



Search for resonances in light-by-light scattering using the forward proton detectors at the LHC-ATLAS

ATLAS-CONF-2023-002

La Thuile 2023 **Gen Tateno** (ICEPP UTokyo) on behalf of the ATLAS Collaboration

Light-by-light scattering @ LHC

Electric field around LHC beam proton is regarded as photons \rightarrow Use LHC as a $\gamma\gamma$ collider

SM $\gamma\gamma \to \gamma\gamma$ observed in lead ion collisions



In *pp* collisions, SM $\gamma\gamma \rightarrow \gamma\gamma$ has too small cross section... But BSM can enhance it!

e.g. Axion-like particle (ALP) (assumed for signal modeling)



AFP detector

In the $\gamma\gamma \rightarrow \gamma\gamma$ event, final state proton can be intact (not broken)



(Re-hadronization into proton may occur)

AFP detector

In the $\gamma\gamma \rightarrow \gamma\gamma$ event, final state proton can be intact (not broken) \rightarrow Use ATLAS forward proton (AFP) detectors AFP



AFP detector

In the $\gamma\gamma \rightarrow \gamma\gamma$ event, final state proton can be intact (not broken) \rightarrow Use ATLAS forward proton (AFP) detectors



Purpose and main strategy

Diphoton resonance search using AFP (Data is 14.6 fb⁻¹ from runs in 2017) Select events where ξ_{AFP} is close to $\xi_{\gamma\gamma}$: matching AFP



Event selection

 $\star \xi_{AFP}$

High

range

acceptance

AFP

~+200 m

- 1. Require diphoton to be back-to-back Acoplanarity $A_{\phi}^{\gamma\gamma} \equiv |\Delta\phi|/\pi < 0.01$
- 2. Require ξ_{AFP} in the high acceptance range $0.035 < \xi_{AFP} < 0.08 \rightarrow \xi_{\gamma\gamma}$ range is also limited



Statistical modeling

s+b unbinned maximum likelihood fit to the $m_{\gamma\gamma}$ distribution



Signal yield modeling

Signal yield

s+b unbinned maximum likelihood fit to the $m_{\gamma\gamma}$ distribution

Signal PDF



BG PDF BG yield

Signal yield modeling

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s+b unbinned maximum likelihood fit to the $m_{\gamma\gamma}$ distribution

Signal PDF Signal yield BG PDF BG yield $\mathcal{F}(m_{\gamma\gamma}; \boldsymbol{\sigma}_X(\boldsymbol{\mu}), m_X, N_b, \boldsymbol{a}) = f_X(m_{\gamma\gamma}; \boldsymbol{x}_X(m_X)) N_X(\boldsymbol{\sigma}_X(\boldsymbol{\mu}); m_X) + f_b(m_{\gamma\gamma}, \boldsymbol{a}) N_b$



Background modeling

s+b unbinned maximum likelihood fit to the $m_{\nu\nu}$ distribution

Signal PDF Signal yield **BG PDF** BG yield $\mathcal{F}(m_{\gamma\gamma}; \boldsymbol{\sigma}_{X}(\boldsymbol{\mu}), m_{X}, N_{\mathrm{b}}, \boldsymbol{a}) = f_{X}(m_{\gamma\gamma}; \boldsymbol{x}_{X}(m_{X})) N_{X}(\boldsymbol{\sigma}_{X}(\boldsymbol{\mu}); m_{X}) + f_{\mathrm{b}}(m_{\gamma\gamma}, \boldsymbol{a}) N_{\mathrm{b}}$



То

- determine parameters *a*
- validate this form
- evaluate uncertainty on signal sterngth μ including
- actual detector response
- fake photons,

Create fully data-driven combinatorial BG sample

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Photons and protons are recorded for each event



Photons and protons are recorded for each event



Reassignment of protons to diphotons

 Reproduce the coincident matching between γγ and proton

- Suppress the single-vertex BG and signal-contamination in data
- → Pure combinatorial BG sample

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Photons and protons are recorded for each event



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Try other combination of the reassignment



