Diagnostic testing approaches for evaluating mastocytosis

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Learning Objectives

- Identify the diagnostic criteria for the clinical diagnosis of mastocytosis
- Interpret biomarkers used to screen for clonal mast cell disease
- Describe how to implement tryptase genotyping
- Recognize that BST is not a good screening tool for clonal mast cell disease in Hymenoptera allergic patients

Diagnosis of Mastocytosis: tissue is (currently) the issue

Table 3.3 WHO diagnosticcriteria for systemicmastocytosis^a

Major criterion

Multifocal dense aggregates of mast cells (\geq 15/HPF) in bone marrow or extracutaneous sections

Minor criteria

>25% of the mast cells are spindle-shaped, atypical, or immature in morphology

KIT p.D816V or other KIT GOF mutation present.

Aberrant expression of CD2 and/or CD25^b and/or CD30

Total serum tryptase >20 ng/mL^b

^aOne major and one minor or three minor criteria must be met for diagnosis

^bInvalid when another clonal myeloid disorder is present

Lyons & Schwartz. Mastocytosis. 2019



Tryptase: a biomarker for anaphylaxis and myeloid dyscrasias

- Mast cell product released during IgE-mediated reactions
- Myeloid diseases
 - Clonal proliferative disease
 - Mastocytosis
 - Myeloid dysplasia/neoplasia
- Genetic disorders affecting the mast cell compartment
 - Hereditary alpha-tryptasemia
 - GATA2 haploinsufficiency
 - PLAID-associated *PLCG2* mutations



Hereditary α-tryptasemia: genetic trait caused by TPSAB1 replications



Canonical tryptase genotypes

$$\beta/\beta, \beta/\beta = 4\beta:0\alpha \qquad 30\%$$

$$\alpha/\beta, \beta/\beta = 3\beta:1\alpha \qquad 44\%$$

$$\alpha/\beta, \alpha/\beta = 2\beta:2\alpha \qquad 21\%$$



Lyons et al. Nat Genet. 2016





Chovanec et al., Lyons. Blood Adv. 2022

Lyons et al. Nat Genet. 2016

Elevated BST in the absence of HaT identifies clonal mast cell disease



KIT p.D816V positive

Diagnosis = MMAS



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Chovanec et al., Lyons. Blood Adv. 2022



Chovanec et al., Lyons. *Blood Adv.* 2022 McMurray et al. *Blood.* 2024

$H\alpha T$ impacts the specificity of using BST as a minor clinical criterion for diagnosing systemic mastocytosis

Table 3.3 WHO diagnosticcriteria for systemicmastocytosis^a

| Major criterion | | | | |
|---|--|--|--|--|
| Multifocal dense aggregates of mast cells (\geq 15/HPF) in | | | | |
| bone marrow or extracutaneous sections | | | | |
| Minor criteria | | | | |
| >25% of the mast cells are spindle-shaped, atypical, or | | | | |
| immature in morphology | | | | |
| KIT p.D816V or other KIT GOF mutation present. | | | | |
| Aberrant expression of CD2 and/or CD25 ^b and/or CD30 | | | | |
| Total serum tryptase >20 ng/mL ^b | | | | |
| | | | | |

^aOne major and one minor or three minor criteria must be met for diagnosis

^bInvalid when another clonal myeloid disorder is present



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BST CALCULATER Basal Serum Tryptase Clinical cut-off Assigned by Locus Copy number of UTR-Linked element and Associated TPSAB1 Encoded Replication

https://bst-calculater.niaid.nih.gov

Chovanec et al., Lyons. medRxiv. 2022



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BST CALCULATER Basal Serum Tryptase Clinical cut-off Assigned by Locus Copy number of UTR-Linked element and Associated TPSAB1 Encoded Replication

| Alpha copy number: | |
|--|-----------|
| 2 | \square |
| Beta copy number: | |
| 3 | ٢ |
| BST (ng/mL) (Optional): | |
| Prediction Interval | |
| 99.5% | • |
| Work-up for Mastocytosis (Optional): Negative Positive Not Perumed | |
| Note: Significantly impaired renal function can also increase BST, and may impact this accuracy of this model. | |
| Analyze my data D Reset | |



The predicted BST is 23.3642 ng/mL; The 99.5% upper prediction bound is 62.1517 ng/mL

