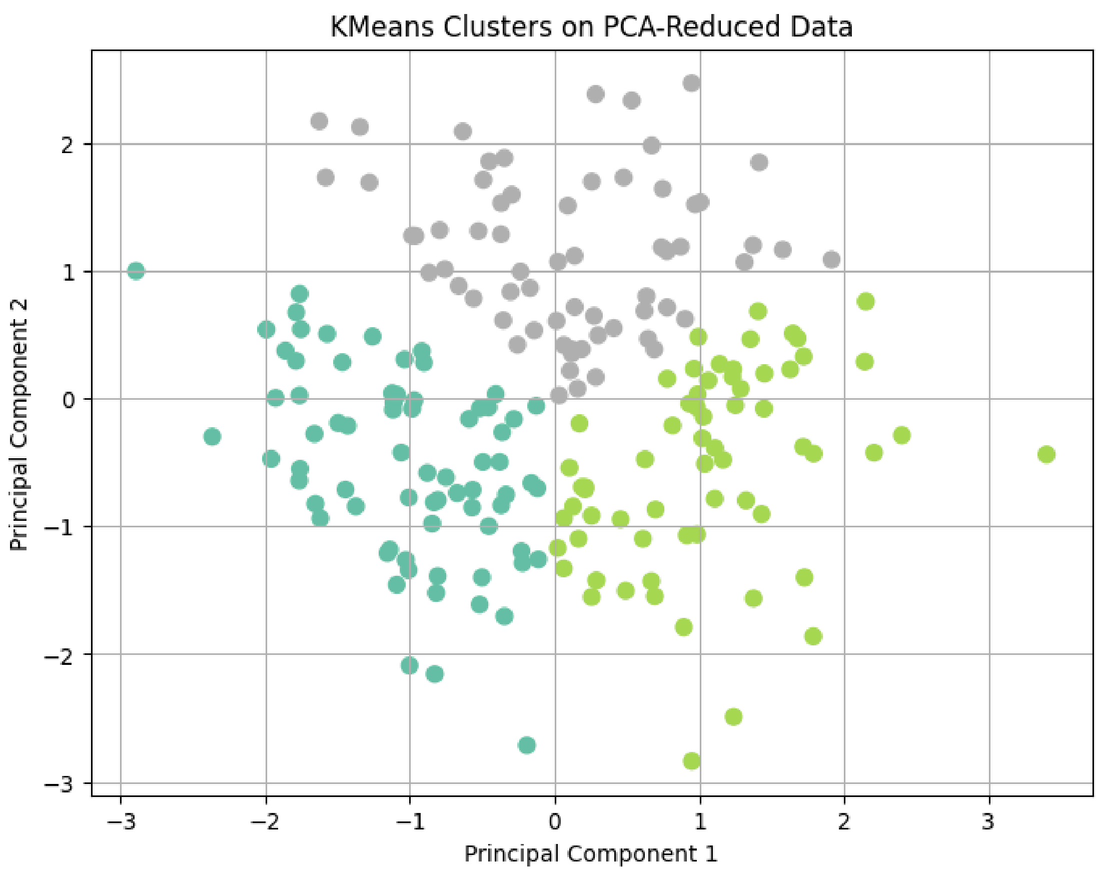
In [61]:
```python
plt.figure(figsize=(8, 6))
plt.scatter(X_pca[:, 0], X_pca[:, 1], c=kmeans_labels, cmap='Set1',
s=50)
plt.title("KMeans Clusters (Original Data Visualized with PCA)")
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.grid(True)
plt.show()
```



```
In [63]: # Apply KMeans directly on PCA data and visualize
         kmeans_pca = KMeans(n_clusters=3, random_state=42)
         pca_labels = kmeans_pca.fit_predict(X_pca)
         print("Silhouette Score (KMeans on PCA data):", silhouette_score(X_p
         ca, pca_labels))

         plt.figure(figsize=(8, 6))
         plt.scatter(X_pca[:, 0], X_pca[:, 1], c=pca_labels, cmap='Set2', s=5
         0)
         plt.title("KMeans Clusters on PCA-Reduced Data")
         plt.xlabel("Principal Component 1")
         plt.ylabel("Principal Component 2")
         plt.grid(True)
         plt.show()
```

```
Silhouette Score (KMeans on PCA data): 0.3625606718282872
```



Step 8: Final Cluster Summary Table

We assign the KMeans cluster labels back to the original dataset, then group by cluster to calculate the **average wellness indicators** per group.
This table gives actionable insights into each cluster’s health behavior profile.

In [94]:
```
df['KMeans_Cluster'] = kmeans_labels
cluster_summary = df.groupby('KMeans_Cluster').mean().round(2)
print("Final Cluster Summary Table:")
display(cluster_summary)
```

```
Final Cluster Summary Table:
```

	Exercise_Time_Min	Healthy_Meals_Per_Day	Sleep_Hours_Per_Night	Stres
KMeans_Cluster				
0	20.88	1.70	6.17	
1	30.15	3.41	7.39	
2	34.15	2.97	6.89	

Step 9: Silhouette Score Comparison Table

We summarize the **Silhouette Scores** for:

- KMeans on original data
- Hierarchical clustering
- KMeans on PCA-reduced data

This allows us to compare and determine which model performs best in terms of cluster cohesion and separation.

In [96]:
```
# Recompute Silhouette Scores (for clarity)
score_kmeans = silhouette_score(X_scaled, kmeans_labels)
score_hierarchical = silhouette_score(X_scaled, agg_labels)
score_kmeans_pca = silhouette_score(X_pca, pca_labels)

# Create a summary DataFrame
silhouette_summary = pd.DataFrame({
    'Clustering Model': ['KMeans (original)', 'Hierarchical', 'KMean
s on PCA'],
    'Silhouette Score': [score_kmeans, score_hierarchical, score_kme
ans_pca]
})

# Display table
print("📊 Silhouette Score Comparison Table:")
display(silhouette_summary.round(4))
```

```
📊 Silhouette Score Comparison Table:
```

	Clustering Model	Silhouette Score
0	KMeans (original)	0.1516
1	Hierarchical	0.1363
2	KMeans on PCA	0.3626

In [ ]:
```
```