Antiproton to proton flux ratio measured by the AMS on ISS

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 08/09/2016, 25th ECRS, Torino



AMS: A TeV precision, multipurpose spectrometer

Transition Radiation Detector Identify p

Particles and nuclei are defined by their charge (Z) and energy (E)

Time of Flight Z, E



Transition Radiation Detector TRD



Ring Imaging Cherenkov detector RICH





Event selection for the p/p analysis

R = -363 GV antiproton

- **Primary cosmic ray particle:**
 - R > 1.2 max cutoff
- TOF:
 - Down-going particle
 - β>0.3
- TRD:
 - at least 12 hits
- TRACKER:
 - Track quality
 - 0.8 < |Q| < 1.2
- ECAL:
 - Hadron shower shape



Antiproton identification

- The number of antiprotons is determined from template fit.
- To maximize the measurement accuracy, different templates are used in three rigidity region
- 1. Low rigidity region:Electron, pion background1.00-4.02 GVmass calculated from TOF and Tracker
- Intermediate region: Electron and small amount of pion background
 3.67-18.0 GV
 RICH and The TRD estimator
- 3. High rigidity region: Electron and charge confusion proton bkg
 16.6-450 GV 2D template in (Λ_{TRD} Λ_{cc}) plane

3.49 x 10⁵ antiprotons and 2.42 x 10⁹ protons are selected in the rigidity range 1<|R|<450 GV

Antiproton identification at intermediate rigidity



Antiproton identification at intermediate rigidity



Charge confusion estimator

Protons may be reconstructed with wrong charge sign, due to

- Finite tracker resolution
- Particle interaction with detector material



Antiproton identification at high rigidity



∧_{cc}

robability

Antiproton identification at high rigidity

PRL 117 091103 (2016)

175<|R|<211 GV



Acceptance correction

The antiproton-to-proton flux ratio is defined as



Number of observed antiprotons and protons

Acceptance ratio of protons to antiprotons

The antiproton acceptance is different from the proton one, due to:

- 1) Softer spectrum at low rigidity
- 2) Larger inelastic cross section



Systematic Error Sources

- Affect the antiproton counting $\sigma_{\!_N}$
 - 1. Cutoff
 - 2. Selection
 - 3. Charge confusion templates
- Affect the acceptance, $\sigma_{\!\scriptscriptstyle A}$
 - 4. Cross sections
 - 5. MC statistic fluctuation
 - 6. Migration matrix
- **<u>Rigidity scale,**</u> σ_{R}

Systematic error from charge confusion templates

- The uncertainty of proton flux above TV region:
- a) Constant spectral index
- b) Continuation of the spectra index variation



Systematic error from charge confusion templates

2. The uncertainty in the proton rigidity resolution function



Systematic error from the cross sections uncertainty



Systematic error from the rigidity scale uncertainty



Error breakdown



Antiproton-to-Proton Flux Ratio

3.49 x 10⁵ antiprotons, 2.42 x 10⁹ protons



Lower rigidity limit for constant behaviour

Study intervals starting with rigidity R_{start}, and ending at the highest rigidity 450 GV:

- Split an interval into two sections (a and b) by any boundary R_{bound}
- Fit with a constant dependence for each section, $(\overline{p}/p) = C$
- Determine the significance of the difference of the two fits C_a and C_b

The limit is defined by the lowest R_{start} that gives consistent C_a and C_b at the 90% C.L. for any boundary yields 60.3 GV



Behaviour of the p/p flux ratio >60 GV



Behavior of Antiproton-to-Proton Flux Ratio



Behavior of Antiproton-to-Proton Flux Ratio

Fit straight line in sliding windows $Ratio = k(|R|-R_0) + C$



Summary

- Antiproton-to-proton flux ratio to 450 GV measured by AMS-02 based on 3.49 x 10⁵ antiprotons and 2.42 x 10⁹ protons
- The antiproton-to-proton flux ratio reaches maximum at 20 GV
- The antiproton-to-proton flux ratio shows no rigidity dependence above 60 GV
- We will collect more data to further explore the high rigidity region
- Fluxes and flux ratios measured by AMS-02 archived in: ASI/ASDC charged cosmic ray DATABASE:

http://tools.asdc.asi.it/cosmicRays.jsp



Unfolding

The antiproton flux is given by



After the completion of the unfolding procedure, the flux is expressed as

$$\Phi_i^{\bar{p}} = \frac{\tilde{N}_i^{\bar{p}}}{\tilde{A}_i^{\bar{p}} T_i \, \Delta R_i}$$
 Folded acceptance

The antiproton-to-proton flux ratio is defined as

$$\begin{pmatrix} \bar{p} \\ \bar{p} \end{pmatrix}_{i} \equiv \frac{\Phi_{i}^{\bar{p}}}{\Phi_{i}^{p}} = \begin{pmatrix} \tilde{N}_{i}^{\bar{p}} \\ \tilde{N}_{i}^{\bar{p}} \end{pmatrix} \begin{pmatrix} \tilde{A}_{i}^{p} \\ \tilde{A}_{i}^{\bar{p}} \end{pmatrix}$$
Counting Acceptance correction

Number of observed events

Mass fit



TRD estimator independent of ECAL acceptance



MC verification with data



The spillover region Comparing MC prediction with data