Use all possible combinations of reassignment



BG PDF initial parameters are determined

Search results



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CL_s limit @ 95% CL 100% ALP $\rightarrow \gamma \gamma$ branching ratio is assumed



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CL_s limit @ 95% CL 100% ALP $\rightarrow \gamma\gamma$ branching ratio is assumed



CL_s limit @ 95% CL 100% ALP $\rightarrow \gamma \gamma$ branching ratio is assumed

"At least one" matching enhances the mass acceptance





Summary

- Search for diphoton resonance in light-by-light scattering
- ATLAS Run 2 experiment (14.6 fb⁻¹) with AFP detector First search for BSM with AFP
- Matching between $\gamma\gamma$ and proton
- "At least one" matching requirement enhances the acceptance
- No excess was observed
- Exclusion limits are set on cross section and coupling constant
- CONF note: <u>ATLAS-CONF-2023-002</u>

Thank you for listening!

Backup slides

Acoplanarity distribution



ξ_{AFP} distribution



$\xi_{\gamma\gamma}$ distribution



Statistical modeling

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• Likelihood Data $\underline{Extended}$ $L(\mu, \nu; m_X, \{m_{\gamma\gamma,i}\}) = e^{-(N_X(\mu) + N_b)} \left[\prod_{i=1}^M \mathcal{F}(m_{\gamma\gamma,i}; \sigma_X(\mu), m_X, N_b, a, \theta)\right] \frac{\underline{Systematics}}{\prod_{\vartheta \in \Theta} e^{-\vartheta^2/2}}$

• PDF

$$\mathcal{F}(m_{\gamma\gamma}; \boldsymbol{\sigma}_{X}(\boldsymbol{\mu}), m_{X}, N_{b}, \boldsymbol{a}, \boldsymbol{\theta})$$

$$= f_{X}\left(m_{\gamma\gamma}; \boldsymbol{x}_{X}(m_{X}, \boldsymbol{\theta}_{CB})\right) N_{X}\left(\boldsymbol{\sigma}_{X}(\boldsymbol{\mu}); m_{X}, \boldsymbol{\theta}_{N_{X}}\right) + f_{b}\left(m_{\gamma\gamma}, \boldsymbol{a}\right) N_{b}$$
Signal PDF Signal yield BG PDF BG yield

- Signal yield $N_{X}(\sigma_{X}(\mu); m_{X}, \theta_{N_{X}})$ $= L_{\text{int}} \sum_{i \in \{\text{EL}, \text{SD}, \text{DD}\}} (\mu \sigma_{\text{std}}^{i}(m_{X}) \varepsilon_{i}(m_{X}) K_{\varepsilon i}(m_{X}, \theta_{\varepsilon i}) K_{S^{2}i}(\theta_{S^{2}i})) \prod_{k \in S_{1}} K_{k}(\theta_{k}) + \delta_{\text{BG}}(m_{X}) \theta_{\text{BG}}$
- μ : Signal strength (unit: $f^{-1} = 0.05 \text{ TeV}^{-1}$)

Signal PDF modeling

s+b unbinned maximum likelihood fit to the $m_{\gamma\gamma}$ distribution

Signal PDF Signal yield BG PDF BG yield $\mathcal{F}(m_{\gamma\gamma}; \boldsymbol{\sigma}_X(\boldsymbol{\mu}), m_X, N_b, \boldsymbol{a}) = f_X(m_{\gamma\gamma}; \boldsymbol{x}_X(m_X)) N_X(\boldsymbol{\sigma}_X(\boldsymbol{\mu}); m_X) + f_b(m_{\gamma\gamma}, \boldsymbol{a}) N_b$

Double-sided crystal ball (DSCB) function

- ALP natural width is negligible
- 6 parameters (x_X)
- Each of them is parametrized as a function of m_X using signal MC

 \rightarrow Modelled signal shape continuously varies with m_X



Signal efficiency × acceptance



Background modeling uncertainty



Signal yield limit



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Stronger limits than CMS-TOTEM in wide range of mass though ATLAS has 7 times lower luminosity – difference is:

"at least one" matching