- 99.5% Upper Prediction Bound • Predicted BST - Predicted Line





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The predicted BST is 23.3642 ng/mL; The 99.5% upper prediction bound is 62.1517 ng/mL

| Alpha copy number: | |
|--|---|
| 3 | ٢ |
| Beta copy number: | |
| 3 | ٢ |
| BST (ng/mL) (Optional): | |
| 35 | |
| Prediction Interval | |
| 99.5% | • |
| Work-up for Mastocytosis (0 | Optional): |
| Negative | |
| O Positive | |
| Not Performed | |
| Note: Significantly impaired re increase BST, and may impac model. | anal function can also t this accuracy of this |

Analyze my data 5 Reset





- 99.5% Upper Prediction Bound • Entered BST • Predicted BST - Predicted Line



Individuals with severe Hymenoptera reactions and *KIT* p.D816V frequently have <u>normal BST</u>



Lyons et al. JACI. 2020 Šelb et al. JACI. 2021

Scoring systems to risk stratify patients for BM biopsy

| Parameter | REMA (124, 199) | NICAS ⁽⁶⁵⁾ |
|--------------------|------------------------|-----------------------|
| Gender | male +1 | male +1 |
| | female -1 | female -1 |
| Clinical Symptoms | pre-/syncope +3 | syncope +3 |
| | angioedema absent +1 | angioedema absent +1 |
| | urticaria absent +1 | - |
| | pruritus absent +1 | - |
| | flushing -1 | flushing -1 |
| | angioedema -1 | - |
| | urticaria -1 | urticaria +1 |
| | pruritus -1 | - |
| BST level (ng/mL) | >25 ng/mL +2 | >11.4 ng/mL +1 |
| | <15 ng/mL -1 | <11.4 ng/mL -1 |
| <i>KIT</i> p.D816V | - | detected +3 |
| | - | undetected -1 |

Table 8. Scoring systems used to stratify individuals with suspected clonal mast cell disease

REMA - Red Española de Mastocitosis (Spanish Mastocytosis Network); NICAS - NIH Idiopathic Clonal Anaphylaxis Score; BST – basal serum tryptase. Total score ≥ 2 is associated with clonal disease in both scoring systems.

Park & Lyons. Allergic and Immunologic Diseases. 2022

Additional biomarkers

Table 6. Mast cell mediator tests to support the diagnosis of clonal MCAD or anaphylaxis

| Analyte | Preferred | Reference range | Level consistent with*: | | CLIA |
|-----------------------------------|---------------|---|----------------------------|-------------------------------|-----------------|
| | method | | anaphylaxis | clonal MCAD | Laboratories |
| Total tryptase | serum/plasma† | ≤11.4 ng/mL | ≥20% + 2ng/mL over BST | >20 ng/mL [‡] | multiple |
| Mature tryptase | serum/plasma† | <1 ng/mL | ≥1 ng/mL | NA | onel |
| N-methylhistamine [§] | 24-hour urine | 0-5yo: 120-510 mcg/g Crt 6-16yo: 70-330 mcg/g Crt >16yo: 30-200 mcg/g Crt | ≥2-fold over baseline¶ | >200 ng/mg Crtt¶ | multiple |
| 2,3-dinor-11β PGF _{2α} § | 24-hour urine | <5,205 pg/mg Crt | ≥4-fold over baseline¶ | >3,263 pg/mg Crt# | one $^{\Delta}$ |
| LTE ₄ | 24-hour urine | <104 pg/mg Crt | ≥10-fold over baseline¶ | >104 pg/mg Crt ^{¶,#} | one $^{\Delta}$ |

Park & Lyons. Allergic and Immunologic Diseases. 2022

Conclusions

- HαT is a common genetic trait caused by increased α-tryptase encoding *TPSAB1* copy number
- Elevated BST when encountered clinically is most often due to $H\alpha T$
- Increased BST in H αT results from increased production of 'normal' alpha-tryptase
- TPSAB1 replication number (when encoding α -tryptase) defines clinical reference ranges for BST
- BST with genotyping and *KIT* p.D816V are the two most useful biomarkers to screen for clonal mast cell disease
- BST >8ng/mL is uncommon
- BST >11.4ng/mL when H α T is not present likely represents a clonal myeloid disorder
- BST levels are frequently normal in patients with clonal mast cell disease and severe HVA; KIT p.D816V should be routinely sent